



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 121855**

**TO: Jeffrey Parkin**  
**Location: REM-3D39&3C18**  
**Art Unit: 1648**  
**May 17, 2004**  
**Case Serial Number: 10/072301**

**From: P. Sheppard**  
**Location: Remsen Building**  
**Phone: (571) 272-2529**

**sheppard@uspto.gov**

### **Search Notes**

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STIC-Biotech/ChemLib

121855

From: Parkin, Jeffrey  
Sent: Wednesday, May 12, 2004 11:32 AM  
To: STIC-Biotech/ChemLib  
Subject: U.S. Serial No. 10/072,301

Would you please search the following SEQ ID NOS.: vis-à-vis the aforementioned application (U.S. 10/072,301) v. all relevant databases: 8, 17, 25, 19, 27, 21, 29, 23, and 31.

Provide a hard copy of the results.

Thanks!

JSP  
AU 1648  
REM 3D39  
2-0908

CRFE

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:48:56 ; Search time 7.40971 Seconds  
(without alignments)  
1372.754 Million cell updates/sec

Title: US-10-072-301-8  
Perfect score: 190  
Sequence: 1 MDYQVSSPIYDINYTSEPCQKINVKQIARLLPPL 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: geneseqp19808:\*  
2: geneseqp19908:\*  
3: geneseqp20008:\*  
4: geneseqp20018:\*  
5: geneseqp20028:\*  
6: geneseqp20038:\*  
7: geneseqp20038:\*  
8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	190	100.0	100	2	AAW88231	Aaw88231 HIV-1 co-
2	190	100.0	184	2	AAW27406	Aaw27406 Inactive
3	190	100.0	215	2	AAW27408	Aaw27408 Inactive
4	190	100.0	215	2	AAW88238	Aaw88238 HIV-1 co-
5	190	100.0	268	7	ADC10142	Adc10142 Human NOV
6	190	100.0	352	2	AAW27407	Aaw27407 Human CCR
7	190	100.0	352	2	AAW27123	Aaw27123 Human CCR
8	190	100.0	352	2	AAW23835	Aaw23835 Human CC
9	190	100.0	352	2	AAW88232	Aaw88232 HIV-1 co-
10	190	100.0	352	4	AAE07048	Aae07048 Human G-p
11	190	100.0	352	4	AAE07048	Aae07048 Human CCR
12	190	100.0	352	4	AAE04321	Aae04321 Human che
13	190	100.0	352	4	AAE07039	Aae07039 Human G-p
14	190	100.0	352	4	AAAB46858	Aab46858 Human HDG
15	190	100.0	352	4	ABBS6342	Abbs6342 Non-endog
16	190	100.0	352	4	AAAB83354	Aab83354 Human CCR
17	190	100.0	352	4	AAAB82948	Aab82948 Human HIV
18	190	100.0	352	5	AAU97152	Aau97152 Human G-p
19	190	100.0	352	5	AAU52829	Aau52829 Human CCR
20	190	100.0	352	5	AAU52828	Aau52828 Human CC
21	190	100.0	352	5	ABG70597	Abg70597 Human G-p
22	190	100.0	352	5	ABG92883	Abg92883 Human imm
23	190	100.0	352	5	AAE25811	Aae25811 Human G-p
24	190	100.0	352	5	ABB81054	Abb81054 G-protein
25	190	100.0	352	5	ABB08343	Abb08343 Human che

26	190	100.0	352	6	ABG75540	Abg75540 Human G-p
27	190	100.0	352	6	ABR58602	AbR58602 Human can
28	190	100.0	352	6	AAO29514	Aao29514 Human C-C
29	190	100.0	352	6	ABU61654	Abu61654 Human G-p
30	190	100.0	352	6	ABP97728	Abp97728 Amino aci
31	190	100.0	352	6	ABP81933	Abp81933 Human C-C
32	190	100.0	352	7	ADC03341	Adc03341 Human che
33	190	100.0	371	2	AAW23834	Aaw23834 Human CC
34	190	100.0	439	2	AAAY41280	Aay41280 Fusion pr
35	184	96.8	352	2	AAW07602	Aaw07602 Human G-p
36	184	96.8	352	3	AAAY80128	Aay80128 Human G-p
37	184	96.8	352	4	AAE07046	Aae07046 Human G-p
38	184	96.8	352	4	AAE07037	Aae07037 Human G-p
39	184	96.8	352	5	AAU97150	Aau97150 Human G-p
40	184	96.8	352	5	ABG92880	Abg92880 Human G-p
41	184	96.8	352	5	AAE25808	Aae25808 Human G-p
42	183	96.3	268	7	ADC10144	Adc10144 Human NOV
43	180	94.7	352	2	AAW27125	Aaw27125 Macaque c
44	180	94.7	352	7	ADC03359	Adc03359 Macaque c
45	170	89.5	352	4	AAG79089	Aag79089 Amino aci

ALIGNMENTS

RESULT 1						
ID	AAW88231	standard; protein; 100 AA.				
XX	AC	AAW88231;				
XX	DT	15-MAR-1999 (first entry)				
XX	DE	HIV-1 co-receptor CCR5 variant CCR5m303.				
XX	KW	HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;				
XX	KV	gene therapy; human.				
XX	OS	Homo sapiens.				
XX	FH	Key				
XX	FT	Domain				
XX	FT	Domain				
XX	FT	Domain				
XX	PN	WO9854317-A1.				
XX	PD	03-DEC-1998.				
XX	PF	29-MAY-1998; 98WO-EP003437.				
XX	PR	30-MAY-1997; 97US-0048057P.				
XX	PA	(MOND-) FOND MONDIALE RECH & PREVENTION SIDA.				
XX	PI	Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;				
XX	DR	WPI; 1999-059835/05.				
XX	DR	N-PSDB; AAW88231.				
XX	PT	New CCR5 variant protein of the HIV-1 co-receptor - useful in developing				
XX	PT	resistance of CCR5-expressing cells to HIV-1 infection.				
XX	PS	Claim 2; Page 37; 55pp; English.				
XX	CC	This is the amino acid sequence of a CCR5 variant protein, designated				
XX	CC	CCR5m303, that comprises the first two transmembrane domains of wild-type				
XX	CC	CCR5 (see AAW88232), but lacks transmembrane domains 3-7. CCR5 serves as				
XX	CC	a co-receptor for infection by macrophage-tropic (M-tropic) strains of				
XX	CC	HIV-1. The presence of the CCR5m303 variant allele (see AAW84125) with				
XX	CC	the wild type CCR5 allele in an individual shows a positive correlation				
XX	CC	with resistance to infection with M-tropic HIV-1 strains, and may				

CC indicate slower progression of the disease. The detection of CCR5  
CC variants may be used to identify individuals at lower risk of infection  
CC relative to the general population who, if infected, may exhibit slower  
CC progression to AIDS. Probes and primers (see AAV84127-36) are provided  
CC for use in diagnostic methods for detecting the presence of such  
CC variants. A method is provided for inhibiting HIV-1 infection of a cell  
CC expressing the CCR5 receptor. This involves introducing a nucleic acid  
CC encoding a CCR5 variant into the cell, thereby reducing the number of  
CC functional CCR5 molecules present on the cell surface  
XX  
SQ Sequence 100 AA;

Query Match 100.0%; Score 190; DB 2; Length 100;  
Best Local Similarity 100.0%; Pred. No. 1.8e-20;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

RESULT 2  
AAW27406  
ID AAW27406 standard; protein; 184 AA.  
XX  
AC AAW27406;  
XX  
DT 14-APR-1998 (first entry)  
XX  
DE Inactive human CCR5.  
XX  
KM Inactive; human Cys-Cys chemokine receptor-5; CCR5;  
KM human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;  
KM predisposition; resistance; diagnosis; treatment; prevention;  
KM inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;  
KM idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;  
XX atherosclerosis; autoimmune disorder.  
OS Homo sapiens.  
XX  
PN WO9732019-A2.  
XX  
PD 04-SEP-1997.  
XX  
PF 28-FEB-1997; 97WO-BE000023.  
XX  
PR 01-MAR-1996; 96EP-00870021.  
PR 06-AUG-1996; 96EP-00870102.  
XX  
PA (EURO-) EUROSCREEN SA.  
XX  
PI Samson M, Parmentier M, Vassart G, Libert F;  
XX WPI; 1997-479829/44.  
DR N-PSDB; AAT90116.  
XX  
XX Active and inactive forms of human CC chemokine receptor CCR-5 - useful  
PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune  
PT disease and viral infection.  
XX  
PS Claim 1; Fig 1a; 94pp; English.  
XX  
CC The present sequence is an inactive human CC (Cys-Cys) chemokine receptor  
CC 5 (CCR5), which is not a receptor of human immunodeficiency virus type 1  
CC or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to diagnose, treat  
CC and/or prevent inflammatory diseases, e.g. rheumatoid arthritis, treat  
CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,  
CC viral infections, especially HIV-1 or HIV-2 infection, cancer,  
CC atherosclerosis and autoimmune disorders. Subjects that express the  
CC inactive receptor have a predisposition, or resistance to HIV-1 and/or  
XX HIV-2  
SQ Sequence 184 AA;

Query Match 100.0%; Score 190; DB 2; Length 184;  
Best Local Similarity 100.0%; Pred. No. 3.6e-20;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

RESULT 3  
AAW27408  
ID AAW27408 standard; protein; 215 AA.  
XX  
AC AAW27408;  
XX  
DT 14-APR-1998 (first entry)  
XX  
DE Inactive human CCR5.  
XX  
KM Inactive; human Cys-Cys chemokine receptor 5; CCR5;  
KM human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;  
KM predisposition; resistance; diagnosis; treatment; prevention;  
KM inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;  
KM idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;  
XX atherosclerosis; autoimmune disorder.  
OS Homo sapiens.  
XX  
PN WO9732019-A2.  
XX  
PD 04-SEP-1997.  
XX  
PF 28-FEB-1997; 97WO-BE000023.  
XX  
PR 01-MAR-1996; 96EP-00870021.  
PR 06-AUG-1996; 96EP-00870102.  
XX  
PA (EURO-) EUROSCREEN SA.  
XX  
PI Samson M, Parmentier M, Vassart G, Libert F;  
XX WPI; 1997-479829/44.  
DR N-PSDB; AAT90118.  
XX  
XX Active and inactive forms of human CC chemokine receptor CCR-5 - useful  
PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune  
PT disease and viral infection.  
XX  
PS Claim 7; Fig 1d-e; 94pp; English.  
XX  
CC The present sequence is an inactive human CC (Cys-Cys) chemokine receptor  
CC 5 (CCR5), which lacks the last 3 transmembrane regions and the regions  
CC involved in G protein-coupling. CCR5 or its cDNA can be used to diagnose,  
CC treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,  
CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,  
CC viral infections, especially human immunodeficiency virus type 1 or type  
CC 2 (HIV-1 or HIV-2) infection, cancer, atherosclerosis and autoimmune  
CC disorders. Subjects that express the inactive receptor have a  
XX predisposition, or resistance to HIV-1 and/or HIV-2  
SQ Sequence 215 AA;

Query Match 100.0%; Score 190; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 4.4e-20;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

RESULT 4





DR N-PSDB; ADC10141.

PT New isolated NOVX polypeptides and nucleic acid molecules useful for  
PT treating, preventing and diagnosing pathological conditions with NOVX-  
PT associated disorders, such as cancer, obesity, diabetes and inflammatory  
PT or CNS diseases.

PS Claim 1; SEQ ID NO 162; 772pp; English.

CC The invention relates to novel isolated polypeptides, mature form of the  
CC polypeptide, a sequence that is 95% identical to the polypeptide or the  
CC polypeptide comprising one or more conservative substitutions. The NOVX  
CC polypeptide is useful for treating or preventing a pathology associated  
CC with the polypeptide e.g. disorders associated with aberrant expression  
CC or activity of the polypeptide, such as cancer, diabetes, obesity, and  
CC endocrine, CNS and inflammatory disorders. They can also be used in  
CC various detection and screening assays, chromosome mapping, tissue typing  
CC and predictive medicine. This sequence corresponds to one of the  
CC polypeptides of the invention.

SQ Sequence 268 AA;

Query Match 100.0%; Score 190; DB 7; Length 268;  
Best Local Similarity 100.0%; Pred. No. 5.7e-20;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYGVSSPIYDINITYTSEPCQKINVKQIARLLPPL 36  
DB 1 MDYGVSSPIYDINITYTSEPCQKINVKQIARLLPPL 36

RESULT 6

AAW27407  
ID AAW27407 standard; protein; 352 AA.

AC AAW27407;  
DT 14-APR-1998 (first entry)

DE Human CCR5.

KW Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;  
KW type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;  
KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;  
KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;  
KW atherosclerosis; autoimmune disorder.

OS Homo sapiens.

PN WO9732019-A2.

PD 04-SEP-1997.

PF 28-FEB-1997; 97WO-BE000023.

PR 01-MAR-1996; 96EP-00870021.  
PR 06-AUG-1996; 96EP-00870102.

PA (EURO-) EUROSCREEN SA.

PI Samson M, Parmentier M, Vaasart G, Libert F;

DR WPI; 1997-479829/44.  
DR N-PSDB; AAT90117.

PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful  
PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune  
PT disease and viral infection.

PS Claim 4; Fig 1b-c; 94pp; English.

CC The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5),  
CC which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but

CC not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3,  
CC interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha)  
CC chemokines. Active CCR-5 is also a receptor of human immunodeficiency  
CC virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can used to  
CC diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid  
CC arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and  
CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer,  
CC atherosclerosis and autoimmune disorders

SQ Sequence 352 AA;

Query Match 100.0%; Score 190; DB 2; Length 352;  
Best Local Similarity 100.0%; Pred. No. 7.9e-20;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYGVSSPIYDINITYTSEPCQKINVKQIARLLPPL 36  
DB 1 MDYGVSSPIYDINITYTSEPCQKINVKQIARLLPPL 36

RESULT 7

AAW27123  
ID AAW27123 standard; protein; 352 AA.

AC AAW27123;

DT 14-DEC-1997 (first entry)

DE Human chemokine receptor 88C.

KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;  
KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;  
KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;  
KW modulator; antibody; human.

OS Homo sapiens.

FH Key

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

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FT Domain

PT	tumours, viral infections, auto-immune diseases, etc.
XX	
PS	Claim 16; Page 47-48; 65pp; English.
XX	
CC	This polypeptide sequence comprises novel human chemokine receptor 88C, a
CC	G protein coupled receptor that is involved in leukocyte trafficking. Its
CC	amino sequence was deduced from a cDNA clone (AA785161) isolated from a
CC	macrophage library. It shows 62% identity to CCR1. Chemokine receptor
CC	88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors
CC	and their polypeptide fragments can be produced in transformed host
CC	cells. The receptors, peptides comprising one or more of the
CC	extracellular or intracellular domains, and anti-receptor antibodies can
CC	be used to modulate receptor activities, particularly ligand and G
CC	protein binding, and are potentially useful in the treatment
CC	of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
CC	infection, AIDS, inflammatory conditions, pathological immune response,
CC	abnormal haematopoietic processes etc
XX	
SO	Sequence 352 AA;
	Query Match 100.0%; Score 190; DB 2; Length 352;
	Best Local Similarity 100.0%; Pred. No. 7.9e-20;
	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MDYQVSSPIYDINYYTSEPCOKINVKQIARLLPPL 36
	1 MDYQVSSPIYDINYYTSEPCOKINVKQIARLLPPL 36
Db	
RESULT 8	
AAW23835	
ID	AAW23835 standard; protein; 352 AA.
XX	
AC	AAW23835;
XX	
DT	08-JUN-1998 (first entry)
XX	
DE	Human CC chemokine receptor 5 (CCR5).
XX	
KW	CC chemokine receptor 5; CCR5; G-protein coupled receptor;
KM	human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Domain
FT	Location/Qualifiers
FT	29..55
FT	/label= I
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FT	104..126
FT	/label= III
FT	/note= "transmembrane domain"
FT	109..120
FT	/note= "extracellular loop-1 (Claim 19)"
FT	143..171
FT	/label= IV
FT	/note= "transmembrane domain"
FT	187..210
FT	/note= "extracellular loop-2 (Claim 19)"
FT	194..219
FT	/label= V
FT	/note= "transmembrane domain"
FT	238..258
FT	/label= VI
FT	/note= "transmembrane domain"
FT	261..276
FT	/note= "extracellular loop-3 (Claim 19)"
FT	277..300
FT	/label= VII
FT	/note= "transmembrane domain"
XX	
PN	WO9745543-A2.
XX	
PD	04-DEC-1997.

Query Match	100.0%;	Score 190;	DB 2;	Length 352;
Best Local Similarity	100.0%;	Pred. No. 7.9e-20;		
Matches 36;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 MDYQVSSPIYDINYYTSEPCQKINVKQIARLPPL 36			
Db	1 MDYQVSSPIYDINYYTSEPCQKINVKQIARLPPL 36			
RESULT 9				
AAW88232				
ID	AAW88232 standard; protein; 352 AA.			
XX				
AC	AAW88232;			
XX				
DT	15-MAR-1999 (first entry)			
XX				
DE	HIV-1 co-receptor CCR5.			
XX				
KW	HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;			
XX	gene therapy; human.			
OS				
XX	Homo sapiens.			
FH	Key	Location/Qualifiers		
FT	Domain	32. .56		
FT		/note= "transmembrane domain 1"		
FT	Domain	67. .87		
FT		/note= "transmembrané domain 2"		
FT	Misc-difference	101		
FT		/note= "corresponds to TGR (Cys) in wild-type CCR5, TGA		
FT		(Stop) in CCR5m303"		
FT	Domain	103. .124		
FT		/note= "transmembrane domain 3"		
FT	Domain	142. .167		
FT		/note= "transmembrane domain 4"		
FT	Domain	200. .223		
FT		/note= "transmembrane domain 5"		

FT Domain 236. .260  
FT /note= "transmembrane domain 6"  
FT Domain 275. .301  
FT /note= "transmembrane domain 7"  
XX  
PN WO9854317-A1.  
XX  
PD 03-DEC-1998.  
XX  
PF 29-MAY-1998; 98MO-EP003437.  
XX  
PR 30-MAY-1997; 97US-0048057P.  
XX  
PA (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.  
XX  
PI Beretta A, Quillent C, Arenzana Siededos F, Braun J;  
XX  
DR WPI; 1999-059835/05.  
DR N-PSDB; AAV84126.  
XX  
PT New CCR5 variant protein of the HIV-1 co-receptor - useful in developing  
PT resistance of CCR5-expressing cells to HIV-1 infection.  
XX  
PS Disclosure; Page 34-35; 55pp; English.  
XX  
CC This is the amino acid sequence of wild-type human CCR5, which serves as  
CC a co-receptor for infection by macrophage-tropic (M-tropic) strains of  
CC HIV-1. The invention relates to the identification of a CCR5 variant (see  
CC AAW88231), designated CCR5m303, comprising the first two transmembrane  
CC domains of wild-type CCR5, but lacking transmembrane domains 3-7. The  
CC presence of the CCR5m303 variant with the wild type CCR5 allele shows a  
CC positive correlation with resistance to infection with M-tropic HIV-1  
CC strains, and may indicate slower progression of the disease. The  
CC detection of CCR5 variants may be used to identify individuals at lower  
CC risk of infection relative to the general population who, if infected,  
CC may exhibit slower progression to AIDS. Probes and primers (see AAV84127-  
CC 36) are provided for use in diagnostic methods for detecting the presence  
CC of such variants. A method is provided for inhibiting HIV-1 infection of  
CC a cell expressing the CCR5 receptor. This involves introducing a nucleic  
CC acid encoding a CCR5 variant into the cell, thereby reducing the number  
CC of functional CCR5 molecules present on the cell surface  
XX  
SQ Sequence 352 AA;  
  
Query Match 100.0%; Score 190; DB 2; Length 352;  
Best Local Similarity 100.0%; Pred. No. 7.9e-20;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
  
RESULT 10  
AAE07048  
ID AAE07048 standard; protein; 352 AA.  
XX  
AC AAE07048;  
XX  
DT 16-OCT-2001 (first entry)  
XX  
DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.  
XX  
KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;  
KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;  
KW cytosatic; immunosuppressive; nootropic; neuroprotective; gene therapy;  
KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;  
KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;  
KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;  
KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;  
KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;  
KW cardiovascular disorder; myocardial ischaemia.  
XX

OS Homo sapiens.  
XX  
PN WO200158916-A2.  
XX  
PD 16-AUG-2001.  
XX  
PF 09-FEB-2001; 2001WO-US004153.  
XX  
PR 09-FEB-2000; 2000US-0181258P.  
PR 09-MAR-2000; 2000US-0187999P.  
PR 22-SEP-2000; 2000US-0234336P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Roschke V, Li Y, Ruben SM;  
XX  
DR WPI; 2001-488966/53.  
DR N-PSDB; AAD13299.  
XX  
PT Isolated nucleic acid encoding a human G-protein chemokine receptor  
PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune  
PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and  
PT neurodegenerative disorders.  
XX  
PS Example 40; Page 504-505; 518pp; English.  
XX  
CC The invention relates to human G-protein chemokine receptor (CCR5)  
CC HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are  
CC useful for treating, preventing or ameliorating a disease or disorder  
CC associated with inflammation, defective or aberrant chemotaxis of immune  
CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's  
CC sarcoma) or defective or aberrant T-cell antigen presenting cell  
CC interaction. The disease or disorder may also be an infectious disease  
CC (e.g. a viral infection such as an early stage HIV infection, a  
CC cytomegalovirus infection, or a poxvirus infection), an autoimmune  
CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The  
CC disease or disorder may be associated with aberrant CCR5 expression, lack  
CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand  
CC function. CCR5 HDGNR10 protein is used as a food additive or preservative  
CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful  
CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,  
CC protein, antibodies, agonists and antagonists are also useful in the  
CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal  
CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,  
CC urogenital); immune disorders (Addison's disease, allergies, autoimmune  
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)  
CC ; cardiovascular disorders (myocardial ischaemia) and wound healing. The  
CC present sequence is human CCR5 HDGNR10 protein  
XX  
SQ Sequence 352 AA;  
  
Query Match 100.0%; Score 190; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 7.9e-20;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
  
RESULT 11  
AAG80111  
ID AAG80111 standard; protein; 352 AA.  
XX  
AC AAG80111;  
XX  
DT 17-JAN-2002 (first entry)  
XX  
DE Human CCR5 protein.  
XX  
KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;  
KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;  
KW



KM chronic bowel inflammation; rheumatoid arthritis; cytostatic;  
KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;  
KV antirheumatic; antiarthritic.  
OS Homo sapiens.  
XX  
XX WO200172830-A2.  
XX  
XX 04-OCT-2001.  
XX  
XX 02-APR-2001; 2001WO-EP003708.  
XX  
XX 31-MAR-2000; 2000DE-01016013.  
XX  
XX (IPFP-) IPF PHARM GMBH.  
XX (FORS/) FORSSMANN U.  
XX  
XX Forssmann W, Adermann K, Heltland A, Spodsberg N;  
XX  
XX WPI; 2001-626256/72.  
XX  
XX  
XX Diagnostic agent containing two or more receptor-specific ligands, useful  
XX for detecting tumors, inflammation etc., also therapeutic use of ligand  
XX inhibitors.  
XX  
XX  
XX Disclosure; Page 10; 26pp; German.  
XX  
XX This invention describes a novel diagnostic agent (A) comprising at least  
XX two different ligands (I) for receptors (II) that are implicated in  
XX disease. (A) are used for the diagnosis of tumors (especially colorectal  
XX or prostatic), organ rejection, inflammation and autoimmune diseases.  
XX Also inhibitors of (I) are used therapeutically against tumors (and their  
XX metastases), inflammation (particularly bronchial asthma or chronic bowel  
XX inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),  
XX where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,  
XX endocrine, motor or urogenital systems or skin are affected, and bone  
XX marrow diseases. The products of the invention are chemokine derivatives  
XX which have cytostatic, antiinflammatory, antiasthmatic,  
XX immunosuppressive, dermatological, antirheumatic, antiarthritic.  
XX Chemokines act on specific tumor and inflammatory cells through a  
XX constellation of chemokine receptors (CR), which control migration and  
XX proliferation of these cells. AAG80045-AAG80128 represent human chemokine  
XX fragments used to illustrate the method of the invention  
XX  
SQ Sequence 352 AA;  
  
Query Match 100.0%; Score 190; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 7.9e-20;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
|||  
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
  
RESULT 12  
AAE04321  
ID AAE04321 standard; protein; 352 AA.  
XX  
XX AAE04321;  
XX  
XX 04-SEP-2001 (first entry)  
XX  
XX Human chemokine receptor (CKR), CC-CKR-5 related protein #2.  
XX  
XX Human; transformed mammalian cell; CD4; reporter gene; translocation;  
XX human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;  
XX chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor;  
XX CC-CKR-5; envelope glycoprotein; anti-HIV.  
XX  
XX Homo sapiens.  
XX  
XX US6258527-B1.  
XX  
XX

XX  
XX 10-JUL-2001.  
XX  
XX 21-MAY-1997; 97US-00861105.  
XX  
XX  
XX 20-MAY-1996; 96US-0017157P.  
XX 19-JUN-1996; 96US-0020043P.  
XX 19-MAY-1997; 97US-00858660.  
XX  
XX (AARO-) AARON DIAMOND AIDS RES CENT.  
XX (UNYNY ) UNIV NEW YORK STATE.  
XX  
XX Littman DR, Deng H, Elmeier W, Landau NR, Liu R;  
XX  
XX WPI; 2001-417127/44.  
XX N-PSDB; AAD08577.  
XX  
XX  
XX Transformed mammalian cell (I) that contains a CD4 gene, reporter gene  
XX and HIV LTR for identification of drugs and antibodies for treatment of  
XX HIV.  
XX  
XX  
XX Disclosure; Col 47-50; 37pp; English.  
XX  
XX  
XX The present invention relates to a transformed mammalian cell that  
XX contains a gene encoding CD4, a construct encoding a reporter gene under  
XX the regulation of an human immuno deficiency virus (HIV) long terminal  
XX repeat (LTR) and that has been transduced with a vector encoding a human  
XX chemokine receptor (CKR) where the CD4 and the CKR are present on the  
XX cell surface of transformed mammalian cell. The invention is useful for  
XX identifying drugs or antibodies that interfere with the translocation of  
XX HIV into transformed mammalian cell or for identifying a human chemokine  
XX receptor that facilitates the infection of a particular HIV strain into  
XX the transformed mammalian cell. Compounds identified can be used to treat  
XX cellular dysfunction and to prevent or combat HIV infection. The present  
XX sequence is a human chemokine receptor (CKR), CC-CKR-5 related protein.  
XX CC-CKR-5 is the principal cofactor for entry mediated by the envelope  
XX glycoproteins of primary macrophage-tropic strains of HIV-1  
XX  
SQ Sequence 352 AA;  
  
Query Match 100.0%; Score 190; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 7.9e-20;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
|||  
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
  
RESULT 13  
AAE07039  
ID AAE07039 standard; protein; 352 AA.  
XX  
XX AAE07039;  
XX  
XX 16-OCT-2001 (first entry)  
XX  
XX Human G-protein chemokine receptor (CCRS) HDGNR10 protein #2.  
XX  
XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;  
XX human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;  
XX cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy;  
XX neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;  
XX rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;  
XX gastrointestinal tract; lung; liver; immune disorder; Addison's disease;  
XX haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;  
XX multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;  
XX cardiovascular disorder; myocardial ischaemia.  
XX  
XX Homo sapiens.  
XX  
XX WO200158915-A2.  
XX  
XX

PD 16-AUG-2001.  
XX  
PF 09-FEB-2001; 2001WO-US004152.  
XX  
PR 09-FEB-2000; 2000US-0181258P.  
PR 09-MAR-2000; 2000US-0187999P.  
PR 22-SEP-2000; 2000US-0234336P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Roschke V, Li Y, Ruben SM;  
XX  
DR WPI; 2001-488965/53.  
DR N-PSDB; AAD13198.  
XX  
PT Isolated nucleic acid encoding a human G-protein chemokine receptor  
PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune  
PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and  
PT neurodegenerative disorders.  
XX  
PS Example 40; Page 486-487; 495pp; English.  
XX  
CC The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10  
CC protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or  
CC ameliorating a disease or disorder associated with inflammation,  
CC defective or aberrant chemotaxis of immune cells, HIV infection (such as  
CC pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or  
CC aberrant T-cell antigen presenting cell interaction. The disease or  
CC disorder may also be an infectious disease (e.g. a viral infection such  
CC as an early stage HIV infection, a cytomegalovirus infection, or a  
CC poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or  
CC a neurodegenerative disorder. The disease or disorder may be associated  
CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5  
CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein  
CC is used as a food additive or preservative to increase or decrease  
CC storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome  
CC identification and in gene therapy. CCR5 HDGNR10 DNA, protein,  
CC antibodies, agonists and antagonists are also useful in the diagnosis,  
CC treatment and prevention of cancer (breast, ovary, adrenal gland, bone,  
CC bone marrow, gastrointestinal tract, liver, lung, urogenital); immune  
CC disorders (Addison's disease, diabetes mellitus, autoimmune haemolytic anaemia,  
CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple  
CC sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular  
CC disorders (myocardial ischaemias) and wound healing  
XX  
SQ Sequence 352 AA;  
SQ  
Query Match  
Best Local Similarity 100.0%; Score 190; DB 4; Length 352;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIARLLPPL 36  
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIARLLPPL 36  
1 MDYQVSSPIYDINYYTSEPCQKINVKQIARLLPPL 36  
RESULT 14  
AAB46858  
ID AAB46858 standard; protein; 352 AA.  
XX  
AC AAB46858;  
XX  
DT 16-AUG-2001 (revised)  
DT 02-AUG-2001 (revised)  
DT 04-MAY-2001 (first entry)  
XX  
DE Human HDGNR10 protein.  
XX  
KW HDGNR10; human; G-protein chemokine receptor; antiinflammatory;  
KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;  
KW cytostatic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic;  
KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;  
KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;

KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;  
KW anaphylaxis; malignancy; inflammation; histamine; IGE; silicosis; shock;  
KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;  
KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;  
KW hyper-eosinophilic syndrome; vulnery.  
XX  
OS Homo sapiens.  
XX  
PN US2001000241-A1.  
XX  
PD 12-APR-2001.  
XX  
PF 29-NOV-2000; 2000US-00725285.  
XX  
PR 06-JUN-1995; 95US-00466343.  
PR 18-NOV-1998; 98US-00195662.  
PR 25-JUN-1999; 99US-00339912.  
XX  
PA (LIYY/) LI Y.  
PA (RUBE/) RUBEN S M.  
XX  
PI Li Y, Ruben SM;  
XX  
DR WPI; 2001-226317/23.  
DR N-PSDB; AAF26390.  
XX  
PT New human G-protein chemokine receptor polypeptides and polynucleotides,  
PT useful for identifying (ant)agonists to the G-protein chemokine receptor.  
XX  
PS Claim 1a; Page 15; 22pp; English.  
XX  
CC This invention describes a novel receptor polypeptide (I) selected from  
CC (i) a fully defined 329 amino acid sequence (II) fully disclosed in the  
CC specification; and (ii) a polypeptide encoded by the cDNA contained in a  
CC plasmid, and fragments, analogs and derivatives of the polypeptide. The  
CC products of the invention have antiinflammatory, immunomodulatory, The  
CC anticoagulant, antiallergic, immunosuppressive, vulnery, cytostatic,  
CC antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic  
CC activity and can be used for gene therapy. The G-protein chemokine  
CC receptors, HDGNR10, (I) are useful for screening for compounds which  
CC also be used for inhibit activation of (I). The products of the invention can  
CC also be used for stimulating haematopoiesis; wound healing, coagulation,  
CC angiogenesis, treating solid tumours, chronic infections, leukemia, T-  
CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and  
CC stimulating growth factor activity. HDGNR10 is useful for treating  
CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute  
CC inflammation, histamine and immunoglobulin E (IGE)-mediated allergic  
CC reactions, prostaglandin-independent fever, bone marrow failure,  
CC bilicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-  
CC eosinophilic syndrome. (N.B. This record was resubmitted to correct  
CC errors in the keyword formatting)  
XX  
SQ Sequence 352 AA;  
SQ  
Query Match  
Best Local Similarity 100.0%; Score 190; DB 4; Length 352;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIARLLPPL 36  
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIARLLPPL 36  
1 MDYQVSSPIYDINYYTSEPCQKINVKQIARLLPPL 36  
RESULT 15  
ABB56342  
ID ABB56342 standard; protein; 352 AA.  
XX  
AC ABB56342;  
XX  
DT 18-FEB-2002 (first entry)  
DT  
XX  
DE Non-endogenous human GPCR protein, SEQ ID NO: 477.  
XX

KM Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;  
KM constitutively activated GPCR; agonist; disease.

KM constitutively activated GPCR; agonist; disease.

**Os Homo sapiens.**

OS Synthetic.

PN W0200177172-A2.

PD 18-OCT-2001.

PF 05-APR-2001; 2001WO-US011098.

PR 07-APR-2000; 2000US-0195747P.

PA (AREN-) ARENA PHARM INC.

PI Lehmann-Bruinsma K, Liaw CW, Lin I;

DR WPI; 2001-648759/74.

DR N-PSDB; ABI97978.

PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in

11 11000000 00000000, compares compounds with reference  
PT of GPCRb.

PT of GPCRs.

PS Claim 1; Page 277-278; 394pp; English.

CC The invention relates to G protein-coupled receptors (GPCRs) for which  
CC the endogenous ligand has been identified. Non-endogenous constitutively  
CC activated versions of known GPCRs are used in the invention for the  
CC direct identification of candidate compounds as receptor agonists,  
CC inverse agonists or partial agonists. Such agonists are useful as  
CC therapeutic agents for diseases or disorders associated with GPCRs. The  
CC present sequence is a non-endogenous version of a known human GPCR

CC The invention relates to G protein-coupled receptors (GPCRs) for which  
CC the endogenous ligand has been identified. Non-endogenous constitutively  
CC activated versions of known GPCRs are used in the invention for the  
CC direct identification of candidate compounds as receptor agonists,  
CC inverse agonists or partial agonists. Such agonists are useful as  
CC therapeutic agents for diseases or disorders associated with GPCRs. The  
CC present sequence is a non-endogenous version of a known human GPCR

CC The invention relates to G protein-coupled receptors (GPCRs) for which  
CC the endogenous ligand has been identified. Non-endogenous constitutively  
CC activated versions of known GPCRs are used in the invention for the  
CC direct identification of candidate compounds as receptor agonists,  
CC inverse agonists or partial agonists. Such agonists are useful as  
CC therapeutic agents for diseases or disorders associated with GPCRs. The  
CC present sequence is a non-endogenous version of a known human GPCR

CC The invention relates to G protein-coupled receptors (GPCRs) for which  
CC the endogenous ligand has been identified. Non-endogenous constitutively  
CC activated versions of known GPCRs are used in the invention for the  
CC direct identification of candidate compounds as receptor agonists,  
CC inverse agonists or partial agonists. Such agonists are useful as  
CC therapeutic agents for diseases or disorders associated with GPCRs. The  
CC present sequence is a non-endogenous version of a known human GPCR

CC The invention relates to G protein-coupled receptors (GPCRs) for which  
CC the endogenous ligand has been identified. Non-endogenous constitutively  
CC activated versions of known GPCRs are used in the invention for the  
CC direct identification of candidate compounds as receptor agonists,  
CC inverse agonists or partial agonists. Such agonists are useful as  
CC therapeutic agents for diseases or disorders associated with GPCRs. The  
CC present sequence is a non-endogenous version of a known human GPCR

CC The invention relates to G protein-coupled receptors (GPCRs) for which  
CC the endogenous ligand has been identified. Non-endogenous constitutively  
CC activated versions of known GPCRs are used in the invention for the  
CC direct identification of candidate compounds as receptor agonists,  
CC inverse agonists or partial agonists. Such agonists are useful as  
CC therapeutic agents for diseases or disorders associated with GPCRs. The  
CC present sequence is a non-endogenous version of a known human GPCR

CC The invention relates to G protein-coupled receptors (GPCRs) for which  
CC the endogenous ligand has been identified. Non-endogenous constitutively  
CC activated versions of known GPCRs are used in the invention for the  
CC direct identification of candidate compounds as receptor agonists,  
CC inverse agonists or partial agonists. Such agonists are useful as  
CC therapeutic agents for diseases or disorders associated with GPCRs. The  
CC present sequence is a non-endogenous version of a known human GPCR

SQ Sequence 352 AA;

Query Match	100.0%;	Score 190;	DB 4;	Length 352;
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Best Local Similarity 100.0%; Pred. No. 7.9e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 7.9e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

**Oy**      1 MDYQVSSPIYDINYYTSEPCOKINVKQIARLLPPL 36  
         |||||  
**Ddb**    1 MDYQVSSPIYDINYYTSEPCOKINVKQIARLLPPL 36

**Oy**      1 MDYQVSSPIYDINYYTSEPCOKINVKQIARLLPPL 36  
         |||||  
**Ddb**    1 MDYQVSSPIYDINYYTSEPCOKINVKQIARLLPPL 36

Search completed: May 13, 2004, 15:00:53  
Job time : 9.40971 secs

Job time : 9.40971 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:53:42 ; Search time 1.97476 Seconds  
(without alignments)  
941.146 Million cell updates/sec

Title: US-10-072-301-8  
Perfect score: 190  
Sequence: 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

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- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/iaa/PCITUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	190	100.0	87	3	US-09-087-232A-18 Sequence 18, Appl
2	190	100.0	100	3	US-09-087-232A-15 Sequence 15, Appl
3	190	100.0	184	4	US-08-833-752-4 Sequence 4, Appl
4	190	100.0	215	3	US-09-087-232A-17 Sequence 17, Appl
5	190	100.0	215	4	US-08-833-752-6 Sequence 6, Appl
6	190	100.0	352	3	US-09-087-232A-13 Sequence 13, Appl
7	190	100.0	352	3	US-08-861-105-14 Sequence 14, Appl
8	190	100.0	352	3	US-08-575-967A-2 Sequence 2, Appl
9	190	100.0	352	4	US-08-833-752-5 Sequence 5, Appl
10	190	100.0	352	4	US-09-502-783A-2 Sequence 2, Appl
11	190	100.0	352	4	US-09-796-202-1 Sequence 1, Appl
12	185	97.4	352	3	US-09-045-583-52 Sequence 52, Appl
13	185	97.4	352	4	US-09-534-185-52 Sequence 52, Appl
14	184	96.8	352	3	US-08-466-343D-2 Sequence 2, Appl
15	170	89.5	352	4	US-09-517-605-5 Sequence 5, Appl
16	131	68.9	354	4	US-08-724-984A-2 Sequence 2, Appl
17	123	64.7	22	3	US-08-861-105-4 Sequence 4, Appl
18	113	59.5	20	2	US-08-889-291-32 Sequence 32, Appl
19	113	59.5	20	3	US-09-098-244-32 Sequence 32, Appl
20	113	59.5	20	4	US-09-375-314-32 Sequence 32, Appl
21	113	59.5	20	4	US-09-767-395-32 Sequence 32, Appl
22	105	55.3	28	3	US-08-861-105-6 Sequence 6, Appl
23	83.5	43.9	26	4	US-09-131-827A-14 Sequence 14, Appl
24	75	39.5	83	4	US-09-131-827A-13 Sequence 13, Appl
25	75	39.5	329	4	US-09-502-783A-9 Sequence 9, Appl
26	75	39.5	344	3	US-08-466-343D-9 Sequence 9, Appl
27	75	39.5	347	1	US-08-461-244-3 Sequence 3, Appl

28	75	39.5	360	1	US-08-450-393A-4	Sequence 4, Appl
29	75	39.5	360	3	US-08-446-669-4	Sequence 4, Appl
30	75	39.5	360	3	US-09-045-583-50	Sequence 50, Appl
31	75	39.5	360	3	US-09-045-583-51	Sequence 51, Appl
32	75	39.5	360	4	US-09-534-185-50	Sequence 50, Appl
33	75	39.5	360	4	US-09-534-185-51	Sequence 51, Appl
34	75	39.5	360	4	US-08-833-752-7	Sequence 7, Appl
35	75	39.5	360	4	US-09-131-827A-2	Sequence 2, Appl
36	75	39.5	360	4	US-09-131-827A-20	Sequence 20, Appl
37	75	39.5	360	5	PCT-US95-00476-4	Sequence 4, Appl
38	75	39.5	374	1	US-08-450-393A-2	Sequence 2, Appl
39	75	39.5	374	3	PCT-US95-00476-2	Sequence 2, Appl
40	75	39.5	374	5	PCT-US95-00476-2	Sequence 2, Appl
41	74.5	39.2	355	1	US-08-012-988A-2	Sequence 2, Appl
42	74.5	39.2	355	1	US-08-450-393A-5	Sequence 5, Appl
43	74.5	39.2	355	3	US-08-446-669-5	Sequence 5, Appl
44	74.5	39.2	355	4	US-09-239-938-1	Sequence 1, Appl
45	74.5	39.2	355	4	US-08-833-752-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1  
US-09-087-232A-18  
Sequence 18, Application US/09087232A  
Patent No. 6153431  
GENERAL INFORMATION:  
APPLICANT: Quillent et al.  
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR  
TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/087,232A  
FILING DATE: 28 MAY 1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/048,057  
FILING DATE: 30 MAY 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KOLE, LISA B.  
REGISTRATION NUMBER: 35,225  
REFERENCE/DOCKET NUMBER: AP 31115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 408-2628  
TELEFAX: (212) 765-2519  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 87 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-087-232A-18  
Query Match 100.0%; Score 190; DB 3; Length 87;  
Best Local Similarity 100.0%; Pred. No. 1.2e-21;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36



## RESULT 2

US-09-087-232A-15

Sequence 15, Application US/09087232A  
Patent No. 6153431

GENERAL INFORMATION:

APPLICANT: Quillent et al.

TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR

TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Baker &amp; Botts, L.L.P. attn. Lisa Kole

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/087,232A

FILING DATE: 28 MAY 1998

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 60/048,057

FILING DATE: 30 MAY 1997

ATTORNEY/AGENT INFORMATION:

NAME: KOLE, LISA B.

REGISTRATION NUMBER: 35,225

REFERENCE/DOCKET NUMBER: AP 31115

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 408-2628

TELEFAX: (212) 765-2519

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 100 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-087-232A-15

## Query Match

Best Local Similarity 100.0%; Score 190; DB 3; Length 100;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MDYQVSSPIYDINITYTSEPCQKINVKQIARLLPPL 36

Db 1 MDYQVSSPIYDINITYTSEPCQKINVKQIARLLPPL 36

## RESULT 3

US-08-833-752-4

Sequence 4, Application US/08833752

Patent No. 6448375

GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL

APPLICANT: PARMENTIER, MARC

APPLICANT: VASSART, GILBERT

APPLICANT: LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Knobe, Martens, Olson &amp; Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: U.S.A.

ZIP: 92660

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/833,752

FILING DATE: 9-APR-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 184 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-833-752-4

## Query Match

Best Local Similarity 100.0%; Score 190; DB 4; Length 184;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MDYQVSSPIYDINITYTSEPCQKINVKQIARLLPPL 36

Db 1 MDYQVSSPIYDINITYTSEPCQKINVKQIARLLPPL 36

## RESULT 4

US-09-087-232A-17

Sequence 17, Application US/09087232A

Patent No. 6153431

GENERAL INFORMATION:

APPLICANT: Quillent et al.

TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR

TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Baker &amp; Botts, L.L.P. attn. Lisa Kole

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/087,232A

FILING DATE: 28 MAY 1998

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 60/048,057

FILING DATE: 30 MAY 1997

ATTORNEY/AGENT INFORMATION:

NAME: KOLE, LISA B.

REGISTRATION NUMBER: 35,225

REFERENCE/DOCKET NUMBER: AP 31115

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 408-2628

TELEFAX: (212) 765-2519

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-087-232A-17

Query Match 100.0%; Score 190; DB 3; Length 215;  
Best Local Similarity 100.0%; Pred. No. 3.6e-21;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36  
|||||  
Db 1 MDYQVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36

## RESULT 5

US-08-833-752-6  
; Sequence 6, Application US/08833752  
; Patent No. 6448375

; GENERAL INFORMATION:

; APPLICANT: SAMSON, MICHEL

; APPLICANT: PARMENTIER, MARC

; APPLICANT: VASSART, GILBERT

; APPLICANT: LIBERT, FREDERICK

; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 620 Newport Center Drive 16th Floor

; CITY: Newport Beach

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/833,752

; FILING DATE: 9-APR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Altman, Daniel E

; REGISTRATION NUMBER: 34,115

; REFERENCE/DOCKET NUMBER:

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 215 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-833-752-6  
Query Match 100.0%; Score 190; DB 4; Length 215;  
Best Local Similarity 100.0%; Pred. No. 3.6e-21;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36  
|||||  
Db 1 MDYQVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36

## RESULT 6

US-09-087-232A-13  
; Sequence 13, Application US/09087232A  
; Patent No. 6153431

; GENERAL INFORMATION:

; APPLICANT: Quillent et al.

; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR

; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/087,232A

; FILING DATE: 28 MAY 1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/048,057

; FILING DATE: 30 MAY 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: KOLE, LISA B.

; REGISTRATION NUMBER: 35,225

; REFERENCE/DOCKET NUMBER: AP 31115

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 408-2628

; TELEFAX: (212) 765-2519

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 352 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-087-232A-13  
Query Match 100.0%; Score 190; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 6.7e-21;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36  
|||||  
Db 1 MDYQVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36

## RESULT 7

US-08-861-105-14  
; Sequence 14, Application US/08861105  
; Patent No. 6258527

; GENERAL INFORMATION:

; APPLICANT: LITTMAN, DAN R.

; APPLICANT: DENG, HONGKUI

; APPLICANT: BLMEIER, WILFRIED

; APPLICANT: LANDAU, NATHANIEL R.

; APPLICANT: LIU, RONG

; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH

; TITLE OF INVENTION: MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: David A. Jackson, Esq.

; STREET: 411 Hackensack Ave, Continental Plaza, 4th

; STREET: Floor

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/861,105

; FILING DATE:

; CLASSIFICATION: 436

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/666,020

; FILING DATE: 19-JUN-1996

; CLASSIFICATION: 436

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,319  
 FILING DATE: 13-APR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 1049-1-004 N1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5800  
 TELEFAX: 201-343-1684  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 352 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 US-08-861-105-14

Query Match  
 Best Local Similarity 100.0%; Score 190; DB 3; Length 352;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINITYTSEPCQKINVKQIARLLPPL 36  
 DB 1 MDYQVSSPIYDINITYTSEPCQKINVKQIARLLPPL 36

RESULT 8

US-08-575-967A-2  
 Sequence 2, Application US/08575967A  
 Patent No. 6265184  
 GENERAL INFORMATION:  
 APPLICANT: Gray et al.  
 TITLE OF INVENTION: Chemokine Receptor Materials and Methods  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 6300 Sears Tower, 233 S. Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/575,967A  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: No. 6265184and, Greta E.  
 REGISTRATION NUMBER: 35,302  
 REFERENCE/DOCKET NUMBER: 32918  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-485-1900  
 TELEFAX: 206-485-1662  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 352 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: misc\_feature  
 OTHER INFORMATION: /= "88C amino acid sequence"  
 US-08-575-967A-2

Query Match 100.0%; Score 190; DB 3; Length 352;

Best Local Similarity 100.0%; Pred. No. 6.7e-21;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9

US-08-833-752-5  
 Sequence 5, Application US/08833752  
 Patent No. 6448375  
 GENERAL INFORMATION:  
 APPLICANT: SAMSON, MICHEL  
 APPLICANT: PARMENTIER, MARC  
 APPLICANT: VASSART, GILBERT  
 APPLICANT: LIBERT, FREDERICK  
 TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Knobbe, Martens, Olson & Bear  
 STREET: 620 Newport Center Drive 16th Floor  
 CITY: Newport Beach  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 92660  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/833,752  
 FILING DATE: 9-APR-1997  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Altman, Daniel E  
 REGISTRATION NUMBER: 34,115  
 REFERENCE/DOCKET NUMBER:  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 352 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-833-752-5

Query Match 100.0%; Score 190; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-21;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINITYTSEPCQKINVKQIARLLPPL 36  
 DB 1 MDYQVSSPIYDINITYTSEPCQKINVKQIARLLPPL 36

RESULT 10

US-09-502-783A-2  
 Sequence 2, Application US/09502783A  
 Patent No. 6511826  
 GENERAL INFORMATION:  
 APPLICANT: Li, Yi  
 APPLICANT: Ruben, Steven M.  
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS  
 FILE REFERENCE: HDGRI10  
 CURRENT APPLICATION NUMBER: US/09/502,783A  
 PRIOR APPLICATION NUMBER: 2001-08-23  
 PRIOR FILING DATE: 1995-06-06  
 NUMBER OF SEQ ID NOS: 9  
 SOFTWARE: Patentin version 3.0



SEQ ID NO 2  
LENGTH: 352  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-502-783A-2

Query Match 100.0%; Score 190; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 6.7e-21;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

RESULT 11  
US-09-796-202-1

Sequence 1, Application US/09796202  
Patent No. 6548636  
GENERAL INFORMATION:  
APPLICANT: Dragic, Tatjana  
APPLICANT: Olson, William  
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPW/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 352  
TYPE: PRT  
ORGANISM: human  
US-09-796-202-1

Query Match 100.0%; Score 190; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 6.7e-21;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

RESULT 12  
US-09-045-583-52

Sequence 52, Application US/09045583  
Patent No. 6287805  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/045,583  
FILING DATE: 20-MAR-98  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-09-045-583-52

Query Match 97.4%; Score 185; DB 3; Length 352;  
Best Local Similarity 97.2%; Pred. No. 3.9e-20;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
Db 1 MDYQVSSPIYDIDYITSEPCQKINVKQIAARLLPPL 36

RESULT 13  
US-09-534-185-52

Sequence 52, Application US/09534185  
Patent No. 6403767  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled  
Heptahelical Receptor Superfamily and Uses  
Therefor  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/534,185  
FILING DATE: 24-Mar-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/045,583  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 52:  
US-09-534-185-52

Query Match 97.4%; Score 185; DB 4; Length 352;  
Best Local Similarity 97.2%; Pred. No. 3.9e-20;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

Db 1 MDYQVSSPIYDIDYTTSEPCQKINVKQIAARLLPPL 36

RESULT 14  
US-08-466-343D-2  
; Sequence 2, Application US/08466343D  
; Patent No. 6025154  
; GENERAL INFORMATION:  
; APPLICANT: LI, YI  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN  
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGMR10 (AS AMENDED)  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,343D  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 352 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-466-343D-2

Query Match 96.8%; Score 184; DB 3; Length 352;  
Best Local Similarity 97.2%; Pred. No. 5.5e-20;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MDYQVSSPIYDIDYTTSEPCQKINVKQIAARLLPPL 36  
Db 1 MDYQVSSPIYDIDYTTSEPCQKINVKQIAARLLPPL 36

RESULT 15  
US-09-517-605-5  
; Sequence 5, Application US/09517605  
; Patent No. 6391567  
; GENERAL INFORMATION:  
; APPLICANT: Littman, Dan R.  
; APPLICANT: Kwon, Douglas S.  
; APPLICANT: van Kooyk, Yvette  
; APPLICANT: Gejtenbeck, Tneo  
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 1049-1-017  
; CURRENT APPLICATION NUMBER: US/09/517,605  
; CURRENT FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-517-605-5

Query Match 89.5%; Score 170; DB 4; Length 352;  
Best Local Similarity 91.7%; Pred. No. 7.6e-18;  
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDIDYTTSEPCQKINVKQIAARLLPPL 36  
Db 1 MDYQVSSPIYDIDYTTSEPCQKINVKQIAARLLPPL 36

Search completed: May 13, 2004, 15:10:44  
Job time: 1.97476 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 15:07:07 ; Search time 5.3301 Seconds  
(without alignments)  
1879.405 Million cell updates/sec

Title: US-10-072-301-8  
Perfect score: 190  
Sequence: 1 MDYQVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
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7: /cgn2\_6/ptodata/2/pubpaa/US08\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*  
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12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	190	100.0	36	14	US-10-072-301-8	Sequence 8, Appli
2	190	100.0	36	14	US-10-071-866-8	Sequence 8, Appli
3	190	100.0	36	15	US-10-360-828-8	Sequence 8, Appli
4	190	100.0	184	9	US-09-938-719-4	Sequence 4, Appli
5	190	100.0	184	9	US-09-939-226-4	Sequence 4, Appli
6	190	100.0	184	9	US-09-938-703-4	Sequence 4, Appli
7	190	100.0	215	9	US-09-938-719-6	Sequence 6, Appli
8	190	100.0	215	9	US-09-939-226-6	Sequence 6, Appli
9	190	100.0	215	9	US-09-938-703-6	Sequence 6, Appli
10	190	100.0	352	9	US-09-725-285-2	Sequence 2, Appli
11	190	100.0	352	9	US-09-759-841-2	Sequence 2, Appli
12	190	100.0	352	9	US-09-779-879A-22	Sequence 22, Appli
13	190	100.0	352	9	US-09-779-880A-22	Sequence 22, Appli
14	190	100.0	352	9	US-09-813-653-15	Sequence 15, Appli
15	190	100.0	352	9	US-09-813-653-17	Sequence 17, Appli

16	190	100.0	352	9	US-09-796-202-1	Sequence 1, Appli
17	190	100.0	352	9	US-09-195-662A-2	Sequence 2, Appli
18	190	100.0	352	9	US-09-339-912A-2	Sequence 2, Appli
19	190	100.0	352	9	US-09-938-719-5	Sequence 5, Appli
20	190	100.0	352	9	US-09-939-226-5	Sequence 5, Appli
21	190	100.0	352	9	US-09-938-703-5	Sequence 5, Appli
22	190	100.0	352	9	US-09-502-783A-2	Sequence 2, Appli
23	190	100.0	352	10	US-09-734-221A-14	Sequence 14, Appli
24	190	100.0	352	11	US-09-826-509-477	Sequence 477, App
25	190	100.0	352	13	US-10-106-623-2	Sequence 2, Appli
26	190	100.0	352	14	US-10-232-686-2	Sequence 2, Appli
27	190	100.0	352	14	US-10-086-814-1	Sequence 1, Appli
28	190	100.0	352	14	US-10-067-800-22	Sequence 22, Appli
29	190	100.0	352	14	US-10-290-058A-6	Sequence 6, Appli
30	190	100.0	352	14	US-10-225-567A-352	Sequence 352, App
31	190	100.0	352	14	US-10-323-314-1	Sequence 1, Appli
32	190	100.0	352	14	US-10-072-301-1	Sequence 1, Appli
33	190	100.0	352	14	US-10-071-866-1	Sequence 1, Appli
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35	190	100.0	352	14	US-10-239-423-67	Sequence 67, Appli
36	190	100.0	352	14	US-10-439-845-2	Sequence 2, Appli
37	190	100.0	352	14	US-10-439-845-4	Sequence 4, Appli
38	190	100.0	352	15	US-10-360-828-1	Sequence 1, Appli
39	185	97.4	352	14	US-10-164-649-52	Sequence 52, Appli
40	184	96.8	352	9	US-09-779-879A-2	Sequence 2, Appli
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44	180	94.7	352	13	US-10-106-623-20	Sequence 20, Appli
45	172	90.5	33	10	US-09-913-238-70	Sequence 70, Appli

## ALIGNMENTS

RESULT 1  
US-10-072-301-8  
; Sequence 8, Application US/10072301  
; Publication No. US20030152913A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF  
; FILE REFERENCE: 25636-718  
; CURRENT APPLICATION NUMBER: US/10/072,301  
; CURRENT FILING DATE: 2002-02-08  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-072-301-8

Query Match 100.0%; Score 190; DB 14; length 36;  
Best Local Similarity 100.0%; Pred. No. 1.1e-19;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36  
Db 1 MDYQVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36

RESULT 2  
US-10-071-866-8  
; Sequence 8, Application US/10071866  
; Publication No. US20030165988A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li

;; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST H  
;; FILE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS  
;; FILE REFERENCE: 25636-717  
;; CURRENT APPLICATION NUMBER: US/10/071,866  
;; CURRENT FILING DATE: 2002-02-08  
;; NUMBER OF SEQ ID NOS: 54  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 8  
;; LENGTH: 36  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-071-866-8

Query Match 100.0%; Score 190; DB 14; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.1e-19;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

RESULT 3  
US-10-360-828-8  
; Sequence 8, Application US/10360828  
; Publication No. US20030206909A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shaobing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS  
; FILE REFERENCE: 25636-727  
; CURRENT APPLICATION NUMBER: US/10/360,828  
; PRIOR FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: US 10/071,866  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/072,301  
; PRIOR FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-360-828-8

Query Match 100.0%; Score 190; DB 15; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.1e-19;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

RESULT 4  
US-09-938-719-4  
; Sequence 4, Application US/09938719  
; Patent No. US20020106742A1  
; GENERAL INFORMATION:  
; APPLICANT: SAMSON, MICHEL  
; APPLICANT: PARMENTIER, MARC  
; APPLICANT: VASSART, GILBERT  
; APPLICANT: LIBERT, FREDERICK  
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach

;; STATE: CA  
;; COUNTRY: U.S.A.  
;; ZIP: 92660  
;; COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
;; CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/938,719  
FILING DATE: 24-Aug-2001  
CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/626,939  
FILING DATE: 27-JULY-2000  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: <Unknown>  
;; INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 184 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-938-719-4

Query Match 100.0%; Score 190; DB 9; Length 184;  
Best Local Similarity 100.0%; Pred. No. 7.2e-19;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

RESULT 5  
US-09-939-226-4  
; Sequence 4, Application US/09939226  
; Patent No. US20020110805A1  
; GENERAL INFORMATION:  
; APPLICANT: SAMSON, MICHEL  
; APPLICANT: PARMENTIER, MARC  
; APPLICANT: VASSART, GILBERT  
; APPLICANT: LIBERT, FREDERICK  
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
;; COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
;; CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/939,226  
FILING DATE: 24-Aug-2001  
CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/626,939  
FILING DATE: 2000-07-27  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: <Unknown>  
;; INFORMATION FOR SEQ ID NO: 4:



## SEQUENCE CHARACTERISTICS:

LENGTH: 184 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-939-226-4

Query Match 100.0%; Score 190; DB 9; Length 184;  
Best Local Similarity 100.0%; Pred. No. 7.2e-19;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MDYQVSSPIYDINYYTSEPCCKINVKQIAARLLPPL 36  
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Db 1 MDYQVSSPIYDINYYTSEPCCKINVKQIAARLLPPL 36

## RESULT 6

US-09-938-703-4  
Sequence 4, Application US/09938703  
Patent No. US20020110870A1

## GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL  
PARMENTIER, MARC  
VASSART, GILBERT  
LIBERT, FREDERICK  
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/938,703  
FILING DATE: 24-Aug-2001  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/626,939  
FILING DATE: 2000-07-27

## ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: <Unknown>

## SEQUENCE CHARACTERISTICS:

LENGTH: 184 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-938-703-4

Query Match 100.0%; Score 190; DB 9; Length 184;  
Best Local Similarity 100.0%; Pred. No. 7.2e-19;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MDYQVSSPIYDINYYTSEPCCKINVKQIAARLLPPL 36  
|||  
Db 1 MDYQVSSPIYDINYYTSEPCCKINVKQIAARLLPPL 36

## RESULT 7

US-09-938-719-6  
Sequence 6, Application US/09938719

Patent No. US20020106742A1

## GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL  
PARMENTIER, MARC  
VASSART, GILBERT  
LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/938,719  
FILING DATE: 24-Aug-2001  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/626,939  
FILING DATE: 27-JULY-2000

## ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: <Unknown>

## INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 215 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-938-719-6

Query Match 100.0%; Score 190; DB 9; Length 215;  
Best Local Similarity 100.0%; Pred. No. 8.6e-19;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MDYQVSSPIYDINYYTSEPCCKINVKQIAARLLPPL 36  
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Db 1 MDYQVSSPIYDINYYTSEPCCKINVKQIAARLLPPL 36

## RESULT 8

US-09-939-226-6  
Sequence 6, Application US/09939226  
Patent No. US20020110805A1

## GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL  
PARMENTIER, MARC  
VASSART, GILBERT  
LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/939,226
;   FILING DATE: 24-Aug-2001
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 09/626,939
;     FILING DATE: 2000-07-27
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Altman, Daniel E
;     REGISTRATION NUMBER: 34,115
;   REFERENCE/DOCKET NUMBER: <Unknown>
;   INFORMATION FOR SEQ ID NO: 6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 215 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-939-226-6

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Query Match      100.0%; Score 190; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 8.6e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

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RESULT 9
US-09-938-703-6
; Sequence 6, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
;   APPLICANT: SAMSON, MICHEL
;   PARMANTIER, MARC
;   VASSART, GILBERT
;   LIBERT, FREDERICK
;   TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;   AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;   NUMBER OF SEQUENCES: 17
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Knobbe, Martens, Olson & Bear
;     STREET: 620 Newport Center Drive 16th Floor
;     CITY: Newport Beach
;     STATE: CA
;     COUNTRY: U.S.A.
;     ZIP: 92660
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/938,703
;     FILING DATE: 24-Aug-2001
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 09/626,939
;     FILING DATE: 2000-07-27
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Altman, Daniel E
;     REGISTRATION NUMBER: 34,115
;   REFERENCE/DOCKET NUMBER: <Unknown>
;   INFORMATION FOR SEQ ID NO: 6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 215 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-703-6

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Query Match      100.0%; Score 190; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 8.6e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

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RESULT 10
US-09-725-285-2
; Sequence 2, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
;   APPLICANT: Li, Yi
;   APPLICANT: Ruben, Steven, M.
;   TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10
;   TITLE OF INVENTION: (CCR5 Receptor)
;   FILE REFERENCE: 1488.1150003
;   CURRENT APPLICATION NUMBER: US/09/725,285
;   CURRENT FILING DATE: 2000-11-29
;   PRIOR APPLICATION NUMBER: 09/339,912
;   PRIOR FILING DATE: 1999-06-25
;   PRIOR APPLICATION NUMBER: 09/195,662
;   PRIOR FILING DATE: 1998-11-18
;   PRIOR APPLICATION NUMBER: 08/466,343
;   PRIOR FILING DATE: 1995-06-06
;   NUMBER OF SEQ ID NOS: 9
;   SOFTWARE: Patentin version 3.0
;   SEQ ID NO 2
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Artificial Sequence: Genomic
;   FEATURE:
;   OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

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Query Match      100.0%; Score 190; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

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RESULT 11
US-09-759-841-2
; Sequence 2, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
;   APPLICANT: Rickett, Graham A
;   APPLICANT: Dobbs, Susan
;   APPLICANT: Perros, Manousos
;   TITLE OF INVENTION: Assay Method
;   FILE REFERENCE: PC10348APME
;   CURRENT APPLICATION NUMBER: US/09/759,841
;   CURRENT FILING DATE: 2001-01-12
;   PRIOR APPLICATION NUMBER: GB 0000661.9
;   PRIOR FILING DATE: 2000-01-12
;   PRIOR APPLICATION NUMBER: GB 0000663.5
;   PRIOR FILING DATE: 2000-01-12
;   PRIOR APPLICATION NUMBER: GB 0000659.3
;   PRIOR FILING DATE: 2000-01-12
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: Patentin Ver. 2.1
;   SEQ ID NO 2
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-759-841-2

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Query Match 100.0%; Score 190; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
|||||  
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

## RESULT 12

US-09-779-879A-22  
; Sequence 22, Application US/09779879A  
; Patent No. US20020048786A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Roschke, Viktor  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10  
; FILE REFERENCE: 1488.115000A  
; CURRENT APPLICATION NUMBER: US/09/779, 879A  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,258  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: US 60/187,999  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/234,336  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 22  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-779-879A-22

Query Match 100.0%; Score 190; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
|||||  
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

## RESULT 13

US-09-779-880A-22  
; Sequence 22, Application US/09779880A  
; Patent No. US20020061834A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Roschke, Viktor  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10  
; FILE REFERENCE: 1488.115000C  
; CURRENT APPLICATION NUMBER: US/09/779, 880A  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,258  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: US 60/187,999  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/234,336  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 22  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-779-880A-22

Query Match 100.0%; Score 190; DB 9; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
|||||  
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

## RESULT 14

US-09-813-653-15  
; Sequence 15, Application US/09813653  
; Patent No. US20020064770A1  
; GENERAL INFORMATION:  
; APPLICANT: Nestor, John  
; APPLICANT: Wilson, Carol  
; APPLICANT: See, Raymond  
; APPLICANT: Tan Hehir, Christina  
; TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds  
; FILE REFERENCE: CNS-005  
; CURRENT APPLICATION NUMBER: US/09/813, 653  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: US 60/190,946  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/190,996  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/191,299  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-813-653-15

Query Match 100.0%; Score 190; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
|||||  
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

## RESULT 15

US-09-813-653-17  
; Sequence 17, Application US/09813653  
; Patent No. US20020064770A1  
; GENERAL INFORMATION:  
; APPLICANT: Nestor, John  
; APPLICANT: Wilson, Carol  
; APPLICANT: See, Raymond  
; APPLICANT: Tan Hehir, Christina  
; TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds  
; FILE REFERENCE: CNS-005  
; CURRENT APPLICATION NUMBER: US/09/813, 653  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: US 60/190,946  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/190,996  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/191,299  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 17  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-813-653-17

Query Match 100.0%; Score 190; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.5e-18;

Matches	36;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Db	1	MDYQVSSPIYDINNYTSEPCKINVKQIAARLLPPL	36						

Search completed: May 13, 2004, 15:43:29  
Job time : 6.3301 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:50:27 ; Search time 1.62524 Seconds  
(without alignments)  
2130.694 Million cell updates/sec

Title: US-10-072-301-8  
Perfect score: 190  
Sequence: 1 MDYQVSSPIVDINYTSEPCQKINVKQIARLLPPL 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pirl:\*  
2: pirl:\*  
3: pirl:\*  
4: pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	190	100.0	352	2	A43113	chemokine (C-C) re
2	75	39.5	360	2	JC2443	chemokine (C-C) re
3	75	39.5	374	2	I38450	chemokine (C-C) re
4	74.5	39.2	355	2	A45177	chemokine (C-C) re
5	65	34.2	355	2	I49339	macrophage inflam
6	65	34.2	359	2	I49341	MIP-1 alpha recept
7	59	31.1	383	2	S55594	G protein-coupled
8	57	30.0	178	2	T20317	hypothetical prote
9	57	30.0	242	2	F84788	hypothetical prote
10	56.5	29.7	360	2	A57160	chemokine (C-C) re
11	56	29.5	211	2	B86864	uracil phosphoribo
12	55.5	29.2	818	2	T40491	hypothetical prote
13	55	28.9	54	2	PT0189	protein-tyrosine k
14	55	28.9	194	2	D87648	conserved hypotet
15	55	28.9	503	2	T29870	hypothetical prote
16	54.5	28.7	130	2	T47540	actin depolymerizi
17	54	28.4	617	2	AF1284	5-methyltetrahydro
18	54	28.4	617	2	AI1655	5-methyltetrahydro
19	53.5	28.2	132	2	G84717	actin depolymerizi
20	53	27.9	516	2	T40181	conserved hypotet
21	53	27.9	1130	2	T29089	alpha-mannosidase
22	53	27.9	2039	2	E64540	probable calcium c
23	52.5	27.6	809	2	E71660	hypothetical prote
24	52	27.4	1162	1	VGTHAK	E2 glycoprotein pr
25	51	26.8	191	2	H70209	decorin binding pr
26	51	26.8	364	2	AE0169	probable exported
27	51	26.8	520	2	S14599	E2 glycoprotein -
28	51	26.8	520	2	S14600	E2 glycoprotein -
29	51	26.8	520	2	S14598	E2 glycoprotein -

30	51	26.8	528	2	T33464	hypothetical prote
31	51	26.8	544	2	S41626	spike protein chai
32	51	26.8	550	1	VGTHD6	E2 glycoprotein pr
33	51	26.8	1154	1	VGTHB	E2 glycoprotein pr
34	51	26.8	1162	2	S14939	E2 glycoprotein pr
35	51	26.8	1162	2	S14940	E2 glycoprotein pr
36	51	26.8	1790	1	MMFEB1	laminin beta-1 cha
37	50.5	26.6	1505	2	T31418	synaptosomal compl
38	50	26.3	849	2	T04242	abdominal segment
39	49.5	26.1	268	2	T50523	hypothetical prote
40	49.5	26.1	477	2	S16383	carboxypeptidase B
41	49.5	26.1	1039	2	T22982	hypothetical prote
42	49.5	26.1	1192	2	H88293	protein F59B10.1 l
43	49	25.8	1487	2	AG2560	hypothetical prote
44	48.5	25.5	126	2	S30934	actin-depolymerizi
45	48.5	25.5	130	2	T05788	actin-depolymerizi

ALIGNMENTS

RESULT 1  
A43113  
chemokine (C-C) receptor 5 - human  
N:Alternate names: C-C CKR-5; CCR5  
C:Species: Homo sapiens (man)  
C:Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000  
C:Accession: A43113; S71808; A58834; A58832; G02653; A58833  
R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.  
Biochemistry 35, 3362-3367, 1996  
A:Title: Molecular cloning and functional expression of a new human CC-chemokine recept  
A:Reference number: A43113; MUID:96241590; PMID:8639485  
A:Accession: A43113  
A:Molecule type: mRNA  
A:Residues: 1-352 <SAM1>  
A:Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811  
R:Samson, M.; Libbert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragost  
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa  
Nature 382, 722-725, 1996  
A:Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles c  
A:Reference number: S71808; MUID:96345670; PMID:8751444  
A:Accession: S71808  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 182-206;207-230 <SAM2>  
A:Accession: A58834  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-184; 'IKDSLHAGAPAAACHGHLILGNPKNSASVSK' <SAM3>  
A:Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063  
A:Note: this frameshift mutation results in a non-functional receptor but confers a degr  
nd may have had a selective advantage by conferring resistance to Yersinia plague infect  
R:Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.  
J. Leukoc. Biol. 60, 147-152, 1996  
A:Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rec  
A:Reference number: A58832; MUID:96295970; PMID:8699119  
A:Accession: A58832  
A:Molecule type: mRNA  
A:Residues: 1-352 <COM1>  
A:Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409  
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes  
R:Combadiere, C.  
Submitted to the EMBL Data Library, May 1996  
A:Reference number: H01541  
A:Accession: G02653  
A:Status: translated from GB/EMBL/DBD  
A:Molecule type: mRNA  
A:Residues: 1-89; 'L', 91-352 <COM2>  
A:Cross-references: EMBL:U57840  
R:Raport, C.U.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.  
J. Biol. Chem. 271, 17161-17166, 1996  
A:Title: Molecular cloning and functional characterization of a novel human CC chemokine  
A:Reference number: A58833; MUID:96291862; PMID:8663314

A/Accession: A58833  
 A/Molecule type: mRNA  
 A/Residues: 1-352 <RAP>  
 A/Cross-references: GB:U54994; NID:G1457945; PIDN:AAC50598.1; PID:G1457946  
 C/Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see PIR:A30574), and dual-tropic strains of HIV-1 bind to a complex of chemokine receptors.  
 C/Genetics:  
 A/Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13  
 A/Cross-references: GDB:1230510; OMIM:601373  
 A/Map position: 3p21-3p21  
 C/Function:  
 A/Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES  
 A/Note: probably acts to control granulocyte proliferation and differentiation  
 C/Superfamily: vertebrate rhodopsin  
 C/Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran  
 F/32-56/Domain: transmembrane #status predicted <TM1>  
 F/103-124/Domain: transmembrane #status predicted <TM2>  
 F/142-166/Domain: transmembrane #status predicted <TM3>  
 F/193-218/Domain: transmembrane #status predicted <TM4>  
 F/236-257/Domain: transmembrane #status predicted <TM5>  
 F/285-300/Domain: transmembrane #status predicted <TM6>  
 F/20-269,101-178/Disulfide bonds: #status predicted <TM7>  
 F/268/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F/336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted  
 F/340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match  
 Best Local Similarity 100.0%; Score 190; DB 2; Length 352;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
 DB 1 MDYQSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36

RESULT 2  
 JC2443  
 chemokine (C-C) receptor 2, splice form B - human  
 N/Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem  
 C/Species: Homo sapiens (man)  
 C/Date: 21-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 20-Jun-2000  
 R/Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.  
 Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994  
 A/Title: CDNA cloning and functional expression of a human monocyte chemoattractant pro  
 A/Reference number: JC2443; MUID:94324942; PMID:8048929  
 A/Accession: JC2443  
 A/Molecule type: mRNA  
 A/Residues: 1-360 <YAM>  
 A/Cross-references: DDBJ:D29984; NID:G531246; PIDN:BAA06253.1; PID:G531247  
 R/Charo, I.F.; Myers, S.J.; Herman, A.; Francis, C.; Connolly, A.J.; Coughlin, S.R.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994  
 A/Title: Molecular cloning and functional expression of two monocyte chemoattractant pro  
 A/Reference number: A53477; MUID:94195821; PMID:8146186  
 A/Accession: I38463  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-360 <RES>  
 A/Cross-references: EMBL:U03905; NID:G472557; PIDN:AAA19120.1; PID:G472558  
 C/Genetics:  
 A/Gene: GDB:CMKBR2  
 A/Cross-references: GDB:337364; OMIM:601267  
 A/Map position: 3p21-3p21  
 C/Superfamily: vertebrate rhodopsin  
 C/Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran  
 F/43-70/Domain: transmembrane #status predicted <TM1>  
 F/81-100/Domain: transmembrane #status predicted <TM2>  
 F/115-136/Domain: transmembrane #status predicted <TM3>  
 F/154-178/Domain: transmembrane #status predicted <TM4>  
 F/207-226/Domain: transmembrane #status predicted <TM5>  
 F/244-268/Domain: transmembrane #status predicted <TM6>  
 F/287-309/Domain: transmembrane #status predicted <TM7>

F/14/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F/113-190/Disulfide bonds: #status predicted

Query Match  
 Best Local Similarity 39.5%; Score 75; DB 2; Length 360;  
 Matches 15; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY 10 YDINYYTSEPCQKINVKQIAARLLPPL 36  
 DB 24 FDYDY--GAPCHKFDVKQIGAQLPPL 48

## RESULT 3

I38450

chemokine (C-C) receptor 2, splice form A - human  
 N/Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte  
 C/Species: Homo sapiens (man)  
 C/Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 13-Aug-1999  
 R/Charo, I.F.; Myers, S.J.; Herman, A.; Francis, C.; Connolly, A.J.; Coughlin, S.R.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994  
 A/Title: Molecular cloning and functional expression of two monocyte chemoattractant  
 A/Reference number: A53477; MUID:94195821; PMID:8146186  
 A/Accession: I38450  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-374 <RES>  
 A/Cross-references: EMBL:U03882; NID:G472555; PIDN:AAA19119.1; PID:G472556  
 C/Genetics:  
 A/Gene: GDB:CMKBR2  
 A/Cross-references: GDB:337364; OMIM:601267  
 A/Map position: 3p21-3p21  
 C/Superfamily: vertebrate rhodopsin  
 C/Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran  
 F/44-68/Domain: transmembrane #status predicted <TM1>  
 F/79-99/Domain: transmembrane #status predicted <TM2>  
 F/115-136/Domain: transmembrane #status predicted <TM3>  
 F/154-178/Domain: transmembrane #status predicted <TM4>  
 F/208-226/Domain: transmembrane #status predicted <TM5>  
 F/244-265/Domain: transmembrane #status predicted <TM6>  
 F/292-309/Domain: transmembrane #status predicted <TM7>  
 F/14/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F/32-277,113-190/Disulfide bonds: #status predicted

Query Match  
 Best Local Similarity 39.5%; Score 75; DB 2; Length 374;  
 Matches 15; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY 10 YDINYYTSEPCQKINVKQIAARLLPPL 36  
 DB 24 FDYDY--GAPCHKFDVKQIGAQLPPL 48

## RESULT 4

A45177

chemokine (C-C) receptor 1 - human  
 N/Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor  
 C/Species: Homo sapiens (man)  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999  
 R/Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.  
 Cell 72, 415-425, 1993  
 A/Title: Molecular cloning, functional expression, and signaling characteristics of a C-  
 A/Reference number: A45177; MUID:93161416; PMID:7679328  
 A/Accession: A45177  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-355 <NEO>  
 A/Cross-references: GB:L10918; NID:G292416; PIDN:AAA36543.1; PID:G292417  
 A/Experimental source: HL60 cells  
 A/Note: sequence extracted from NCBI backbone (NCBIP:124876)  
 R/Gao, J.  
 J. Exp. Med. 177, 1421-1427, 1993

A;Title: Structure and functional expression of the human macrophage inflammatory 1 alph  
A;Reference number: I55671; MUID:93240122; PMID:7683036  
A;Accession: I55671  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-355 <RES>  
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417  
C;Genetics:  
A;Gene: GDB:CMKBR1; CMKR-1  
A;Cross-references: GDB:138446; OMIM:601159  
A;Map position: 3p21-3p21  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; tr  
F;36-60/Domain: transmembrane #status predicted <TM1>  
F;71-91/Domain: transmembrane #status predicted <TM2>  
F;108-129/Domain: transmembrane #status predicted <TM3>  
F;147-171/Domain: transmembrane #status predicted <TM4>  
F;205-223/Domain: transmembrane #status predicted <TM5>  
F;240-264/Domain: transmembrane #status predicted <TM6>  
F;288-305/Domain: transmembrane #status predicted <TM7>  
F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;24-273,106-183/Disulfide bonds: #status predicted  
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 39.2%; Score 74.5; DB 2; Length 355;  
Best Local Similarity 40.0%; Pred. No. 0.012;  
Matches 14; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

QY 2 DYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36  
Db 9 DYDTT---EFDYGDATPCQKVNERRAFGAQLLPPL 40

RESULT 5  
149339  
macrophage inflammatory protein-1 alpha receptor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999  
C;Accession: I49339  
R;Gao, J.L.; Murphy, P.M.  
J. Biol. Chem. 270, 17494-17501, 1995  
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki  
A;Reference number: I49339; MUID:95340546; PMID:7542241  
A;Accession: I49339  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-355 <RES>  
A;Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548  
C;Superfamily: vertebrate rhodopsin

Query Match 34.2%; Score 65; DB 2; Length 355;  
Best Local Similarity 50.0%; Pred. No. 0.27;  
Matches 13; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 11 DINYYTSBPCQKINVKQIAARLLPPL 36  
Db 15 EFDYGDSTPCQKTAVRAFGAGLLPPL 40

RESULT 6  
149341  
MIP-1 alpha receptor like-2 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 02-Jul-1998  
C;Accession: I49341  
R;Gao, J.L.; Murphy, P.M.  
J. Biol. Chem. 270, 17494-17501, 1995  
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki  
A;Reference number: I49339; MUID:95340546; PMID:7542241  
A;Accession: I49341  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-359 <RES>

A;Cross-references: EMBL:U28406; NID:g881551; PID:g881552  
C;Superfamily: vertebrate rhodopsin

Query Match 34.2%; Score 65; DB 2; Length 359;  
Best Local Similarity 43.5%; Pred. No. 0.27;  
Matches 10; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 14 YTTSEPCQKINVKQIAARLLPPL 36  
Db 22 YEWAPPCEKVRKEIGSWLPPL 44

RESULT 7  
55594  
G protein-coupled receptor E1 - equine herpesvirus 2  
C;Species: equine herpesvirus 2  
C;Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 13-Aug-1999  
C;Accession: 55594  
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.  
J. Mol. Biol. 249, 520-528, 1995  
A;Title: The DNA sequence of equine herpesvirus 2.  
A;Reference number: 55594; MUID:95302501; PMID:7783207  
A;Accession: 55594  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-383 <TEL>  
A;Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor

Query Match 31.1%; Score 59; DB 2; Length 383;  
Best Local Similarity 38.5%; Pred. No. 2;  
Matches 10; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 11 DINYYTSEPCQKINVKQIAARLLPPL 36  
Db 53 DVDYESAPCYKSDYTRLAAQVVPAL 78

RESULT 8  
T20317  
hypothetical protein D1081.6 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T20317  
R;Dobson, R.  
submitted to the EMBL Data Library, July 1996  
A;Reference number: Z19256  
A;Accession: T20317  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-178 <WIL>  
A;Cross-references: EMBL:Z75710; PIDN:CAB00027.1; GSPDB:GN00019; CESP:D1081.6  
A;Experimental source: clone D1081  
C;Genetics:  
A;Gene: CESP:D1081.6  
A;Map position: 1  
A;Introns: 95/3; 114/3

Query Match 30.0%; Score 57; DB 2; Length 178;  
Best Local Similarity 52.9%; Pred. No. 1.7;  
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 YQVSSPIYDINYYTSEP 19  
Db 47 FQVQIPLYDLNITYAPEP 63

RESULT 9  
F84788  
hypothetical protein At2g37110 (imported) - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001



C/Accession: F84788  
R./In, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: F84788  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-242 <STO>  
A/Cross-references: GB:AE002093; NID:94371290; PIDN:AAD18148.1; GSPDB:GN00139  
C/Genetics:  
A/Gene: At2g37110  
A/Map position: 2

Query Match 30.0%; Score 57; DB 2; Length 242;  
Best Local Similarity 38.2%; Pred. No. 2.3;  
Matches 13; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 2 DYQVSSPIYDINYYTSEPCQKINVKQIARLLP 35  
Db 14 EYESSPLLKVNENDGKICSKDAK--AAPLVVP 45

RESULT 10  
A57160  
chemokine (C-C) receptor 4 - human  
N/Alternate names: C-C CKR-4  
C/Species: Homo sapiens (man)  
C/Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 21-Jul-2000  
C/Accession: A57160  
R./Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; W  
J. Biol. Chem. 270, 19495-19500, 1995  
A/Title: Molecular cloning and functional expression of a novel CC chemokine receptor CD  
A/Reference number: A57160; MUID:95370289; PMID:7642634  
A/Accession: A57160  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-360 <POW>  
A/Cross-references: GB:X85740; NID:91370103; PIDN:CAA59743.1; PID:9971452  
A/Note: source clone K5-5  
C/Genetics:  
A/Gene: GDB:CMKBR4  
A/Cross-references: GDB:677463  
A/Map position: 3p21-3p21  
C/Superfamily: vertebrate rhodopsin  
C/Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot  
F/40-65/Domain: transmembrane #status predicted <TM1>  
F/76-97/Domain: transmembrane #status predicted <TM2>  
F/112-133/Domain: transmembrane #status predicted <TM3>  
F/151-175/Domain: transmembrane #status predicted <TM4>  
F/208-226/Domain: transmembrane #status predicted <TM5>  
F/243-264/Domain: transmembrane #status predicted <TM6>  
F/291-308/Domain: transmembrane #status predicted <TM6>  
F/29-276, 110-187/Disulfide bonds: #status predicted <TM7>  
F/72, 350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicte  
F/145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
F/183, 194/Binding site: carboxylate (Asn) (covalent) #status predicted  
F/321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 29.7%; Score 56.5; DB 2; Length 360;  
Best Local Similarity 38.5%; Pred. No. 4.3;  
Matches 15; Conservative 2; Mismatches 17; Indels 5; Gaps 2;

QY 2 DYQVSSPIYDINYYTSE----PCQKINVKQIARLLP 36  
Db 8 DTTLDSEIYS-NYLYESIPKPCCTKEGIKARGELFLP 45

RESULT 11  
B86864  
uracil phosphoribosyltransferase (EC 2.4.2.9) [imported] - Lactococcus lactis subsp. lad

C/Species: Lactococcus lactis subsp. lactis  
C/Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C/Accession: B86864  
R./Bolotin, A.; Wincker, P.; Mauger, S.; Tallon, O.; Malarne, K.; Weissenbach, J.; Eh  
Genome Res. 11, 731-753, 2001  
A/Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis*  
A/Reference number: A86625; MUID:21235186; PMID:11337471  
A/Accession: B86864  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-211 <STO>  
A/Cross-references: GB:AE005176; PID:912724952; PIDN:AAK06012.1; GSPDB:GN00146  
A/Experimental source: strain IL1403  
C/Genetics:  
A/Gene: upp  
C/Superfamily: uracil phosphoribosyltransferase upp  
C/Keywords: glycosyltransferase; pentosyltransferase

Query Match 29.5%; Score 56; DB 2; Length 211;  
Best Local Similarity 45.7%; Pred. No. 2.8;  
Matches 16; Conservative 4; Mismatches 11; Indels 4; Gaps 2;

QY 1 MDYQVSS--PIYDINYYTSEPCQKINVKQIARLL 33  
Db 40 MAYEVSRLDPLEDVEIET--PVQKTVKQIAGKRL 72

RESULT 12  
T40491  
hypothetical protein SPBC4C3.06 - fission yeast (*Schizosaccharomyces pombe*)  
C/Species: Schizosaccharomyces pombe  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C/Accession: T40491  
R./Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A.  
submitted to the EMBL Data Library, February 1998  
A/Reference number: Z21910  
A/Accession: T40491  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-818 <WOO>  
A/Cross-references: EMBL:AL021730; PIDN:CAA16828.1; GSPDB:GN00067; SPDB:SPBC4C3.06  
A/Experimental source: strain 972h-; cosmid c4C3  
C/Genetics:  
A/Gene: SPDB:SPBC4C3.06  
A/Map position: 2  
A/Introns: 14/3

Query Match 29.2%; Score 55.5; DB 2; Length 818;  
Best Local Similarity 41.9%; Pred. No. 15;  
Matches 13; Conservative 8; Mismatches 7; Indels 3; Gaps 2;

QY 4 QVSSPIYD--INYYTSEPCQKINVKQIARL 32  
Db 99 QIASQVYKPLIDYTTSP-QTATLRLAERL 128

RESULT 13  
PT0189  
protein-tyrosine kinase (EC 2.7.1.112) tyro-7 - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 04-Feb-2000  
C/Accession: PT0189  
R./Lai, C.; Lemke, G.  
Neuron 6, 691-704, 1991  
A/Title: An extended family of protein-tyrosine kinase genes differentially expressed in  
A/Reference number: PT0183; MUID:91222560; PMID:2025425  
A/Accession: PT0189  
A/Molecule type: mRNA  
A/Residues: 1-54 <LAI>  
A/Experimental source: sciatic nerve  
C/Genetics:  
A/Gene: tyro-7  
C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

**Keywords:** ATP; phosphotransferase; tyrosine-specific protein kinase C; KeyWords: ATP; phosphotransferase; tyrosine-specific protein kinase F;1-54/Domain: protein kinase homology (fragment) <KIN>

**Job time : 2.62524 secs**

Query Match	28.9%	Score 55;	DB 2;	Length 54;
Best Local Similarity	40.6%	Pred. No. 0.83;		
Matches 13; Conservative	5;	Mismatches 14;	Indels 0;	Gaps 0;

```

QY      2 DYQVSSPIYDINYYTSEPCCKINTKQIAARLL 33
      11 : : : : : : : : : : : : : : : :
      14 DFGLSKKIYNGDYRRQGFPAKMPYKMAIAEST 45
DB

```

## RESULT 14

**D87648**

conserved hypothetical protein CC3222 (imported) - Caulobacter crescentus  
C/Species: Caulobacter crescentus  
C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001  
C/Accession: D87648  
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A/Title: Complete Genome Sequence of Caulobacter crescentus.  
A/Reference number: A87249, MUID:21173698; PMID:11259647  
A/Accession: D87648  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-194 <STO>  
A/Cross-references: GB:AE005673; NID:g13424904; PIDN:AAK25184.1; GSPDB:GN00148  
C/Genetics:  
A/Gene: CC3222

Query Match	28.9%	Score 55;	DB 2;	Length 194;
Best Local Similarity	33.3%	Pred. No. 3.5;		
Matches 13; Conservative	8;	Mismatches 12;	Indels 6;	Gaps 2;

Oy 2 DYQVSSPIYDINYY-----TSEPCQKINVKQIARLLPPL 36  
|| : || : || : : : || ||  
Db 55 DYGIKD--YDVAYHDDSDTSYEADVVIKRVAALAEFPP 91

## RESULT 15

**T29870**

hypothetical protein F32B5.6 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T29870  
R:ledwith, J.; Graves, T.; Biewald, T.  
submitted to the EMBL Data Library, May 1997  
A:Description: The sequence of *C. elegans* cosmid F32B5.  
A:Reference number: Z20702  
A:Accession: T29870  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-503 <LED>  
A:Cross-references: EMBL:AF003148; PIDN:AAB54212.1; GSPDB:GN00019; CESP:F32B5.6  
A:Experimental source: strain Bristol N2; clone F32B5  
C:Genetics:  
A:Gene: CESP:F32B5.6  
A:Map position: 1  
A:Introns: 31/2; 71/1; 210/3; 249/3; 299/3; 358/2; 398/2; 415/1; 453/3  
C:Superfamily: *Caenorhabditis elegans* hypothetical protein F32B5.6

Query Match	28.94;	Score 55;	DB 2;	Length 503;
Best Local Similarity	34.84;	Pred. No. 10;		
Matches	8;	Conservative	8;	Mismatches 7;
			Indels	0;
			Gaps	0;

Qy	14	Y	T	S	E	P	C	O	K	I	N	V	K	Q	I	A	R	L	L	P	L	36
				:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:		
Db	84	Y	K	E	G	P	C	P	E	V	A	E	E	V	R	A	Q	I	L	D	P	106

Search completed: May 13, 2004, 15:08:39

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:01 ; Search time 1.01359 Seconds  
(without alignments)  
1849.388 Million cell updates/sec

Title: US-10-072-301-8  
Perfect score: 190  
Sequence: 1 MDYQVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	190	100.0	352 1 CKR5_HUMAN	P51681 homo sapien
2	185	97.4	352 1 CKR5_PANTR	P56440 pan troglod
3	180	94.7	352 1 CKR5_CERY	Q9tv42 cercopithe
4	180	94.7	352 1 CKR5_CERTO	Q62743 cercocobus
5	180	94.7	352 1 CKR5_HYLSY	Q95nc5 hylobates s
6	180	94.7	352 1 CKR5_MACMU	P79436 macaca mula
7	180	94.7	352 1 CKR5_PAPHA	P56441 papio hamad
8	180	94.7	352 1 CKR5_PONPY	O97881 pongo pygma
9	179	94.2	352 1 CKR5_PYGBI	O97880 pygathrix b
10	179	94.2	352 1 CKR5_PYGBE	O97882 pygathrix n
11	179	94.2	352 1 CKR5_TRAFR	O97878 trachypithe
12	179	94.2	352 1 CKR5_TRAPH	O97879 trachypithe
13	175	92.1	352 1 CKR5_GORGO	P56439 gorilla gor
14	173	91.1	352 1 CKR5_HYLMU	Q95nc0 hylobates m
15	171	90.0	352 1 CKR5_CERAB	P56493 cercopithe
16	170	89.5	352 1 CKR5_HYLB	O97883 hylobates l
17	131	68.9	354 1 CKR5_MOUSE	P51682 mus musculu
18	131	68.9	354 1 CKR5_MOUSE	O08556 rattus norv
19	76.5	40.3	373 1 CKR2_MOUSE	P51683 mus musculu
20	76.5	40.3	373 1 CKR2_MOUSE	O55193 rattus norv
21	75	39.5	360 1 CKR2_MACMU	O18793 macaca mula
22	75	39.5	374 1 CKR2_HUMAN	P41597 homo sapien
23	74.5	39.2	355 1 CKR1_HUMAN	P32246 homo sapien
24	73.5	38.7	355 1 CKR1_MACMU	P56482 macaca mula
25	65	34.2	355 1 CKR1_MOUSE	P51675 mus musculu
26	65	34.2	359 1 CKR3_MOUSE	P51678 mus musculu
27	63	33.2	359 1 CKR3_MOUSE	O54814 rattus norv
28	61	32.1	357 1 CKR3_MOUSE	P51686 homo sapien
29	57	30.0	369 1 CKR9_MOUSE	O9wt7 mus musculu
30	56.5	29.7	360 1 CKR4_HUMAN	P51679 homo sapien
31	56	29.5	211 1 UPP_IACIA	O9cec9 lactococcus
32	56	29.5	211 1 UPP_IACLC	P50926 lactococcus
33	54.5	28.7	137 1 ADF2_ARATH	Q39251 arabidopsis

34	54.5	28.7	139 1 ADF4_ARATH	Q9zsk3 arabidopsis
35	53.5	28.2	139 1 ADF1_PETHY	Q9fv12 petunia hyb
36	53.5	28.2	146 1 ADF6_ARATH	Q9zsk2 arabidopsis
37	53	27.9	143 1 ADF_VITVI	Q8sag3 vitis vinif.
38	53	27.9	358 1 CKR3_CAVPO	Q9z213 cavia porce
39	53	27.9	516 1 YB4F_SCHPO	014360 schizosacch
40	53	27.9	721 1 THIC_SHEON	Q8ed7 shewanella
41	53	27.9	2039 1 CCH1_YEAST	P50077 saccharomyc
42	52	27.4	1162 1 VGL2_IBVK	P12650 avian infec
43	52	27.4	1790 1 LMB1_DROME	P11046 drosophila
44	51.5	27.1	537 1 IL2B_RAT	P26896 rattus norv
45	51	26.8	139 1 ADF1_ARATH	Q39250 arabidopsis

## ALIGNMENTS

RESULT 1  
ID CKR5\_HUMAN STANDARD; PRT; 352 AA.  
AC P51681; 014692; 014693; 014695; 014696; 014697; 014698; 014699;  
AC 014700; 014701; 014702; 014703; 014704; 014705; 014706; 014707;  
AC 014708; 015538; Q9UPA4;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5)  
DE (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).  
GN CCR5 OR CMKRS.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=96241590; PubMed=8639485;  
RX Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;  
RT "Molecular cloning and functional expression of a new human  
RT CC-chemokine receptor gene."  
RL Biochemistry 35:3362-3367(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96291862; PubMed=8663314;  
RA Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;  
RT "Molecular cloning and functional characterization of a novel human  
RT CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha."  
RL J. Biol. Chem. 271:17161-17166(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96295970; PubMed=8699119;  
RA Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;  
RT "Cloning and functional expression of CC CKR5, a human monocyte CC  
RT chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and  
RT RANTES."  
RL J. Leukoc. Biol. 60:147-152(1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,  
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,  
RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell B.,  
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,  
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98001387; PubMed=9343222;  
RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;  
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice  
RT implicate specific amino acids in infections by simian and human  
RT immunodeficiency viruses."  
RL J. Virol. 71:8642-8656(1997).

[6]  
RN SEQUENCE FROM N.A., AND POLYMORPHISMS.  
RX MEDLINE=98022612; PubMed=9359654;  
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,  
RA Ho D.D.;  
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."  
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).  
RN [7]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98049523; PubMed=9388201;  
RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;  
RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts  
RT with 5'-end heterogeneity, dual promoter usage, and evidence for  
RT polymorphisms within the regulatory regions and noncoding exons."  
RL J. Biol. Chem. 272:30662-30671(1997).  
RN [8]  
RP SEQUENCE FROM N.A., AND VARIANT ARG-178.  
RA Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,  
RL Debre P.;  
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP SEQUENCE FROM N.A.  
RX Kopatz S.A., Aronstam R.S., Sharma S.V.;  
RT "cDNA clones of human proteins involved in signal transduction  
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.  
RX MEDLINE=96260017; PubMed=8649511;  
RA Deng H., Liu R., Elmelel W., Choe S., Unutmaz D., Burkhardt M.,  
RA di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,  
RA Pelzer S.C., Schall T.J., Littman D.R., Landau N.R.;  
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RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.  
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RA Paxton W.A.;  
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RT CC-CKR-5."  
RL Nature 381:667-673(1996).  
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RP SULFATION.  
RX MEDLINE=99189752; PubMed=10089882;  
RA Parzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,  
RA Gerard N.P., Gerard C., Sodroski J., Choe H.;  
RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1  
RT entry."  
RL Cell 96:667-676(1999).  
RN  
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
CC MIP-1-beta and rantes and subsequently transduces a signal by  
CC increasing the intracellular calcium ions level. May play a role  
CC in the control of granulocytic lineage proliferation or  
CC differentiation. Acts as co-receptor with CD4 for primary non-  
CC syncytium-inducing strains (NSI) (macrophage-tropic) of HIV-1  
CC virus. It promotes Env-mediated fusion of the virus.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: Found in promyelocytic cells.  
CC -1- PTM: Sulfation contributes to the efficiency of HIV-1 entry.  
CC -1- PTM: Modified by O-linked glycosylation, but not by N-linked  
CC glycosylation.  
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC -----  
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DR EMBL; AF011867; AAB66069.1; -  
DR EMBL; AF011868; AAB66070.1; -  
DR EMBL; AF011869; AAB66071.1; -  
DR EMBL; AF011870; AAB66072.1; -  
DR EMBL; AF011871; AAB66073.1; -  
DR EMBL; AF011872; AAB66074.1; -  
DR EMBL; AF011873; AAB66075.1; -  
DR EMBL; AF011874; AAB66076.1; -  
DR EMBL; AF011875; AAB66077.1; -  
DR EMBL; AF011876; AAB66078.1; -  
DR EMBL; AF011877; AAB66079.1; -  
DR EMBL; AF011878; AAB66080.1; -  
DR EMBL; AF011879; AAB66081.1; -  
DR EMBL; AF011880; AAB66082.1; -  
DR EMBL; AF011881; AAB66083.1; -  
DR EMBL; AF011882; AAB66084.1; -  
DR EMBL; AF011883; AAB66085.1; -  
DR EMBL; AF011884; AAB66086.1; -  
DR EMBL; AF011885; AAB66087.1; -  
DR EMBL; AF011886; AAB66088.1; -  
DR EMBL; AF011887; AAB66089.1; -  
DR EMBL; AF011888; AAB66090.1; -  
DR EMBL; AF011889; AAB66091.1; -  
DR EMBL; AF011890; AAB66092.1; -  
DR EMBL; AF011891; AAB66093.1; -  
DR EMBL; AF011892; AAB66094.1; -  
DR EMBL; AF011893; AAB66095.1; -  
DR EMBL; AF011894; AAB66096.1; -  
DR EMBL; AF011895; AAB66097.1; -  
DR EMBL; AF011896; AAB66098.1; -  
DR EMB



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Query Match      100.0%; Score 190; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.9e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 MDYQVSSPIYDINITYTSEPCQKINVKQIAARLLPPL 36
      |||
Db      1 MDYQVSSPIYDINITYTSEPCQKINVKQIAARLLPPL 36

RESULT 2
ID_CKRS_PANTR STANDARD; PRT; 352 AA.
AC P56440; O02778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Zimmerman P.A., Buckler-White A., Alkhatib G.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97426118; PubMed=9282822;
RA Zacharova V., Zachar V., Goustin A.S.;
RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
RT HIV type 1 host.";
RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=98090115; PubMed=9430250;
RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
RN [6]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny.";
RN Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF005663; AAB62557.1; -.
DR EMBL; U94329; AAB58446.1; -.
DR EMBL; AF011542; AAB65742.1; -.
DR EMBL; U97666; AAC51670.1; -.
DR EMBL; AF011540; AAB65740.1; -.
DR EMBL; U89797; AAC03717.1; -.
DR EMBL; AF177894; AAK43377.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPE_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPE_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 123 123 T -> S (IN REF. 1).
SQ SEQUENCE 352 AA; 40539 MW; 4A33E698B80F334C CRC64;

Query Match      97.4%; Score 185; DB 1; Length 352;
Best Local Similarity 97.2%; Pred. No. 2.5e-18;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      1 MDYQVSSPIYDINITYTSEPCQKINVKQIAARLLPPL 36
      |||
Db      1 MDYQVSSPIYDINITYTSEPCQKINVKQIAARLLPPL 36

RESULT 3
ID_CKRS_CERPY STANDARD; PRT; 352 AA.
AC Q9TV42;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Cercopithecus pygerythrus (Vervet monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=60710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=100;
RX MEDLINE=99335215; PubMed=10408730;
RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C.,
RA Diop O., Rigoulet J., Barre-Sinoussi F., Ponsgaard A.;
RT "Mutations in CCR5-coding sequences are not associated with SIV
RT carrier status in African nonhuman primates.";
```

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RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF035222; AAD44015.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40558 MW; EF17D67CBCC3DB0 CRC64;

Query Match
Best Local Similarity 94.7%; Score 180; DB 1; Length 352;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36
Db 1 MDYQVSSPTDYDIDYTTSEPCQKINVKQIAARLLPPL 36

RESULT 4
CKRS_CERTO STANDARD; PRT; 352 AA.
AC 062743; 062744; 062745; 062746;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercocebus.
OX NCBI_TaxId=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate 079, 085, 087, and 089;
RX MEDLINE=98321155; PubMed=9656999;
RA Chen Z., Gettle A., Ho D.D., Marx P.A.;
```

```
RT "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys
RT naturally infected in west Africa: a comparison of coreceptor usage
RT of primary SIVsm, HIV-2, and SIVmac."
RL Virology 246:113-124(1998).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF051902; AAC39830.1; -
DR EMBL; AF051903; AAC39831.1; -
DR EMBL; AF051904; AAC39832.1; -
DR EMBL; AF051905; AAC39833.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT VARIANT 2 2 D -> E (IN ISOLATE 087).
FT VARIANT 3 3 Y -> D (IN ISOLATE 079).
FT VARIANT 25 25 V -> G (IN ISOLATE 087).
FT VARIANT 100 100 M -> K (IN ISOLATE 079).
FT VARIANT 107 107 L -> V (IN ISOLATE 089).
FT VARIANT 134 134 V -> G (IN ISOLATE 079).
FT VARIANT 146 146 V -> L (IN ISOLATES 085 AND 089).
FT VARIANT 340 340 T -> I (IN ISOLATE 079).
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;

Query Match
Best Local Similarity 94.7%; Score 180; DB 1; Length 352;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36
Db 1 MDYQVSSPTDYDIDYTTSEPCQKINVKQIAARLLPPL 36

RESULT 5
CKRS_HYLSY STANDARD; PRT; 352 AA.
AC 095NC5;
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DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CCR-5) (CCR-5) (CCRS)
GN CCR5 OR CMKBR5.
OS Hylobates syndactylus (Simang) (Symphalangus syndactylus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9590;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF177884; AAK43367.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_REC_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_REC_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;

Query Match 94.7%; Score 180; DB 1; Length 352;
Best Local Similarity 94.4%; Pred. No. 1.2e-17;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSEPCOKINVKQIAARLPL 36
Db 1 MDYQVSSPTYDIDYTTSEPCOKINVKQIAARLPL 36

RESULT 6
ID CKR5_MACMU STANDARD; PRT; 352 AA.
AC P79436; O02746;
DT 01-NOV-1997 (Rel. 35, Created)
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DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CCR-5) (CCR-5) (CCRS).
GN CCR5 OR CMKBR5.
OS Macaca mulatta (Rhesus macaque),
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544, 9541, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RX SPECIES=M.mulatta;
RX MEDLINE=97184592; PubMed=9032394;
RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
RA Newman W., Gerard N., Gerard C., Sodroski J.;
RT "Utilization of C-C chemokine receptor 5 by the envelope
RT glycoproteins of a pathogenic simian immunodeficiency virus,
RT SIVmac239.";
RL J. Virol. 71:2522-2527(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX SPECIES=M.mulatta; STRAIN=Indian macaque;
RX MEDLINE=97213934; PubMed=9060623;
RA Chen Z., Zhou P., Ho D.D., Jandau N.R., Marx P.A.;
RT "Genetically divergent strains of simian immunodeficiency virus use
RT CCR5 as a coreceptor for entry.";
RL J. Virol. 71:2705-2714(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX SPECIES=M.mulatta;
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors.";
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amodee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U77672; AAC51109.1; -.
DR EMBL; U73739; AAC51158.1; -.
DR EMBL; U96762; AAC34132.1; -.
DR EMBL; AF005660; AAB62554.1; -.
DR EMBL; AF005661; AAB62555.1; -.
DR EMBL; AF005662; AAB62556.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_REC_F1_1; 1.
```



DR PROSITE; PS50262; G-PROTEIN RECEPTOR\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 31 58 1 (POTENTIAL).  
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 69 89 2 (POTENTIAL).  
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 103 124 3 (POTENTIAL).  
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 142 166 4 (POTENTIAL).  
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 199 218 5 (POTENTIAL).  
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 236 260 6 (POTENTIAL).  
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 278 301 7 (POTENTIAL).  
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 101 178 BY SIMILARITY.  
FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 241 241 M -> I (IN REF. 3).  
FT CONFLICT 292 292 I -> M (IN REF. 3).  
SQ SEQUENCE 352 AA; 40507 MW; 58B96C85909FACB2 CRC64;

Query Match 94.7%; Score 180; DB 1; Length 352;  
Best Local Similarity 94.4%; Pred. No. 1.2e-17;  
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCCKINVKQIARLLPPL 36  
Db 1 MDYQVSSPTDYDIDYTTSEPCCKINVKQIARLLPPL 36

RESULT 7  
CKRS\_PAPHA STANDARD; PRT; 352 AA.  
AC P56441;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE C-C chemokine receptor type 5 (C-C-CCR-5) (CCR-5) (CCR5).  
GN CCR5 OR CMKBR5.  
OS Papio hamadryas (Hamadryas baboon), and  
OS Papio anubis (Olive baboon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Papio.  
OX NCBI\_TaxID=9557, 9555;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=P.hamadryas;  
RX MEDLINE=97268687; PubMed=9108095;  
RA Edinger A.L., Amodee A., Miller K., Doranz B.J., Endres M.,  
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,  
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;  
RT "Differential utilization of CCR5 by macrophage and T cell tropic  
RT simian immunodeficiency virus strains.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES=P.hamadryas;  
RX MEDLINE=99210133; PubMed=10195758;  
RA Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;  
RT "Species-specific changes in the CCR5 gene from African and Asian  
RT nonhuman primates.";  
RL AIDS Res. Hum. Retroviruses 15:479-483(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES=P.anubis;  
RA Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;

RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
CC MIP-1-beta and RANTES and subsequently transduces a signal by  
CC increasing the intracellular calcium ions level. May play a role  
CC in the control of granulocytic lineage proliferation or  
CC differentiation.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF005658; AAB62552.1; -  
DR EMBL; AF105287; AAD20556.1; -  
DR EMBL; AF105288; AAD20557.1; -  
DR EMBL; AF105289; AAD20558.1; -  
DR EMBL; AF105290; AAD20559.1; -  
DR EMBL; AF023452; AAC63830.1; -  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_HODOPSIN.  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR\_F1\_1; 1.  
DR PROSITE; PS50262; G-PROTEIN RECEPTOR\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 31 58 1 (POTENTIAL).  
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 69 89 2 (POTENTIAL).  
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 103 124 3 (POTENTIAL).  
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 142 166 4 (POTENTIAL).  
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 199 218 5 (POTENTIAL).  
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 236 260 6 (POTENTIAL).  
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 278 301 7 (POTENTIAL).  
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 101 178 BY SIMILARITY.  
FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 352 AA; 40489 MW; 5E1504A9BA1FE8B2 CRC64;

Query Match 94.7%; Score 180; DB 1; Length 352;  
Best Local Similarity 94.4%; Pred. No. 1.2e-17;  
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCCKINVKQIARLLPPL 36  
Db 1 MDYQVSSPTDYDIDYTTSEPCCKINVKQIARLLPPL 36

RESULT 8  
CKRS\_PONPY STANDARD; PRT; 352 AA.  
AC O97881;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE C-C chemokine receptor type 5 (C-C-CCR-5) (CCR-5) (CCR5).  
GN CCR5 OR CMKBR5.  
OS Pongo pygmaeus (Orangutan).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.

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OX NCBI_TaxID=96600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
DR EMBL; AF075446; AAD19858.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;

Query Match 94.7%; Score 180; DB 1; Length 352;
Best Local Similarity 94.4%; Pred. No. 1.2e-17;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36
Db 1 MDYQVSSPTYDIDYTTSEPCQKINVKQIAARLLPPL 36

RESULT 9
CKR5_PYGBI STANDARD; PRT; 352 AA.
ID CKR5_PYGBI
AC O97880;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
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OC Pygathrix.
OX NCBI_TaxID=61621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF075445; AAD19857.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;

Query Match 94.2%; Score 179; DB 1; Length 352;
Best Local Similarity 91.7%; Pred. No. 1.7e-17;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSEPCQKINVKQIAARLLPPL 36
Db 1 MDYQVSSPTYDIDYTTSEPCQKINVKQIAARLLPPL 36

RESULT 10
CKR5_PYGBI STANDARD; PRT; 352 AA.
ID CKR5_PYGBI
AC O97882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-----
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-----
DR EMBL; AF075448; AAD19860.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_HODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40532 MW; F84F9D98D3B3E861 CRC64;

Query Match
Best Local Similarity 94.2%; Score 179; DB 1; Length 352;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36
DB 1 MDYQVSSPTDYDIDYTTSEPCQKVNKQIAARLLPPL 36

RESULT 11
CKR5_TRAFR
ID CKR5_TRAFR STANDARD; PRT; 352 AA.
AC 097878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN Trachypithecus francoisi (Francois' langur) (Indochinese langur).
```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=54180;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-----
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-----
DR EMBL; AF075442; AAD19854.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_HODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40496 MW; 4366F148C255938F CRC64;

Query Match
Best Local Similarity 94.2%; Score 179; DB 1; Length 352;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36
DB 1 MDYQVSSPTDYDIDYTTSEPCQKVNKQIAARLLPPL 36

RESULT 12
CKR5_TRAPH
ID CKR5_TRAPH STANDARD; PRT; 352 AA.
AC 097879;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN Trachypithecus francoisi (Francois' langur) (Indochinese langur).
```

```
OS Trachypithecus phayrei (Phayre's leaf monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=61618;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
DR EMBL; AF075443; AAD19855.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40509 MW; 4366F148D3A5938F CRC64;

Query Match 94.2%; Score 179; DB 1; Length 352;
Best Local Similarity 91.7%; Pred. No. 1.7e-17;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPTIDINYTSEPCQKINVKQIAARLPL 36
Db 1 MDYQVSSPTIDIDYITSEPCQKVNKQIAARLPL 36

RESULT 13
CKR5_GORGO STANDARD; PRT; 352 AA.
AC P56439;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DB C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
```

```
GN CCR5 OR CCR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF005659; AAB62553.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9FE5EAC84 CRC64;

Query Match 92.1%; Score 175; DB 1; Length 352;
Best Local Similarity 91.7%; Pred. No. 6.1e-17;
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDYQVSSPTIDINYTSEPCQKINVKQIAARLPL 36
Db 1 MDYQVSSPTIDIDYITSEPCQKTNVKQIAARLPL 36

RESULT 14
CKR5_HYML STANDARD; PRT; 352 AA.
AC Q95NC0;
DT 15-MAR-2004 (Rel. 43, Created)
```

```

DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Hylobates moloch (Silvery gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=81572;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF177899; AAK43382.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1, 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR;
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 SULFATION (BY SIMILARITY).
FT MOD_RES 14 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;

Query Match 91.1%; Score 173; DB 1; Length 352;
Best Local Similarity 91.7%; Pred. No. 1.2e-16;
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDYQVSSPIVDINYYTSEPCQKINVKQIARLLPPL 36
Db 1 MDYQVSSPTDYDIDYTTSGPCQKINVKQIARLLPPL 36

RESULT 15
ID _CKR5 CERAE STANDARD; PRT; 352 AA.
AC P56493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CCR-5) (CC-CCR-5) (CCR-5) (CCR5).
GN CCR5 OR CCR5R5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT "cDNA sequence of African green monkey CCR-5 chemokine receptor
RT gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U83324; AAC51795.1; -.
DR EMBL; U83325; AAC51796.1; -.
DR EMBL; AB015944; BAA31328.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHRHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW Polymorphism.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 CYTOPLASMIC (POTENTIAL).
FT MOD_RES 3 3 BY SIMILARITY.
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT VARIANT 14 14 SULFATION (BY SIMILARITY).
FT VARIANT 352 352 N -> Y.
FT VARIANT 352 352 F -> L.
SQ SEQUENCE 352 AA; 40561 MW; 7F52E690C72BC29A CRC64;
Query Match 90.0%; Score 171; DB 1; Length 352;

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Mon May 17 11:04:01 2004

us-10-072-301-8.rsp

Page 11

Best Local Similarity 91.7%; Pred. No. 2.2e-16;  
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

**Oy**      1 MDYQVSSPIYDINITYTSECCQIKNVKQIAARLLPPL 36  
         ||||| : |||||  
**Db**      1 MDYQVSSPTYDIDNNTSECCQIKNVKQIAARLLPPL 36

Search completed: May 13, 2004, 15:02:03  
Job time : 2.01359 secs

NOISE BLANK (USPTO)



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:31 ; Search time 4.84078 Seconds  
(without alignments)  
2346.453 Million cell updates/sec

Title: US-10-072-301-8  
Perfect score: 190  
Sequence: 1 MDYQVSSPIYDINYTSEPCOKINVKQIARLLPPL 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	190	100.0	215	4	075303	075303 homo sapien
2	185	97.4	352	6	Q95NC3	Q95nc3 miopithecus
3	185	97.4	352	6	018771	018771 pan troglod
4	185	97.4	352	6	018772	018772 pan troglod
5	185	97.4	352	6	Q9TQX0	Q9tqx0 cercopithec
6	180	94.7	344	6	Q9TQR8	Q9tqr8 cercocobus
7	180	94.7	344	6	077833	077833 cercocobus
8	180	94.7	352	6	Q9TSK1	Q9tsk1 cercopithec
9	180	94.7	352	6	Q95NC5	Q95nc5 hylobates s
10	180	94.7	352	6	Q9TV48	Q9tv48 cercopithec
11	180	94.7	352	6	Q9TV49	Q9tv49 cercocobus
12	180	94.7	352	6	Q9XT76	Q9xt76 cercopithec
13	180	94.7	352	6	018770	018770 pan troglod
14	180	94.7	352	6	Q9TV44	Q9tv44 cercopithec
15	180	94.7	352	6	Q97975	Q97975 macaca arct
16	180	94.7	352	6	Q9XT12	Q9xt12 cercopithec

17	180	94.7	352	6	Q9TV42	Q9tv42 cercopithec
18	180	94.7	352	6	Q9XT13	Q9xt13 papio anubi
19	180	94.7	352	6	Q95ND2	Q95nd2 mandrillus
20	180	94.7	352	6	077776	077776 cercocobus
21	180	94.7	352	6	Q9TV46	Q9tv46 cercopithec
22	180	94.7	352	6	Q9MZA2	Q9mza2 cercopithec
23	180	94.7	352	6	Q9TV50	Q9tv50 pan troglod
24	180	94.7	352	6	Q95NE1	Q95ne1 cercocobus
25	180	94.7	352	6	Q95ND0	Q95nd0 erythrocebu
26	180	94.7	352	6	Q95NE8	Q95ne8 cercopithec
27	179	94.2	352	6	Q9XT14	Q9xt14 colobus gue
28	179	94.2	352	6	Q95NC6	Q95nc6 trachypithe
29	179	94.2	352	6	Q95NC8	Q95nc8 colobus pol
30	179	94.2	352	6	Q95NC7	Q95nc7 nasalis lar
31	179	94.2	352	6	Q97962	Q97962 pygathrix a
32	176	92.6	352	6	Q95NC1	Q95nc1 theropithec
33	175	92.1	352	6	Q9XS35	Q9xs35 macaca neme
34	175	92.1	352	6	Q9TV93	Q9tv93 macaca arct
35	175	92.1	352	6	Q95ND1	Q95nd1 mandrillus
36	175	92.1	352	6	Q9XS99	Q9xs99 gorilla gor
37	174	91.6	352	6	Q9TV43	Q9tv43 cercopithec
38	173	91.1	352	6	Q95NC0	Q95nc0 hylobates m
39	173	91.1	352	6	Q9MZA3	Q9mza3 hylobates a
40	171	90.0	352	6	Q9BGN5	Q9bgn5 cercopithec
41	171	90.0	352	6	Q9BGN6	Q9bgn6 cercopithec
42	170	89.5	352	6	Q9TSQ7	Q9tsq7 cercopithec
43	170	89.5	352	6	Q9TV45	Q9tv45 cercopithec
44	161	84.7	352	6	Q9TV47	Q9tv47 cercopithec
45	155	81.6	339	4	Q9UN26	Q9un26 homo sapien

ALIGNMENTS

RESULT 1						
ID	075303	PRELIMINARY;	PRT;	215	AA.	
AC	075303;					
DT	01-NOV-1998 (TREMBLrel. 08, Created)					
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)					
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)					
DE	CC-chemokine receptor.					
GN	CCR-5.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Butheria; Primates; Catarrhini; Homiidae; Homo.					
OX	NCBI_Taxid=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Tse L., Ehrenberg P.K., Chang G., Michael N.L.;					
RT	"Genomic Organization and Functional Characterization of the Complete					
RT	Transcription Unit for the Chemokine Receptor CCR-5, a Major Entry Co-					
RT	Receptor for HIV-1."					
RL	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.					
DR	EMBL; AF009962; AAC23944.1; -.					
DR	GO; GO:0016021; C:integral to membrane; IEA.					
DR	GO; GO:0004872; F:receptor activity; IEA.					
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.					
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.					
DR	InterPro; IPR000276; GPCR_Rhodpsn.					
DR	Pfam; PF00001; 7tm_1; 1.					
DR	PRINTS; PR00237; GPCR_RHODPSN.					
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.					
DR	PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.					
KW	Receptor.					
SQ	SEQUENCE 215 AA; 23946 MW; 3C9146C76BA416F7 CRC64;					
Query Match 100.0%; Score 190; DB 4; Length 215;						
Best Local Similarity 100.0%; Pred. No. 1.3e-19;						
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
OY	1 MDYQVSSPIYDINYTSEPCOKINVKQIARLLPPL 36					

Db 1 MDYQVSSPIYDINYTSEPCQKINVKQIARLLPPL 36

## RESULT 2

Q95NC3

AC Q95NC3; PRELIMINARY; PRT; 352 AA.

DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE C-C chemokine receptor 5.  
GN CCR5.

OS Miopithecus talapoin (Talapoin) (Cercopithecus talapoin).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Miopithecus.  
OX NCBI\_TaxID=36231;  
RN [1]

RP SEQUENCE FROM N.A.

RA Zhang Y., Ryder O.A., Zhang Y.

RT "Sequence comparison of the CCR5 gene in primates and primate phylogeny."

RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF177886; AAK43369.1; -  
DR GO; GO:016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PRO0237; GPCR\_RHODOPSN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.

KW Receptor.  
SQ SEQUENCE 352 AA; 40546 MW; 6464152F3E566AE5 CRC64;

## Query Match

Best Local Similarity 97.4%; Score 185; DB 6; Length 352;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MDYQVSSPIYDINYTSEPCQKINVKQIARLLPPL 36  
Db 1 MDYQVSSPTDYDINYTSEPCQKINVKQIARLLPPL 36  
|||||  
1 MDYQVSSPTDYDINYTSEPCQKINVKQIARLLPPL 36

## RESULT 3

018771

ID 018771; PRELIMINARY; PRT; 352 AA.

DT 01-JAN-1998 (TReMBLrel. 05, Created)  
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE CCR5 receptor (Fragment).  
GN CCR5.

OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ChCCR5-141a;

RA Zhang L., Caruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,  
Ho D.D.;

RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism."  
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).

DR EMBL; AF011539; AAB65739.1; -  
DR GO; GO:016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PRO0237; GPCR\_RHODOPSN.

DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
FT NON\_TER  
SQ SEQUENCE 352 AA; 40466 MW; 3FFFACT7ABAE1D4FB CRC64;

Query Match  
Best Local Similarity 97.4%; Score 185; DB 6; Length 352;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDYQVSSPIYDINYTSEPCQKINVKQIARLLPPL 36  
Db 1 MDYQVSSPIYDIDYITSEPCQKINVKQIARLLPPL 36  
|||||  
1 MDYQVSSPIYDIDYITSEPCQKINVKQIARLLPPL 36

## RESULT 4

018772

ID 018772; PRELIMINARY; PRT; 352 AA.

DT 01-JAN-1998 (TReMBLrel. 05, Created)  
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE CCR5 receptor (Fragment).  
GN CCR5.

OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ChCCR5-142a;

RA Zhang L., Caruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,  
Ho D.D.;

RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism."  
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).

DR EMBL; AF011541; AAB65741.1; -  
DR GO; GO:016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PRO0237; GPCR\_RHODOPSN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.

FT NON\_TER  
SQ SEQUENCE 352 AA; 40598 MW; 39688FA7004C952F CRC64;

Query Match  
Best Local Similarity 97.4%; Score 185; DB 6; Length 352;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDYQVSSPIYDINYTSEPCQKINVKQIARLLPPL 36  
Db 1 MDYQVSSPIYDIDYITSEPCQKINVKQIARLLPPL 36  
|||||  
1 MDYQVSSPIYDIDYITSEPCQKINVKQIARLLPPL 36

## RESULT 5

09TQX0

ID 09TQX0; PRELIMINARY; PRT; 352 AA.

DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE CC chemokine receptor 5.  
GN CCR5.

OS Cercopithecus aethiops (Green monkey) (Grivet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=9534;  
RN [1]





OS Cercopithecus aethiops (Green monkey) (Grivet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=9534;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Holkamp N., Baier M., Werner A.;  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF019379; AAD01639.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro; IPR00276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 352 AA; 40588 MW; 0F1869D9A6668DBB CRC64;

Query Match  
Best Local Similarity 94.7%; Score 180; DB 6; Length 352;  
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSBPCQKINVKQIAARLLPPL 36  
Db 1 MDYQVSSPTDYDIDYTSBPCQKINVKQIAARLLPPL 36

RESULT 9  
Q95NC5 PRELIMINARY; PRT; 352 AA.  
AC Q95NC5;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE C-C chemokine receptor 5.  
GN CCR5.  
OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
OX NCBI\_TaxID=9590;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zhang Y., Ryder O.A., Zhang Y.;  
RT "Sequence comparison of the CCR5 gene in primates and primate  
RT phylogeny."  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF177884; AAK43367.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro; IPR00276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;

Query Match  
Best Local Similarity 94.7%; Score 180; DB 6; Length 352;  
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSBPCQKINVKQIAARLLPPL 36  
Db 1 MDYQVSSPTDYDIDYTSBPCQKINVKQIAARLLPPL 36

RESULT 10  
Q9TV48

ID Q9TV48 PRELIMINARY; PRT; 352 AA.  
AC Q9TV48;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE CC chemokine receptor type 5.  
GN CCR5.  
OS Cercopithecus aethiops (black-cheeked white-nosed monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=36223;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mueller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,  
RC STRAIN=52;  
RX MEDLINE=99335215; PubMed=10408730;  
RA Mueller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,  
RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;  
RT "Mutations in CCR5-coding sequences are not associated with SIV  
RT carrier status in African nonhuman primates."  
RL AIDS Res. Hum. Retroviruses 15:931-939(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Mueller-Trutwin M.C., Corbet S., Hansen J., Diop O.,  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF035216; AAD44009.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro; IPR00276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 352 AA; 40650 MW; 7906256AA3945266 CRC64;

Query Match  
Best Local Similarity 94.7%; Score 180; DB 6; Length 352;  
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSBPCQKINVKQIAARLLPPL 36  
Db 1 MDYQVSSPTDYDIDYTSBPCQKINVKQIAARLLPPL 36

RESULT 11  
Q9TV49 PRELIMINARY; PRT; 352 AA.  
AC Q9TV49;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE CC chemokine receptor type 5 (C-C chemokine receptor 5).  
GN CCR5.  
OS Cercopithecus galeritus (Agile mangabey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=9532;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=4;  
RX MEDLINE=99335215; PubMed=10408730;  
RA Mueller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,  
RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;  
RT "Mutations in CCR5-coding sequences are not associated with SIV  
RT carrier status in African nonhuman primates."  
RL AIDS Res. Hum. Retroviruses 15:931-939(1999).  
RN [2]

```
RP SEQUENCE FROM N.A.
RC STRAIN=4;
RA Mueller-Trutwin M.C., Corbet S., Hansen J., Diop O.,
RA Georges-Courbot M.-C., Barre-Sinoussi F., Fomsgaard A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF035215; AAD44008.1; -.
DR EMBL; AF177898; AAK43381.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40479 MW; 5E1504A9B87278B2 CRC64;

Query Match          94.7%; Score 180; DB 6; Length 352;
Best Local Similarity 94.4%; Pred. No. 6.4e-18;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36
Db 1 MDYQVSSPTYDIDYITSEPCQKINVKQIAARLLPPL 36

RESULT 12
O9XT76 PRELIMINARY; PRT; 352 AA.
AC O9XT76;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE CC chemokine receptor type 5.
GN CCR5.
OS Cercopithecus lhoesti (L'Hoeest's monkey), and
OS Cercopithecus preussi.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=100224, 147649;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=C.lhoesti;
RX MEDLINE=99335215; PubMed=10408730;
RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,
RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
RT "Mutations in CCR5-coding sequences are not associated with SIV
RT carrier status in African nonhuman primates."
RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=C.preussi;
RA Beer B.E., Kulkarni C.L., Bailes E., Korber B., Sharp P.M., Hirsch V.M.;
RT "Phylogeny and cross-species transmission of simian and human
RT immunodeficiency viruses."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF081579; AAD45497.1; -.
DR EMBL; AF212102; AAG53467.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
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DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40408 MW; 2D354E5128C779E0 CRC64;

Query Match          94.7%; Score 180; DB 6; Length 352;
Best Local Similarity 94.4%; Pred. No. 6.4e-18;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36
Db 1 MDYQVSSPTYDIDYITSEPCQKINVKQIAARLLPPL 36

RESULT 13
O18770 PRELIMINARY; PRT; 352 AA.
ID O18770;
AC O18770;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE CCR5 receptor (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MACCR5-140a;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism."
RT AIDS Res. Hum. Retroviruses 0:0-0(1997).
RL EMBL; AF011538; AAB65738.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 352 AA; 40523 MW; 4513DB983A28ACB2 CRC64;

Query Match          94.7%; Score 180; DB 6; Length 352;
Best Local Similarity 94.4%; Pred. No. 6.4e-18;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL 36
Db 1 MDYQVSSPTYDIDYITSEPCQKINVKQIAARLLPPL 36

RESULT 14
O9TV44 PRELIMINARY; PRT; 352 AA.
ID O9TV44;
AC O9TV44;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE CC chemokine receptor type 5.
GN CCR5.
OS Cercopithecus patas.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=27677;
RN [1]
```



RP SEQUENCE FROM N.A.  
RC STRAIN=04;  
RX MEDLINE=99335215; Pubmed=10408730;  
RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,  
RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;  
RT "Mutations in CCR5-coding sequences are not associated with SIV  
RT carrier status in African nonhuman primates."; AIDS Res. Hum. Retroviruses 15:931-939(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=04;  
RA Mueller-Trutwin M.C., Corbet S., Hansen J., Diop O.,  
RA Georges-Courbot M.C., Barre-Sinoussi F., Fomsgaard A.;  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF035220; AAD44013.1; -  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCR\_RHODOPSN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 352 AA; 40747 MW; 3A56E90D3528D94C CRC64;  
  
Query Match 94.7%; Score 180; DB 6; Length 352;  
Best Local Similarity 94.4%; Pred. No. 6.4e-18;  
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MDYQVSSPIYDINYYTSEPCOKINVKQIAARLLPPL 36  
|||:|||||  
Db 1 MDYQVSSPTYDIDYTTSEPCOKINVKQIAARLLPPL 36  
  
RESULT 15  
O97975 PRELIMINARY; PRT; 352 AA.  
ID O97975;  
AC O97975;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE C-C chemokine receptor type 5.  
GN CCR5.  
OS Macaca arctoides (Stump-tailed macaque), and  
OS Macaca assamensis (Assam's macaque) (Assam's monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9540, 9551;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zhang Y.-W., Zhang Y.-P.;  
RT "Sequence evolution of chemokine receptor CCR5 gene in primates.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF075450; AAD19862.1; -  
DR EMBL; AF075449; AAD19861.1; -  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCR\_RHODOPSN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 352 AA; 40521 MW; 5F276C85909FACB2 CRC64;  
  
Query Match 94.7%; Score 180; DB 6; Length 352;  
Best Local Similarity 94.4%; Pred. No. 6.4e-18;  
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCOKINVKQIAARLLPPL 36  
|||:|||||  
Db 1 MDYQVSSPTYDIDYTTSEPCOKINVKQIAARLLPPL 36

Search completed: May 13, 2004, 15:06:53  
Job time : 5.84078 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:48:56 ; Search time 52.0738 Seconds  
(without alignments)  
1372.754 Million cell updates/sec

Title: US-10-072-301-17

Perfect score: 1351  
Sequence: 1 QVTLKESGPTLVKPTQTLTL.....CQAMDSTAVFGTGTKLTVL 253

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1:	geneseqp19808:*
2:	geneseqp19908:*
3:	geneseqp20008:*
4:	geneseqp20018:*
5:	geneseqp20028:*
6:	geneseqp20038:*
7:	geneseqp2003bs:*
8:	geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	788.5	58.4	245	4	AAB67620	Aab67620 Human leu
2	783	58.0	250	5	ABP45537	Abp45537 Human Bly
3	779.5	57.7	247	5	ABP45640	Abp45640 Human Bly
4	771.5	57.1	249	6	AAB36257	Aae36257 TRAIL rec
5	756.5	56.0	245	4	AAB67621	Aab67621 Human leu
6	753.5	55.8	245	4	AAB67622	Aab67622 Human leu
7	753	55.7	237	6	ABR62332	Abrc62332 Anti-EBV
8	752.5	55.7	245	4	AAB67623	Aab67623 Human leu
9	752.5	55.7	280	4	AAE02186	Aae02186 PAM2 sing
10	751.5	55.6	245	4	AAB67619	Aab67619 Human leu
11	747	55.3	254	5	ABP45955	Abp45955 Human Bly
12	742	54.9	250	5	ABP45469	Abp45469 Human Bly
13	736	54.5	256	5	ABP45596	Abp45596 Human Bly
14	734.5	54.4	251	5	ABP44979	Abp44979 Human Bly
15	733	54.3	252	5	ABP45318	Abp45318 Human Bly
16	732.5	54.2	245	4	AAB67617	Aab67617 Human leu
17	731	54.1	254	5	ABP44833	Abp44833 Human Bly
18	730	54.0	252	6	ABJ19827	Abj19827 Human VEG
19	729.5	54.0	245	4	AAB67618	Aab67618 Human leu
20	728.5	53.9	247	5	ABP45007	Abp45007 Human Bly
21	723.5	53.6	251	5	ABP45305	Abp45305 Human Bly
22	723.5	53.6	253	5	ABP45608	Abp45608 Human Bly
23	722.5	53.5	251	5	ABP44941	Abp44941 Human Bly
24	721.5	53.4	255	5	ABP44830	Abp44830 Human Bly
25	721	53.4	248	5	ABP45984	Abp45984 Human Bly

26	719.5	53.3	249	5	ABP45714	Abp45714 Human Bly
27	718.5	53.2	249	5	ABP45713	Abp45713 Human Bly
28	718.5	53.2	251	5	ABP45527	Abp45527 Human Bly
29	718	53.1	244	5	ABP45831	Abp45831 Human Bly
30	717	53.1	244	2	AAy06718	Aay06718 Antibody
31	717	53.1	266	5	ABG97835	Abg97835 Single ch
32	717	53.1	266	5	ABG35336	Abg35336 Thrombopo
33	716.5	53.0	253	5	ABP45491	Abp45491 Human Bly
34	716	53.0	254	5	ABP45648	Abp45648 Human Bly
35	715.5	53.0	249	5	ABP45104	Abp45104 Human Bly
36	715.5	53.0	249	5	ABP45991	Abp45991 Human Bly
37	715.5	53.0	251	5	ABP44971	Abp44971 Human Bly
38	715	52.9	234	6	ABR62333	Abrc62333 Anti-EBV
39	714.5	52.9	247	5	ABP45459	Abp45459 Human Bly
40	714.5	52.9	247	5	ABP45195	Abp45195 Human Bly
41	714.5	52.9	253	5	ABP44927	Abp44927 Human Bly
42	712.5	52.7	247	5	ABP45311	Abp45311 Human Bly
43	711	52.6	250	5	ABP44982	Abp44982 Human Bly
44	710.5	52.6	249	5	ABP44946	Abp44946 Human Bly
45	710	52.6	246	3	AAy15126	Aay15126 Anti-muri

ALIGNMENTS

RESULT 1  
AAB67620 ID AAB67620 standard; protein; 245 AA.  
AC AAB67620;  
DT 29-MAY-2001 (first entry)  
DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6\_4.  
KW Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing; miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.  
OS Homo sapiens.  
PN WO200114558-A1.  
PD 01-MAR-2001.  
PF 28-AUG-2000; 2000WO-EP008388.  
PR 26-AUG-1999; 99EP-00116691.  
PA (MORP-) MORPHOSYS AG.  
PI Kretzschmar T, Tesar M, Marget M, Kroenke M;  
DR WPI; 2001-218451/22.  
XX Novel isolated human immunoglobulin or functional immunoglobulin fragment specific for human leukocyte antigen Cw6, useful for treatment of humans and for human leukocyte antigen phenotyping.  
PS Claim 3; Fig 1; 23pp; English.  
XX AAB67617-23 represent single chain antibody (scFv) fragments which are specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived from a synthetic human combinatorial antibody library based on molecular consensus frameworks and CDRs randomised with trinucleotides. The specification describes a human immunoglobulin fragments specific for HLA -Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of natural killer cell silencing as well as miscarriages. HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions. Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are useful for the preparation of a pharmaceutical for the treatment of humans. They are also useful for HLA phenotyping  
SQ Sequence 245 AA;

Query Match  
Best Local Similarity 58.4%; Score 788.5; DB 4; Length 245;  
Matches 159; Conservative 30; Mismatches 53; Indels 13; Gaps 4;

Qy 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVGIRQPPGKALEWLASINWDDKC 60  
Db 1 EVQLVESGGGLVQPGSLRLSCAASGFTSSVAMS--WVRQAPGKGLEWVASISGSGST 58  
Qy 61 -YSPSLKSRLLTITKDTPKNOVVLAMSNMADPADTATYSCALDMPHDSGQSFDSVWGP 119  
Db 59 YVADSVKGRFTISRDNKNTLYIQMNSLRADTAVYYCA-----RYSFSWFDVWGQ 109  
Qy 120 GTMTVSSSGGGSGGGSGGGSGGGSSYEIMQLPSVSVSPGQTASITCGDNLGDKYA 179  
Db 110 GTLVTVSSAGGGSGGGSGGGSGGGSDIELTQPSVSVAPGQTARISGSGDALGDKYA 169  
Qy 180 CMYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCOAMD 239  
Db 170 SMYQOKPGQAPVLVIYDDSDRPSGIPERFSGNSGNTATLTISGTQAEDEADYYCOASYDN 229  
Qy 240 -STAVFGTGKLTVL 253  
Db 230 FDSPVFGGKLTVL 244

RESULT 2  
ABP45537  
ID ABP45537 standard; protein; 250 AA.  
XX  
AC ABP45537;  
XX  
DT 19-AUG-2002 (first entry)  
XX

Human Blys binding scFv SEQ ID 1548.  
XX  
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
tumour necrosis factor; B cell proliferation; B cell differentiation;  
immunomodulatory; immunosuppressive; immunostimulant; antirheumatic;  
antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
common variable immunodeficiency; acquired immunodeficiency syndrome;  
XX  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US019110.  
XX  
PR 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX  
DR WPI, 2002-114799/15.  
XX  
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
XX  
PT diagnosis and treatment of cancers and immune disorders.  
XX  
PS Claim 1; Page 2250-2251; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have

CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 250 AA;

Query Match  
Best Local Similarity 58.0%; Score 783; DB 5; Length 250;  
Matches 162; Conservative 29; Mismatches 56; Indels 8; Gaps 4;

Qy 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVGIRQPPGKALEWLASINWDDKC 60  
Db 1 QVQLQESGPGLVKPSRSETISLTCAVSGYSIS--SGYYGWIRQPPGKLEWIGSIYHSGSTY 59  
Qy 61 YSPSLKSRLLTITKDTPKNOVVLAMSNMADPADTATYSCALDMPHDSGQSFDSVWGP 120  
Db 60 YNPSLKSRTVTSVDTISKNQPSLKLSSVTADTAVYYCA--RVHYDILLTGWLAFDIWGQ 117  
Qy 121 TMVTVSSGGSGGGSGGGSGGGSGGGSSYEIMQLPSVSVSPGQTASITCGDNLGDKYAC 180  
Db 118 TMVTVSSGGSGGGSGGGSGGGSGGGSDIELTQPSVSVAPGQTARISGSGDALGDKYA 174  
Qy 181 WYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCOAMD 240  
Db 175 WYQOKPGQAPVLVIYGNKMRPSGIPDRFSGSSGNTASLTITGTQAEDEADYYCNSRDS 234  
Qy 241 --TAVFGTGKLTVL 253  
Db 235 GNHVFVGGGTQLTVL 249

RESULT 3  
ABP45640  
ID ABP45640 standard; protein; 247 AA.  
XX  
AC ABP45640;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scFv SEQ ID 1651.  
XX  
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
tumour necrosis factor; B cell proliferation; B cell differentiation;  
immunomodulatory; immunosuppressive; immunostimulant; antirheumatic;  
antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US019110.  
XX  
PR 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.  
XX  
PS Claim 1; Page 2373-2374; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 247 AA;

Query Match 57.7%; Score 779.5; DB 5; Length 247;  
Best Local Similarity 60.5%; Pred. No. 1.2e-44;  
Matches 161; Conservative 28; Mismatches 44; Indels 33; Gaps 5;  
QY 1 QVTLKESGPTLVKPTQTTLTCTLSGSLSTGVSVMIRQPPGKALEWLASIMNDDKC 60  
Db 1 QVQLDPSGPGLVKPKSETLSLTCTVSNYSIS-SGYWGWIRQPPGKLEWIGSITYSGSTY 59  
QY 61 YSPSLKSRLLTTKDTPKNOVLAMSNMDPADTATYSCA-----LDMPPHDSGPQ 109  
Db 60 YNPSTLKRVTISVDTSKNQFSLKLSVTAAADTAVYYCARFRYDILLGYDDM----- 111  
QY 110 SFDASDVWGPGTMTVTVSSGGGGSGGGSGGGSGGGSSYEIMOLPSVSVPQTASITC 169  
Db 112 -----DVWGRGTLTVTVSSGGGGSGGGSGGGSS-----ELTQDPAVSVALGQTVRITC 160  
QY 170 SGGNLTGDKYACWYQOKRGRSPVLVIYEDNKRPSGIPERFSSGNSGNTATLTISGTQAMDE 229  
Db 161 QGDSLRSRYTASWYQOKPGQAPVLVIYGNKRRPSPGIPDRFSGSSSGNTASLTITGAQAEDE 220  
QY 230 ADYYCQAWDTS--TAVFGTGKLTVL 253  
Db 221 ADYYCNSRDSGSHVVFGGGTKLTVL 246

RESULT 4  
AAE36257  
ID AAE36257 standard; protein; 249 AA.  
XX  
AC AAE36257;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE TRAIL receptor protein binding scFv protein, T1006F07.  
XX  
KW TRAIL receptor; TR4; cancer; Kaposi's sarcoma; cerebellar degeneration;  
KW hyperproliferative disorder; neurodegenerative disorder; immune disorder;  
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
KW retinitis pigmentosa; Huntington's disease; Hashimoto's thyroiditis;  
KW rheumatoid arthritis; multiple sclerosis; Sjogren's syndrome; asthma;  
KW biliary cirrhosis; Behcet's disease; Crohn's disease; allergic disorder;  
KW glomerulonephritis; immune deficiency syndrome; myasthenia gravis;

KW polymyositis; inflammatory disorder; rheumatoid arthritis; septic shock;  
KW infectious disease; acquired immunodeficiency syndrome; viral infection;  
KW AIDS; proliferative disorder; myelodysplastic syndrome; aplastic anaemia;  
KW ischaemic injury; myocardial infarction; reperfusion injury; cachexia;  
KW anorexia; stroke; cardiovascular disorder; peripheral artery disease;  
KW limb ischaemia; arrhythmia; congestive heart failure; neovascularisation;  
KW ocular disorder; wound healing; angiogenesis; transplantation.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Domain 1..125  
FT /note= "VH domain"  
FT Region 26..35  
FT /note= "VH domain complementarity determining region 1  
FT (CDR1)"  
FT Region 50..66  
FT /note= "VH domain complementarity determining region 2  
FT (CDR2)"  
FT Region 99..114  
FT /note= "VH domain complementarity determining region 3  
FT (CDR3)"  
FT Domain 142..249  
FT /note= "VL domain"  
FT Region 164..174  
FT /note= "VL domain complementarity determining region 1  
FT (CDR1)"  
FT Region 190..196  
FT /note= "VL domain complementarity determining region 2  
FT (CDR2)"  
FT Region 229..238  
FT /note= "VL domain complementarity determining region 3  
FT (CDR3)"  
PN WO200297033-A2.  
XX  
PD 05-DEC-2002.  
XX  
PF 07-MAY-2002; 2002WO-US014268.  
XX  
PR 25-MAY-2001; 2001US-0293473P.  
PR 04-JUN-2001; 2001US-0294981P.  
PR 02-AUG-2001; 2001US-0309176P.  
PR 21-SEP-2001; 2001US-0323807P.  
PR 09-OCT-2001; 2001US-0327364P.  
PR 07-NOV-2001; 2001US-0331044P.  
PR 14-NOV-2001; 2001US-0331310P.  
PR 20-DEC-2001; 2001US-0341237P.  
PR 05-APR-2002; 2002US-0369860P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Salcedo T, Ruben SM, Rosen CA, Albert VR, Dobson CL, Vaughan TJ;  
XX WPI; 2003-140454/13.  
XX  
DR N-PSDB; AAD54858.  
XX  
PT Novel antibody useful for treating cancers and other hyperproliferative  
PT disorders, immunospecifically binds to TRAIL receptor and comprises  
PT variable heavy or light chain complementarity determining regions.  
XX  
PS Claim 1; Page 294-295; 301pp; English.  
XX  
CC The present invention relates to novel antibodies that immunospecifically  
CC bind to TRAIL receptor (TR4). Sequences of the invention are useful for  
CC treating, preventing or ameliorating cancer (e.g. colon, breast, uterine,  
CC pancreatic, lung, gastrointestinal or central nervous system cancer e.g.  
CC medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in  
CC human. They are useful for detecting expression of TR4 polypeptide and  
CC detecting, diagnosing, prognosing or monitoring cancers and other hyper-  
CC proliferative disorders. Antibodies of the invention are useful for  
CC treating, preventing or ameliorating neurodegenerative disorders (e.g.  
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,



CC retinitis pigmentosa, cerebellar degeneration and Huntington's disease),  
CC immune disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis,  
CC Sjogren's syndrome, biliary cirrhosis, Behcet's disease, Crohn's disease,  
CC polymyositis, immune-related glomerulonephritis, myasthenia gravis,  
CC Hashimoto's thyroiditis and immune deficiency syndrome), inflammatory  
CC disorders (e.g. asthma, allergic disorders and rheumatoid arthritis),  
CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS),  
CC herpes viral infections and other viral infections) and proliferative  
CC disorders. They are also useful for treating myelodysplastic syndromes  
CC (e.g. aplastic anaemia), ischaemic injury (such as that caused by stroke,  
CC myocardial infarction and reperfusion injury), septic shock, cachexia,  
CC anorexia and toxin-induced liver diseases (such as alcohol). They are  
CC also useful for treating cardiovascular disorders including peripheral  
CC artery diseases such as limb ischaemia, arrhythmia, congestive heart  
CC failure and cardiovascular tuberculosis, diseases or disorders associated  
CC with neovascularisation and ocular disorders, for wound healing, for  
CC promoting angiogenesis and as adjuvants to enhance immune responsiveness  
CC to specific antigen e.g. viral antigen. They are also useful in the  
CC preparation or recovery from surgery, trauma, radiation therapy and  
CC transplantation. The present sequence is T106F07 single chain Fv (scFv)  
CC antibody that immunospecifically bind to TR4 protein. This sequence is  
XX used in the invention

SQ Sequence 249 AA;

Query Match 57.1%; Score 771.5; DB 6; Length 249;  
Best Local Similarity 62.4%; Pred. No. 4e-44;  
Matches 159; Conservative 28; Mismatches 59; Indels 9; Gaps 5;

OY 1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSGVSVMIRQPPGKALEWLASINMNDKC 5;  
Db 1 EVQLVDSGGGLVQPGSLRLSCAASGFTFSYAMS--WVRQAPGKLEWVASISGSGST 60  
OY 61 -YSPSLKSRLLTITKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGQSFDAVDWGP 58  
Db 59 YVADSVKGRFTISRDNKNTLLYLQMSLRAEDTAVYYCARPSFQQWGHYSY-CMDVWGQ 119  
OY 120 GTMTVTSSGGGSGGGSGGGSGGGSSYEIMQLPSVSVSPGQTASITCSGDNLDGKYA 117  
Db 118 GTMTVTSSGGGSGGGSGGGSGGGSSYEIMQLPSVSVSPGQTASITCSGDNLDGKYA 179  
OY 180 CWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAWDT 173  
Db 174 SWYQORPGQSPVLVIYQDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAWDT 239  
OY 240 STA-VFGTGTKLTVL 253  
Db 234 SADWVFGGSGTKVTVL 248

RESULT 5  
AAB67621  
ID AAB67621 standard; protein; 245 AA.  
XX  
AC AAB67621;  
XX  
DT 29-MAY-2001 (first entry)  
XX  
DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6\_5.  
XX  
KW Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;  
XX  
OS miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.  
XX Homo sapiens.  
XX  
PN WO200114558-A1.  
XX  
PD 01-MAR-2001.  
XX  
PF 28-AUG-2000; 2000WO-EP008388.  
XX  
PR 26-AUG-1999; 99EP-00116691.  
XX

PA (MORP-) MORPHOSYS AG.  
XX  
PI Kretzschmar T, Tesar M, Marget M, Kroenke M;  
XX  
DR WPI; 2001-218451/22.  
XX  
PT Novel isolated human immunoglobulin or functional immunoglobulin fragment  
PT specific for human leukocyte antigen Cw6, useful for treatment of humans  
XX and for human leukocyte antigen phenotyping.  
PS Claim 3; Fig 1; 23pp; English.  
XX

CC AAB67617-23 represent single chain antibody (scFv) fragments which are  
CC specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived  
CC from a synthetic human combinatorial antibody library based on molecular  
CC consensus frameworks and CDRs randomised with trinucleotides. The  
CC -Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of  
CC natural killer cell silencing as well as miscarriages. HLA-Cw6  
CC demonstrates a disequilibrium in some recurrent abortions. Psoriasis may  
CC also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are  
CC useful for the preparation of a pharmaceutical for the treatment of  
CC humans. They are also useful for HLA phenotyping  
XX

SQ Sequence 245 AA;

Query Match 56.0%; Score 756.5; DB 4; Length 245;  
Best Local Similarity 60.2%; Pred. No. 4e-43;  
Matches 154; Conservative 32; Mismatches 55; Indels 15; Gaps 5;

OY 1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSGVSVMIRQPPGKALEWLASINMND-DK 59  
Db 1 EVQLVDSGAEVKKPGEISLTKISCKSGSYFTS--YWGVRQMPGKLEWVGIIYPGSDST 58  
OY 60 CYSPSLKSRLLTITKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGQSFDAVDWGP 118  
Db 59 RYSPSFGQVTTISADKSIATAVLQWSSLKASDTAMYCA-----RSWDYPFDIWG 108  
OY 119 PGTMVTSSGGGSGGGSGGGSGGGSSYEIMQLPSVSVSPGQTASITCSGDNLDGKY 178  
Db 109 QGTLVTSSAGGSGGGSGGGSGGGSSYEIMQLPSVSVSPGQTASITCSGDNLDGKY 168  
OY 179 ACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAWD 238  
Db 169 ASWYQOKPGRSPVLVIYDDSDRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQSYD 228  
OY 239 T-STAVFGTGTKLTVL 253  
Db 229 DHDRIVFGGSGTKLTVL 244

RESULT 6  
AAB67622  
ID AAB67622 standard; protein; 245 AA.  
XX  
AC AAB67622;  
XX  
DT 29-MAY-2001 (first entry)  
XX  
DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6\_6.  
XX  
KW Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;  
XX  
OS miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.  
XX Homo sapiens.  
XX  
PN WO200114558-A1.  
XX  
PD 01-MAR-2001.  
XX  
PF 28-AUG-2000; 2000WO-EP008388.  
XX  
PR 26-AUG-1999; 99EP-00116691.  
XX



Query Match	55.8%;	Score 753.5;	DB 4;	Length 245;
Best Local Similarity	60.3%;	Pred. No. 6.3e-43;		
Matches 155; Conservative	29;	Mismatches 56;	Indels 17;	Gaps 5;

RESULT	7
ID	ABR62332
ABR62332	standard; protein; 237 AA.
XX	
AC	ABR62332;
XX	
DT	22-SEP-2003 (first entry)
XX	
DE	Anti-EBV latent membrane protein scFv antibody FG-1.
XX	
KW	Latent membrane protein; LMP; antibody; scFv; Epstein-Barr virus; EBV;
KW	lymphoma; lymphoproliferative disease; carcinoma; malignancy.
XX	
OS	Homo sapiens.

FH	Key	Location/Qualifiers
FT	Region	1. .29
FT		/label= VH_FR1
FT	Region	31. .35
FT		/label= VH_CDRI
FT	Region	36. .48

CC The present sequence is the protein sequence of anti-Epstein-Barr virus  
 CC (EBV) latent membrane protein (LMP) scFv FG-1. The scFv was isolated from  
 CC a human antibody phage display library. It comprises a DP-88/hv1051K VH  
 CC germ line and 3r.9C5/DPL23 VL germ line. It is an example of antibodies of  
 CC the invention directed against EBV LMP proteins (LMP1, LMP2A or LMP2B).  
 CC Claimed methods of generating an immune reaction comprise administering  
 CC an antibody with specificity for EBV LMP, or an immune cell endowed with  
 CC antibody specificity for an EBV LMP by transformation, to an individual  
 CC having an EBV-associated disease such as malignancy, Hodgkin's disease,  
 CC chronic EBV syndrome or oral hairy cell leukoplakia. The malignancy is  
 CC especially Burkitt's lymphoma, lymphoproliferative disease, B-  
 CC lymphoproliferative disease, non-Hodgkin's lymphoma (NHL), T-NHL, NK-NHL,  
 CC lymphonasoaryngeal carcinoma or gastric carcinoma. Alternatively, the  
 CC lymphocytes of an individual having an EBV associated malignancy are  
 CC transformed with a chimeric gene encoding e.g. a single chain antibody as  
 CC a means of treatment  
 CC  
 SQ Sequence 237 AA;

Query Match	55.7%;	Score 753;	DB 6;	Length 237;
Best Local Similarity	59.2%;	Pred. No. 6.6e-43;		

Matches 154; Conservative 25; Mismatches 51; Indels 30; Gaps 5;  
QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLASI----- 53  
Db 1 QVQLVQSGSEELKPKGSSVKVSCASGCTPSSYAIS--WVRQAPGQGLEWMGILIPFGTA 58  
QY 54 NWNDKCYSPSLKSLRTITKDTPRKQVVLAMSNMDPADTATYSCALDMPHDSGPQSFDA 113  
Db 59 N-----YAQKFQGRVTITADKSTSTAYMELSLRSEDYAVYYCA-----RGRDG 102  
QY 114 SDVMGPGMTVTVSSSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASITCSGDN 173  
Db 103 MDVMGQGTLVTVSSSGGGSGGGSGGGSGQPG-----LTQPPSVSVSPGQTASITCSGDE 157  
QY 174 LGDKRACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYY 233  
Db 158 LGNRYAYWYQOKPGQSPVLVIYQDRKRPISGIPERFSGNSGNTATLTISGTQAMDEADYY 217  
QY 234 COAMDSTAVFGTGTCLTVL 253  
Db 218 COAMASGTGVFGTGTCLTVL 237

RESULT 8  
AAB67623  
ID AAB67623 standard; protein; 245 AA.  
XX  
AC AAB67623;  
XX  
DT 29-MAY-2001 (first entry)  
XX  
DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6\_7.  
XX  
KW Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;  
XX miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.  
OS Homo sapiens.  
XX  
PN WO200114558-A1.  
XX  
PD 01-MAR-2001.  
XX  
PF 28-AUG-2000; 2000WO-EP008388.  
XX  
PR 26-AUG-1999; 99EP-00116691.  
XX  
PA (MORP-) MORPHOSYS AG.  
XX  
PI Kretzschmar T, Tesar M, Marget M, Kroenke M;  
XX  
DR WPI; 2001-218451/22.  
XX  
PT Novel isolated human immunoglobulin or functional immunoglobulin fragment  
PT specific for human leukocyte antigen Cw6, useful for treatment of humans  
PT and for human leukocyte antigen phenotyping.  
XX  
PS Claim 3; Fig 1; 23pp; English.  
XX  
CC AAB67617-23 represent single chain antibody (scFv) fragments which are  
CC specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived  
CC from a synthetic human combinatorial antibody library based on molecular  
CC consensus frameworks and CDRs randomised with trinucleotides. The  
CC specification describes a human immunoglobulin fragments specific for HLA  
CC -Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of  
CC natural killer cell silencing as well as miscarriages. HLA-Cw6  
CC demonstrates a disequilibrium in some recurrent abortions. Psoriasis may  
CC also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are  
CC useful for the preparation of a pharmaceutical for the treatment of  
CC humans. They are also useful for HLA phenotyping  
XX  
SQ Sequence 245 AA;

Query Match 55.7%; Score 752.5; DB 4; Length 245;

Best Local Similarity 60.0%; Pred. No. 7.4e-43;  
Matches 153; Conservative 31; Mismatches 58; Indels 13; Gaps 4;  
QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLASINWD-DK 59  
Db 1 EVQLVQSGAEVKKPGESLKISCKSGYSFTS--YMGVWRQMPGKGLEWMGITTPGDSDT 58  
QY 60 CYSPSLKSLRTITKDTPRKQVVLAMSNMDPADTATYSCALDMPHDSGPQSFDAVDVWGP 119  
Db 59 RYSPSFQGVTVISADKSIISTAYLQWMSLKAADTAMYYCARFVYY-----MDNWGQ 109  
QY 120 GTMTVTVSSSGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYA 179  
Db 110 GTLVTVSSAGGSGGGSGGGSGGGSGGGSDIELTQPPSVSVAFGQTARISGSDALGDKYA 169  
QY 180 CWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCOAMD- 238  
Db 170 SWYQOKPGQAPVLVIYDDSDRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQSYDY 229  
QY 239 TSTAVFGTGTCLTVL 253  
Db 230 FRDVVFGGTGTCLTVL 244

RESULT 9  
AAE02186  
ID AAE02186 standard; protein; 280 AA.  
XX  
AC AAE02186;  
XX  
DT 10-AUG-2001 (first entry)  
XX  
DE PAM2 single chain variable region (scFv) antibody.  
XX  
KW Pectin; PAM1 antibody; single chain variable region; scFv; food; jam;  
XX yogurt; gel; homogalacturonan; HG; plant cell wall.  
OS Unidentified.  
XX  
FH Key  
FT Peptide  
FT 1..22  
FT /label= pe1B\_leader\_sequence  
FT 23..138  
FT /label= Heavy\_chain\_fragment  
FT 139..154  
FT /label= Linker  
FT 155..275  
FT /label= Light\_chain\_fragment  
FT 265..275  
FT /label= Myc\_epitope  
FT Misc-difference 279..80  
FT /note= "Encoded by TAGACT"  
XX  
PN US6228599-B1.  
XX  
PD 08-MAY-2001.  
XX  
PF 26-FEB-1999; 99US-00260527.  
XX  
PR 24-DEC-1998; 98GB-00028700.  
XX  
PA (DANI-) DANISCO AS.  
XX  
PI Knox JP, Willats WGT, Mikkelsen JD;  
XX  
DR WPI; 2001-342672/36.  
XX  
DR N-PSDB; AAD06194.  
XX  
PT New PAM1 and PAM2 antibodies capable of binding de-esterified  
PT homogalacturonan, useful for identifying a pectin moiety, for quantifying  
PT the amount of pectin in a sample or for extracting pectin from a sample.  
XX  
PS Claim 2; Fig 4B; 21pp; English.





PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.

PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
DR WPI; 2002-114799/15.

PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.

PS Claim 1; Page 2746-2747; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to  
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantify the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention

SQ Sequence 254 AA;

Query Match 55.3%; Score 747; DB 5; Length 254;  
Best Local Similarity 59.8%; Pred. No. 1.8e-42;  
Matches 155; Conservative 34; Mismatches 58; Indels 12; Gaps 5;

OY 1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSSTSGSVGWIRQPPGKALEWLASINWDDKC 60  
DB 1 QVQLVQSGEGLVPSGTLSTCAVSGASISSNNL-MSWVRQPPGKGLWIGEIYHSGSTS 59  
OY 61 YSPSLKSLRLTITKDTPKNQVVLAMSNMADPATATYSCALDMPHDSGQS---FDASDV 116  
DB 60 YNPSLRGRVTISVDKSTNQSLKLTSTVDADTDVYYCARDY--YDSSSYSSGDIYYVMDV 117  
OY 117 WGPQTMVTVSSGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASITCSGDNLGD 176  
DB 118 WGGQTTVTVSSGGGSGGGSGGGSGGGSS---ALSYELTQPPSVSVSPGQTATITCSGDLPRK 174  
OY 177 KYACWYQOKPGRSPVLVIYGDNKRPSGIPRFGSGNSGNTATLITISGTOAMDEADYYCQA 236  
DB 175 QNAYWYQOKPGQAPVLVIYRDSERRSGIPERFSGSSSGTTATLITISGVAEDEADYYCQS 234  
OY 237 WDTSTA--VEGTGKLTVL 253  
DB 235 ADSTVSYVFGGKTVTL 253

RESULT 12

ABP45469  
ID ABP45469 standard; protein; 250 AA.

AC ABP45469;

XX 19-AUG-2002 (first entry)

DE Human Blys binding scfv SEQ ID 1480.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;

KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

DR WPI; 2002-114799/15.

PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the

PT diagnosis and treatment of cancers and immune disorders.

PS Claim 1; Page 2169-2170; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to  
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantify the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention

SQ Sequence 250 AA;

Query Match 54.9%; Score 742; DB 5; Length 250;  
Best Local Similarity 56.9%; Pred. No. 3.8e-42;  
Matches 152; Conservative 30; Mismatches 53; Indels 32; Gaps 6;

OY 1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSSTSGSVGWIRQPPGKALEWLASINWDDKC 59  
DB 1 QVQLVQSGAEVKKPGASVKVSCKTSGYSFNDYGIT--WVRQAPGGGLEWGWISAYDGR 58  
OY 60 CYSPLKSLRLTITKDTPKNQVVLAMSNMADPATATYSCALDMPHDSGQSFDASDV--- 116  
DB 59 NYAQKLRGRVTMTTDTSTAYMELRLRPDTRAVYYCAR-----DDRDILTN 106  
OY 117 -----WGPQTMVTVSSGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASIT 168  
DB 107 YYLEYFQHWGKGLTVTVSSGGGSGGGSGGGSGGGSS---AQSVLTQPPSVSVSPGQTASIT 162  
OY 169 CSGDNLGDKYACWYQOKPGRSPVLVIYGDNKRPSGIPRFGSGNSGNTATLITISGTOAMD 228  
DB 163 CSGHNLGDKYVSWYQOKPGQSPVLVIYQDTKRPSGIPRFGSGNSGNTATLITISGTOAMD 222  
OY 229 EADYYCQAMD--TSTAVFGTGTCLTVL 253



DB 223 EADYSCQTWDGSTSSVFEGGTKLTVL 249

RESULT 13

ABP45596

ID ABP45596 standard; protein; 256 AA.

XX

AC ABP45596;

XX

DT 19-AUG-2002 (first entry)

XX

DE Human Blys binding scFv SEQ ID 1607.

XX

KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

XX

OS Homo sapiens.

XX

PN WO200202641-A1.

XX

PD 10-JAN-2002.

XX

PF 15-JUN-2001; 2001WO-US019110.

XX

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX

DR WPI; 2002-114799/15.

XX

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.

XX

PS Claim 1; Page 2320-2321; 3148pp; English.

XX

CC This invention describes novel antibodies that immunospecifically bind to B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of Blys. The antibodies bind to Blys and so may be used to detect and quantitate the presence of Blys in biological samples and may be used in this way to diagnose disease associated with aberrant expression of Blys. They may also be administered to treat diseases associated with aberrant Blys expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention

CC

XX

SQ Sequence 256 AA;

Query Match 54.5%; Score 736; DB 5; Length 256; Best local Similarity 58.5%; Pred. No. 9.8e-42; Matches 152; Conservative 33; Mismatches 63; Indels 12; Gaps 5;

Qy 1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSGVSVMGWIROPKGALEWLASINWMDKC 60

Db 1 QVQLQESGSGLVKPSQTLSTLCAVSGSGSISGGYSWSWIRQPGKLEWIGYIYHSGSTY 60

Qy 61 YSPSLKSRLLITTKDTPKNQVVLAMSNMDPADTATYSCA-IDMPPHD--SGPQSFADSDW 117

Db 61 YNPSLKSRYTISVDRSKNQPSLKLSSVTAADTAVYYCARQRGRDYDILLTGYLGYAFDIW 120

Qy 118 GPGTMVTYSSGGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASITCSG--DNLG 175

Db 121 GRGTPVTVS-----SGGGSGGGSGGGSGGSQSVLTQPPSVSAAPGQKVTISCSGSTSNIG 175

Qy 176 DKYACWYQQKEGRSPVLVIYGDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYCCQ 235

Db 176 NMYVSWYQQHFGKAPKLMITDVSKRPSGVPRFRSGSKSGNSASLDISGLQSEADYCYCA 235

Qy 236 AWDSTRA--VEGTGTKLTVL 253

Db 236 AWDSTLSEFLFGTGTKLTVL 255

RESULT 14

ABP44979

ID ABP44979 standard; protein; 251 AA.

XX

AC ABP44979;

XX

DT 19-AUG-2002 (first entry)

XX

DE Human Blys binding scFv SEQ ID 990.

XX

KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

XX

OS Homo sapiens.

XX

PN WO200202641-A1.

XX

PD 10-JAN-2002.

XX

PF 15-JUN-2001; 2001WO-US019110.

XX

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX

DR WPI; 2002-114799/15.

XX

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.

XX

PS Claim 1; Page 1583-1584; 3148pp; English.

XX

CC This invention describes novel antibodies that immunospecifically bind to B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of Blys. The antibodies bind to Blys and so may be used to detect and quantitate the presence of Blys in biological samples and may be used in this way to diagnose disease associated with aberrant expression of Blys. They may also be administered to treat diseases associated with aberrant Blys expression and activity such as cancer, immune, and autoimmune disorders and

CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
XX the invention  
SQ Sequence 251 AA;

Query Match 54.4%; Score 734.5; DB 5; Length 251;  
Best Local Similarity 59.9%; Pred. No. 1.2e-41;  
Matches 154; Conservative 30; Mismatches 62; Indels 11; Gaps 4;

QY 1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSGVSVCWIRQPPGKALEWLASINWDDKC 60  
Db 1 QVQLQESGPGLVKPSSETLSLCTVSGGSISSSYWGWIRQPPGKLEWIGSIYSGSTY 60  
QY 61 YSPSLKSRLLTITKDTPKNQVLAWSNMDPADTATYSCALDMPHDSGPGSFDASDVWGP 120  
Db 61 YNPSLKSRLVTISVDTSKNQFSLKSSVTADTAVYCARFR--YDILTSYYGMDVWGRG 118  
QY 121 TMVTYSSGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASITCSG---DNLGDK 177  
Db 119 TMVTYS-----SGGGSGGGSGGGSGGSSVLTQPASVSGSPGQSTITCTGSSSDVGVN 173  
QY 178 YACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCOAW 237  
Db 174 YVSWYQOHQPKAPKLMIEGSKRPSGVSNNRFSGSKSGNTASLTISGLQAEDEADYYCSSY 233  
QY 238 DT-STAVFGTGTKLTVL 253  
Db 234 TTRSTRVFGGGLTVL 250

RESULT 15  
ABP45318  
ID ABP45318 standard; protein; 252 AA.  
XX  
AC ABP45318;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scFv SEQ ID 1329.  
XX  
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US019110.  
XX  
PR 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX  
DR WPI; 2002-114799/15.

PT Antibodies against B lymphocyte stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.

XX Claim 1; Page 1989-1990; 3148pp; English.

PS This invention describes novel antibodies that immunospecifically bind to  
XX B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
XX the invention  
SQ Sequence 252 AA;

Query Match 54.3%; Score 733; DB 5; Length 252;  
Best Local Similarity 58.0%; Pred. No. 1.5e-41;  
Matches 153; Conservative 31; Mismatches 56; Indels 24; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSGVSVCWIRQPPGKALEWLASINWDDKC 60  
Db 1 QVQLQESGPGLVKPSSETLSLCTVSGGSISSSYWGWIRQPPGKLEWIGSIYSGSTY 60  
QY 61 YSPSLKSRLLTITKDTPKNQVLAWSNMDPADTATYSCA-----LDMPHDSGPGSFD 113  
Db 61 YNPSLKSRLVTISVDTSKNQFSLKLSVTADTAVYCARGDYDILTYPLH-----A 112  
QY 114 SDVWGPSTMTVYSSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASITCSGDN 173  
Db 113 FDIWKGKTLTVS-----SGGGSGGGSGGGSGGSSVLTQPASVSGSPGQSTITISCTGTS 167  
QY 174 L---GDKYACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEA 230  
Db 168 SAVGGYNYVSWYQOHQPKAPKLMIEGSKRPSGVSNNRFSGSKSGNTASLTISGLQAEDEA 227  
QY 231 DYCCQAMD-STAVFGTGTKLTVL 253  
Db 228 DYCCSYTTRSTRVFGGGLTVL 251

Search completed: May 13, 2004, 15:00:55  
Job time : 54.0738 secs





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QY 120 GTMTVSSGGGGGGGGGGSSSYELMQLPSVSVSPGQTASITCSGDNLGDKYA 179
DB 118 GTMTVSSGGGGGGGGGGSSSYELMQLPSVSVSPGQTASITCSGDNLGDKYA 173
QY 180 CWYQKPGRSPLVLYIGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAWDT 239
DB 174 SWYQKPGRSPLVLYIGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAWDT 233
QY 240 STA-VFGTGTCLTVL 253
DB 234 SADWVFGGCTKTVL 248
```

```
RESULT 2
US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelsen, J.D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 278
; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected
; OTHER INFORMATION: from a naive phage display library known as the
; OTHER INFORMATION: Synthetic scfv library (#1) from the Centre for
US-09-260-527-3
```

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Query Match 55.7%; Score 752.5; DB 3; Length 278;
Best Local Similarity 60.4%; Pred. No. 3.4e-49;
Matches 154; Conservative 31; Mismatches 51; Indels 19; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMNDKC 60
DB 23 QVQLQESGPGLVKPSDITSLTCAVSGYSSISN-WGWIRQPGKLEWIGYIYSGSTY 81
QY 61 YSPSLKRLTITKDTPKNQVVLAMSNMPPADTATYSCALDMPHDSGQSFDAADYWGPG 120
DB 82 YNPSLKSRLTITKDTPKNQVVLAMSNMPPADTATYSCALDMPHDSGQSFDAADYWGPG 120
QY 121 TMVTVSSGGGGGGGGGGSSSYELMQLPSVSVSPGQTASITCSGDNLGDKYA 180
DB 132 TLVTVSRGGGGGGGGGGSSSYELMQLPSVSVSPGQTASITCSGDNLGDKYA 180
QY 181 WYQKPGRSPLVLYIGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAWDT 240
DB 186 WYQKPGRSPLVLYIGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAWDT 240
QY 241 --TAVFGTGTCLTVL 253
DB 246 GNHVVFGGCTKTVL 260
```

```
RESULT 3
US-08-918-148-79
; Sequence 79, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
```

```
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 79
; LENGTH: 244
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-79
```

```
Query Match 53.1%; Score 717; DB 4; Length 244;
Best Local Similarity 59.1%; Pred. No. 1.3e-46;
Matches 152; Conservative 30; Mismatches 53; Indels 22; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINMNDKC 60
DB 3 QVQLQESGPGLVKPSDITSLTCAVSGYSSISN-WGWIRQPGKLEWIGYIYSGSTY 81
QY 61 YSPSLKRLTITKDTPKNQVVLAMSNMPPADTATYSCALDMPHDSGQSFDAADYWGPG 120
DB 61 YNPSLKSRLTITKDTPKNQVVLAMSNMPPADTATYSCALDMPHDSGQSFDAADYWGPG 120
QY 121 TMVTVSSGGGGGGGGGGSSSYELMQLPSVSVSPGQTASITCSG--DNLGDK 177
DB 110 TMVTVS-----SGGGGGGGGGGGSSSYELMQLPSVSVSPGQTASITCSG--DNLGDK 177
QY 178 YACWYQKPGRSPLVLYIGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAW 237
DB 165 YSWYQKPGRSPLVLYIGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAW 237
QY 238 DT-STAVFGTGTCLTVL 253
DB 225 TTRSTRVFGGCTKTVL 241
```

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RESULT 4
US-10-039-785-50
; Sequence 50, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
```



OTHER INFORMATION: T1015A02 scfv  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (250)  
OTHER INFORMATION: Xaa equals either Gly or Ser  
US-10-039-785-50

Query Match 51.4%; Score 694; DB 4; Length 250;  
Best Local Similarity 54.5%; Pred. No. 7.3e-45;  
Matches 140; Conservative 36; Mismatches 69; Indels 12; Gaps 4;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTSGSVSGWIRPPGKALEWLASINWDDKC 60  
DB 1 QVQLQESGPGILVKPSQTLSLKCNVSGSGSIGTDYYSWIRQPGKLEWIGYIHSSGSTY 60  
QY 61 YSPSLKSRLLITKDTPKNQVVLAMSNMDPADTATYSCALDMPHDSPQSFSDASDVWGPG 120  
DB 61 YKPSLRSLTVSMDSRNQFSLKLTSTVTAADTALYYCVREWANGD---HMSAFDLWGQG 116  
QY 121 TMVTYSSGGGGSGGGSGGGSGGGSSYELMQLPSVSPGQTASITCSG--DNLGDKY 178  
DB 117 TLVTYSSGGGGSGGGSGGGSGGGG---AAVLTQPSASGTPGQRTIIPCSGSSNIGNT 172  
QY 179 ACWYQKRGKSPVLVIYGNKRPSPGIPERFSGNSGNTATLTISGTQAMDEADYCCQAMD 238  
DB 173 VMWYQQLPQTAPKLLIYGNDRPSPGVDRFSGSKSGTSASLALTGQSEDEADYCCQAMD 232  
QY 239 TSTA--VFGTGTKLTVL 253  
DB 233 DSLIGYVFGTGTQLTVL 249

#### RESULT 5

US-09-079-029-9  
Sequence 9, Application US/09079029  
Patent No. 6342369

#### GENERAL INFORMATION:

APPLICANT: Adams, Camilia W.  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Chuntharapai, Anan  
APPLICANT: Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

#### COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,029  
FILING DATE:  
CLASSIFICATION:

#### ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881

#### INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-079-029-9

Query Match 51.2%; Score 692; DB 4; Length 309;  
Best Local Similarity 55.9%; Pred. No. 1.3e-44;  
Matches 143; Conservative 33; Mismatches 64; Indels 16; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTSGSVSGWIRPPGKALEWLASINWDDKC 60  
DB 40 EVQLVQSGGVERPQGSRLSLSCASGFTFDYGMS--WVRQAPGKLEWVSGINWNGST 97  
QY 61 -YSPSLKSRLLITKDTPKNQVVLAMSNMDPADTATYSCALDMPHDSPQSFSDASDVWGPG 119  
DB 98 GYADSVKGRVTTISRDNKNSLYLQMSLRADTAVYYCAKIL-----GAGRGWYFDLWGK 152  
QY 120 GTMTYSSGGGGSGGGSGGGSGGGSSYELMQLPSVSPGQTASITCSGDNLGDKYA 179  
DB 153 GTTIVTSSGGGGSGGGSGGGSGGGG-----ELTQDPVAVVALCQTVRITCQGDLSRYIA 206  
QY 180 CWYQKRGKSPVLVIYGNKRPSPGIPERFSGNSGNTATLTISGTQAMDEADYCCQAMD 239  
DB 207 SWYQKRGKQAPVLVIYGNKRPSPGIPDRFSGSSGNTASLTITGAQAEDEADYCCNSRDS 266  
QY 240 S--TAVFGTGTKLTVL 253  
DB 267 SGNHVFGGGTKLTVL 282

#### RESULT 6

US-09-079-029-10  
Sequence 10, Application US/09079029  
Patent No. 6342369

#### GENERAL INFORMATION:

APPLICANT: Adams, Camilia W.  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Chuntharapai, Anan  
APPLICANT: Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

#### COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,029  
FILING DATE:  
CLASSIFICATION:

#### ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881

#### INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:  
LENGTH: 312 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-079-029-10

Query Match 51.0%; Score 688.5; DB 4; Length 312;  
Best Local Similarity 56.9%; Pred. No. 2.4e-44;  
Matches 145; Conservative 31; Mismatches 66; Indels 13; Gaps 5;

QY 2 VTLKESGPTLVKPTQTLTLTCTLSGFSLSSTSGSVSGWIRPPGKALEWLASINWN-DDKC 60  
DB 41 VQLVESGGGLVQPGSLRLSCAASGFTFSYWM--WVRQAPGKLEWVANIKQDSSEK 98

[illegible]

## RESULT 7

```

US-10-039-785-44
; Sequence 44, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014A02 scFv
US-10-039-785-44

```

Query Match	50.6%	Score 684	DB 4	Length 244
Best Local Similarity	55.6%	Pred. No.	4e-44	
Matches 143	Conservative			

```

QY      1 QVTLKESGFLVKEPTQTTLTCTISGFSLSSTSGSVSGWIRQPPGKALEWLASINWDDKC 60
Db      1 QVQLQESGPGELVKPSETLSLTCTVSGSGISDYWYS--WVRQSPGKGLHWIGSIDYAGSTN 58
QY      61 YSPSLKSRLLITKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGPQSFDAADYWGPG 120
Db      59 YNPSLSKSRVTMTIDKSKKQFPFLKIDSVTAADATMYCA-----RQLGRISDYWGQ 109
QY      121 TMVTYSSGGGGSGGGSGGGSGGGSSYELMQLPSPSVSPGQTASITCSG--DNLGDKY 178
Db      110 TLVTYSSGGGGSGGGSGGGSGGGSS--ALSYVLTQPPSASGTPGQRTVISCAGSSSNIGCNT 166

```

[illegible]

RESULT 8  
US-09-26

```

/ Sequence1, Application US/09260527A
/ Patent No. 6228599
/ GENERAL INFORMATION:
/   APPLICANT: Knox, J.P.
/   APPLICANT: Mikkelsen, J.D.
/   APPLICANT: Willats, W. G.
/   TITLE OF INVENTION: ANTIBODY
/   FILE REFERENCE: DYOU19.001AUS
/   CURRENT APPLICATION NUMBER: US/09/260,527A
/   CURRENT FILING DATE: 1999-02-26
/   NUMBER OF SEQ ID NOS: 7
/   SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/   LENGTH: 280
/   TYPE: PRT
/   ORGANISM: UNKNOWN
/   FEATURE:
/   OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
/   OTHER INFORMATION: phase display library known as the Synthetic scFv
/   OTHER INFORMATION: Library (#1) from the Centre for Protein
US-09-260-527-1 Engineering, MRC Centre, Cambridge, UK.

```

Query Match	49.5%;	Score 668.5;	DB 3;	Length 280;
Best Local Similarity	54.7%;	Pred. No. 6.8e-43;		
Matches 141;	Conservative 31;	Matmatch 100;		

```

QY      1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTSGVSGVMIRQPPGKALEWLASINMND-- 58
Db      23 EVOLVESGGGLVKKPGGSLRLSCAASGFTFSNAMS--WVRQAPGKGLEWVGRISKTDGG 80
QY      59 -KCYSPSLKSLRLTITKDTPKQVVLAMSNMNPADTATYSCALDMPHDSGPQSFDAQVW 117
Db      61 TTDYAAPVKGRFTISRDSKNTLTLYQMNSLKTEDTAVYYCA-----RKWRKALRW 130
QY      118 GPGTMYTVSSGGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASITCSGDMIGDK 177
Db      131 GGGTLTVSRGGGSGGGSGGGSGGGSS-----ELTQDPAVSVALGQTVRITCQGSLSRSY 184
QY      178 YACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGSNSGNTATLTISGTOAMDEADYYCQAW 237
Db      185 YASWYQOKPGQAPVLVIYKNNRPSGIPDRFGSSSSGNTASLTITGAQAEADYDYCNRSR 244
QY      238 DTS--TAVFGTGTKLTVL 253
Db      245 DSSGNHVVFGGGTKLTVL 262

```

## RESULT 9

US-09-079-029-11  
 ; Sequence 11, Application US/09079029  
 ; Patent No. 6342369  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Adams, Camilla W.  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Chuntcharapai, Anan  
 ; APPLICANT: Kim, Kyung J.  
 ; TITLE OF INVENTION: Apo-2 Receptor  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA way

```

: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/079,029
: FILING DATE:
:
: CLASSIFICATION:
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Marschang, Diane L.
: REGISTRATION NUMBER: 35,600
: REFERENCE/DOCKET NUMBER: P1101R2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5416
: TELEFAX: 650/952-9881
:
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 310 amino acids
: TYPE: Amino acid
: TOPOLOGY: Linear
:
:
US-09-079-029-11

```

Query Match 46.7%; Score 630.5; DB 4; Length 310;  
Best Local Similarity 51.4%; Pred. No. 5.4e-40;  
Matches 133; Conservative 42; Mismatches 63; Indels 21; Gaps 7;

QY	1 QVTLKESGPTLVKPTQTLTITLTCISGFSLSTSGVSVGMIRÖPPKALEWLASINWN-DDK	59
Dd	40 QVQLVDSGGGVNQPRSLRLSCAASGFISSYGMA--WRQAPKGLEWYAGIFYDGSK	97
QY	60 CYPSPLSKRLTITKDTPKNOVLAMSNMDEADATATYSCALDMPPHDSGPDSFSDSVMGP	119
Dd	98 YYADSVKGRFTISRDNISKNTLYQMNSLRRAEDTAIVYYCARD-----RGYYMDVMWGK	149
QY	120 GTMTVTSSGGSGSGSGSGSGSGSSYEIMQLPSVSVPQTASTITCSG--DNIGDK	177
Dd	150 GTTVTVS-----SGGGSGSGSGSGSGSQSVLTQPSPVSGAPGQRVTISCTGRSSNIGAG	204
QY	178 Y-ACWYQQKPKRSPVLVIYGDNRKRPSCIPEFSGSNSGNATLTISGTQAMDEADYYCQA	236
Dd	205 HDVHWYQQLPGTAPKLIIYDSDNPSPGVDFRFGSGRSSTASLAITGLQADEADYYCCQS	264
QY	237 WDTST--AVFGTGTKLTVL	253
Dd	265 YDSSLRGSVFGGGTKVTVL	283

RESULT 10  
US-08-665-202-5  
; Sequence 5, Application US/08665202  
; Patent No. 5977322  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D.  
; APPLICANT: Schier, Robert  
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to  
; TITLE OF INVENTION: Tumor Antigens  
; NUMBER OF SEQUENCES: 141  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 258 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-665-202-5

```

Query Match	45.7%;	Score 617.5;	DB 2;	Length 258;
Best Local Similarity	49.3%;	Pred. NO. 4.1e-39;		
Matches 132;	Conservative 39;	Mismatches 68;	Indels 29;	Gaps 8;

```
QY      1 QVTLKESGPTLVKFTQTLLTCTLSGSFSLSTSGSVSGMIROPPGKALENTLASINMND-DK 59
Db      1 QVQLLQGSAELKKPESLKIICKSGSYFTSYWIA--WVRQMPEGKLEYMGLIYPGDSDT 58
QY      60 CYSPLSKRLTTTKDTPKNQVVLAWSNMDPADTATYSCALDMPEPHDC-----PQ 109
Db      59 KISPSPFGQGVTTISVDKSVSTAYLQWSSLKPSPDSAVYFCA---RHVDGYCSSSNCAKWPE 114
QY      110 SFDASDVWGPGTMVTIVSSGGGSGCGGSGGGGSSSXYEIMQLPSVSVPGQTASITC 169
Db      115 YFOH---WGQGTIVTVS-----SCGGSGGGGSGGGGQSQSVLTQPVSAAAPQKVITISC 166
QY      170 SG--DNLGDKYACWYQQKPKRSPLVIYGDNKRPSGIPIRFSGNSGNATLTIISGTQAM 227
Db      167 SGSSSNIGNNYVSWYQQLPEGIAPKLIIYGHTNRPAVGPDPRFSGSKGSTASLASIGFRSE 226
QY      228 DEADYYCQAMDTSIA--VFGTGTKLTVL 253
Db      227 DEADYYCAAMDSDLSCGWVFGGGTKLTVL 254
```

RESULT 11  
US-09-315-574-5  
; Sequence 5, Application US/09315574  
; Patent No. 6512097  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D.  
; APPLICANT: Schier, Robert  
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to  
; TITLE OF INVENTION: Tumor Antigens  
; NUMBER OF SEQUENCES: 141  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.  
; STREET: Four Embarcadero Center, Suite 1100  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-4106  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/315,574  
FILING DATE: 20-MAY-99  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,238  
FILING DATE: 14-JUN-1995  
APPLICATION NUMBER: US 60/000,250  
FILING DATE: 15-JUN-1995  
APPLICATION DATA:  
APPLICATION NUMBER: US 08/665,202  
FILING DATE: 13-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 02307E-061411  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 258 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-315-574-5

Query Match 45.7%; Score 617.5; DB 4; Length 258;  
Best Local Similarity 49.3%; Pred. No. 4.1e-39;  
Matches 132; Conservative 39; Mismatches 68; Indels 29; Gaps 8;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMGIRPPGKALEWLASINWMD-DK 59  
DB 1 QVQLQSGAEIKKPEGLSKISCKSGYSFTSYWIA--WVRQMPGKGLVYMGILYPGDSDT 58  
QY 60 CYSPLSKRLITKDTPKNQVLAAMSNMADPADTATYSCALDMPPHDSG-----PQ 109  
DB 59 KYSPLKSGPTLVKPTQTTLTCTLSGFSLSSTGVSVMGIRPPGKALEWLASINWMD-DK 114  
QY 110 SFDASDVWPGTMTVSSSGGGSGGGSGGGSGGGSSYELMQLPSVSVSGQTASITC 169  
DB 115 YFQH---WGQGLTVTS-----SGGGSGGGSGGGSGGGSSVLTQPSVSAAPGQKVTISC 166  
QY 170 SG--DNLGDKYACWYQKPRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAM 227  
DB 167 SGSSSNIGNNYSWYQQLPGTAPKLLIYGHTRPAGVDPDRFSGSKSGTSASLAIISGRSE 226  
QY 228 DEADYYCAQAMDSTA--VFGTGKLTVL 253  
DB 227 DEADYYCAAMDSDLGSGWVFGGKLTVL 254

## RESULT 12

US-08-190-199A-61  
Sequence 61, Application US/08190199A  
Patent No. 5830663  
GENERAL INFORMATION:  
APPLICANT: EMBLETON, Michael J.  
APPLICANT: GOROCHOV, Guy  
APPLICANT: JONES, Peter T.  
APPLICANT: WINTER, Gregory P.  
TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

## COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/190,199A  
FILING DATE: 13-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/01483  
FILING DATE: 10-AUG-1992  
APPLICATION NUMBER: GB 9212419.7  
FILING DATE: 11-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9117352.6  
FILING DATE: 10-AUG-1991  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-190-199A-61

Query Match 45.0%; Score 607.5; DB 2; Length 235;  
Best Local Similarity 51.0%; Pred. No. 2.1e-38;  
Matches 128; Conservative 31; Mismatches 71; Indels 21; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMGIRPPGKALEWLASINWMDKC 60  
DB 1 QVQLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMGIRPPGKALEWLASINWMDKC 58  
QY 61 YSPSLKRLITKDTPKNQVLAAMSNMADPADTATYSCALDMPPHDSGPGSFDASDVWPG 120  
DB 59 YNSALMSRLSISKDNSKQVFLKMSLQTDTDAMYCCARDGAY-----WGQG 106  
QY 121 TMVTVSSGGSGGGSGGGSGGGSGGGSSYELMQLPSV-SVSPGQTASITCSGDNLDKYA 179  
DB 107 TLVTVS-----AGGGSGGGSGGGSGGGSSVLTQSPALMSASPGQKVTMTCSASS-SVSYM 160  
QY 180 CWYQKPRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCAQAMD 239  
DB 161 HWYQKSGTSPKRWITDTSKLASGVPARFSGSGSATSYSLTISMEAEADAATYYCCQWSS 220  
QY 240 STAVFGTGTL 250  
DB 221 NPLTFGAGTKL 231

## RESULT 13

US-08-918-148-74  
Sequence 74, Application US/08918148A  
Patent No. 6342220  
GENERAL INFORMATION:  
APPLICANT: Adams, Camellia  
APPLICANT: W.  
APPLICANT: Carter, Paul J.  
APPLICANT: Fendly, Brian M.  
APPLICANT: Gurney, Austin L.  
TITLE OF INVENTION: Agonist Antibodies  
FILE REFERENCE: P0979  
CURRENT APPLICATION NUMBER: US/08/918,148A  
FILING DATE: 1997-08-25  
NUMBER OF SEQ ID NOS: 79  
SEQ ID NO 74  
LENGTH: 249  
TYPE: PRT  
ORGANISM: artificial  
US-08-918-148-74

Query Match 44.9%; Score 606.5; DB 4; Length 249;  
Best Local Similarity 49.6%; Pred. No. 2.6e-38;  
Matches 128; Conservative 41; Mismatches 70; Indels 19; Gaps 6;



```

QY      1 QVTLKESGPTLVKPTOTLTTLTCTLSGFSLSITSGVSGWIRPPGKALEWLASI--NWANDK 59
Db      3 QVQLQESGGEMKKKPGESLKISCKGYGYSPFATSW--IGWVRQMPGRGLEWMAIMYPCNSDT 60
QY      60 CYPSPILSKRLTITTKDTPKQNVVLAMSNMDPADTATYSCALDMPHDSGPQSFPDASDVWGP 119
Db      61 RHNPSPFEDQVTMSADTSINTAYLQWSLSKASDPTAMYCA-----RAGVAGGAFDLWGK 113
QY      120 GIMTVTVSSGGGGSGGGSGGGSSGYELMQLPSVSVSPGQTASITCSGDNL---GD 176
Db      114 GIMTVTVS-----SGGGSGGGSGGGSSQSVLTQPASVSGSPQISITISCTGTSAGVGY 168
QY      177 KYACWYQOKPGRSPVLVITYGDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYVQA 236
Db      169 NYVSWYQOHFGKAPKLLITYGNSNRPSCGVDRFSASKSGNTASLTISGLQAEADYDFCST 228
QY      237 W-DTSTAVFGTGTCLTVL 253
Db      229 YAPPGIIMFGGGLTVL 246

```

RESULT 14  
US-08-752-844-66  
; Sequence 66, Application US/08752844

```

GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Foon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

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Query Match	43.9%	Score 592.5;	DB 2;	length 263;
Best Local Similarity	51.7%;	Pred. No. 3.1e-37;		
Matches 134;	Conservative 30;	Mismatches 72;	Indels 23;	Gaps 7;

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RESULT 15  
US-09-293-533-66  
; Sequence 66, Application US/09293533  
; Patent No. 6509016

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: GENERAL INFORMATION:
: APPLICANT: Chatterjee, Malaya
: APPLICANT: Foon, Kenneth A.
: APPLICANT: Chatterjee, Sunil K.
: TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
: TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
: NUMBER OF SEQUENCES: 66
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 PAGE MILL ROAD
: CITY: PALO ALTO
: STATE: CA
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/293,533
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/752,844
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Schiff, J. Michael
: REGISTRATION NUMBER: 40,253
: REFERENCE/DOCKET NUMBER: 30414-20002.21
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 706141
: INFORMATION FOR SEQ ID NO: 66:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 263 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
US-293-533-66

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Query Match	43.9%;	Score 592.5;	DB 4;	Length 263;
Best Local Similarity	51.7%;	Pred. No. 3.1e-37;		
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Search completed: May 13, 2004, 15:10:45  
Job time : 14.8782 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 15:07:07 ; Search time 37.4587 Seconds  
(without alignments)  
1879.405 Million cell updates/sec

Title: US-10-072-301-17  
Perfect score: 1351  
Sequence: 1 QVTLKESGPTLVKPTQTLL.....CQAMDSTAVFGTGTKLTVL 253

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.peg:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1351	100.0	253	14	US-10-072-301-17	Sequence 17, Appl
2	1351	100.0	253	14	US-10-072-301-25	Sequence 25, Appl
3	1351	100.0	253	14	US-10-071-866-17	Sequence 17, Appl
4	1351	100.0	253	14	US-10-071-866-25	Sequence 25, Appl
5	1351	100.0	253	15	US-10-360-828-17	Sequence 17, Appl
6	1351	100.0	253	15	US-10-360-828-25	Sequence 25, Appl
7	794	58.8	253	14	US-10-072-301-23	Sequence 23, Appl
8	794	58.8	253	14	US-10-072-301-31	Sequence 31, Appl
9	794	58.8	253	14	US-10-071-866-23	Sequence 23, Appl
10	794	58.8	253	14	US-10-071-866-31	Sequence 31, Appl
11	794	58.8	253	15	US-10-360-828-23	Sequence 23, Appl
12	794	58.8	253	15	US-10-360-828-31	Sequence 31, Appl
13	783	58.0	250	10	US-09-880-748-1548	Sequence 1548, Ap
14	783	58.0	250	12	US-10-293-418-1548	Sequence 1548, Ap
15	779.5	57.7	247	10	US-09-880-748-1651	Sequence 1651, Ap

16	779.5	57.7	247	12	US-10-293-418-1651	Sequence 1651, Appl
17	771.5	57.1	249	13	US-10-039-785-53	Sequence 53, Appl
18	771.5	57.1	249	14	US-10-139-785-53	Sequence 53, Appl
19	747	55.3	254	10	US-09-880-748-1966	Sequence 1966, App
20	747	55.3	254	12	US-10-293-418-1966	Sequence 1966, App
21	742	54.9	250	10	US-09-880-748-1480	Sequence 1480, App
22	742	54.9	250	12	US-10-293-418-1480	Sequence 1480, App
23	739.5	54.7	258	14	US-10-072-301-27	Sequence 27, Appl
24	739.5	54.7	258	14	US-10-071-866-27	Sequence 27, Appl
25	739.5	54.7	258	15	US-10-360-828-27	Sequence 27, Appl
26	736	54.5	256	10	US-09-880-748-1607	Sequence 1607, App
27	736	54.5	256	12	US-10-293-418-1607	Sequence 1607, App
28	734.5	54.4	251	10	US-09-880-748-990	Sequence 990, App
29	734.5	54.4	251	12	US-10-293-418-990	Sequence 990, App
30	733	54.3	252	10	US-09-880-748-1329	Sequence 1329, App
31	733	54.3	252	12	US-10-293-418-1329	Sequence 1329, App
32	731	54.1	254	10	US-09-880-748-844	Sequence 844, App
33	731	54.1	254	12	US-10-293-418-844	Sequence 844, App
34	730	54.0	252	14	US-10-120-414-73	Sequence 73, Appl
35	728.5	53.9	247	10	US-09-880-748-1018	Sequence 1018, App
36	728.5	53.9	247	12	US-10-293-418-1018	Sequence 1018, App
37	723.5	53.6	251	10	US-09-880-748-1316	Sequence 1316, App
38	723.5	53.6	251	12	US-10-293-418-1316	Sequence 1316, App
39	723.5	53.6	253	10	US-09-880-748-1619	Sequence 1619, App
40	723.5	53.6	253	12	US-10-293-418-1619	Sequence 1619, App
41	722.5	53.5	251	10	US-09-880-748-952	Sequence 952, App
42	722.5	53.5	251	12	US-10-293-418-952	Sequence 952, App
43	721.5	53.4	255	10	US-09-880-748-841	Sequence 841, App
44	721.5	53.4	255	12	US-10-293-418-841	Sequence 841, App
45	721	53.4	248	10	US-09-880-748-1995	Sequence 1995, App

## ALIGNMENTS

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RESULT 1
US-10-072-301-17
; Sequence 17, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODE
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.186.35
US-10-072-301-17

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	Query Match	100.0%;	Score 1351;	DB 14;	Length 253;
	Best Local Similarity	100.0%;	Pred. No. 2.8e-87;		
	Matches 253;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
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Db	1 QVTLKESGPTLVKPTQTLLTLLTCTLSGSFSLSTSGSVSWGIRPPGKALEWLASINWNDDKC				60
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Db	61 YSPSLKSRLTTITKDTPKNQVYLAMSNDPADTATYSICALDMPPHDSGPQSFDASDVWGPG				120
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Db	121 TMTVTSSGGGSGGGGSGGGGSSSYELMQLPSVSVPGGQTASITCSGDNLGDKYAC				180

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## RESULT 2

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US-10-072-301-25
; Sequence 25, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.186.35 Variant
US-10-072-301-25
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Query Match
Best Local Similarity 100.0%; Score 1351; DB 14; Length 253;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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## RESULT 3

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US-10-071-866-17
; Sequence 17, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST F
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 17
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; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Clone 15.186.35
US-10-071-866-17
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Best Local Similarity 100.0%; Score 1351; DB 14; Length 253;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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## RESULT 4

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US-10-071-866-25
; Sequence 25, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST F
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.186.35 Variant
US-10-071-866-25
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Query Match
Best Local Similarity 100.0%; Score 1351; DB 14; Length 253;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 5

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; Sequence 17, Application US/10360828  
; Publication No. US20030206909A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shaobing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS  
; FILE REFERENCE: 25636-727  
; CURRENT APPLICATION NUMBER: US/10/360,828  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: US 10/071,866  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/072,301  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/133,978  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.186.35  
US-10-360-828-17

Query Match 100.0%; Score 1351; DB 15; Length 253;  
Best Local Similarity 100.0%; Pred. No. 2.8e-87;  
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 TMVTWSSGGGGSGGGGGGGGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 180  
QY 181 WYQOKPGRSPVLVIYGDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDTS 240  
Db 181 WYQOKPGRSPVLVIYGDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDTS 240  
QY 241 TAVFGTGTKLTVL 253  
Db 241 TAVFGTGTKLTVL 253

RESULT 6

US-10-360-828-25  
; Sequence 25, Application US/10360828  
; Publication No. US20030206909A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shaobing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS  
; FILE REFERENCE: 25636-727  
; CURRENT APPLICATION NUMBER: US/10/360,828  
; CURRENT FILING DATE: 2003-02-07

; PRIOR APPLICATION NUMBER: US 10/071,866  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/072,301  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/133,978  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.186.35 Variant  
US-10-360-828-25

Query Match 100.0%; Score 1351; DB 15; Length 253;  
Best Local Similarity 100.0%; Pred. No. 2.8e-87;  
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLASINWDDKC 60  
QY 61 YSPSLKSRLTTTKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGPQSFSDASDVWGP 120  
Db 61 YSPSLKSRLTTTKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGPQSFSDASDVWGP 120  
QY 121 TMVTWSSGGGGSGGGGGGGGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 180  
Db 121 TMVTWSSGGGGSGGGGGGGGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 180  
QY 181 WYQOKPGRSPVLVIYGDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDTS 240  
Db 181 WYQOKPGRSPVLVIYGDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDTS 240  
QY 241 TAVFGTGTKLTVL 253  
Db 241 TAVFGTGTKLTVL 253

RESULT 7

US-10-072-301-23  
; Sequence 23, Application US/10072301  
; Publication No. US20030152913A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF  
; FILE REFERENCE: 25636-718  
; CURRENT APPLICATION NUMBER: US/10/072,301  
; CURRENT FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.24  
US-10-072-301-23

Query Match 58.8%; Score 794; DB 14; Length 253;  
Best Local Similarity 62.8%; Pred. No. 3.5e-48;  
Matches 159; Conservative 24; Mismatches 68; Indels 2; Gaps 2;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLASINWDDKC 60  
Db 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSRTTGEVWVRQPPGKALEWLALTYWDDDKR 60  
QY 61 YSPSLKSRLTTTKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGPQSFSDASDVWGP 120

```
Db 61 YSPSLKSRLLITTKDTSKKQVLLMTNVDPADTATYCTHEQYYYDTSQPY-YFDWGGG 119
Qy 121 TMTVSSGGGGSGGGSGGGSSYELMQLP-SVSVSPGQTASITCSGDNLGDKYA 179
Db 120 TLVTVSSGGGGSGGGSGGGSSNIQVTSPLSASVGDRTMTCRASQDIRKNL 179
Qy 180 CMYQOKPGRSPVLVIYGDNRKPSGIPERFSGNSGNTATLTISGTQAMDEADYCCQAMDY 239
Db 180 NMWQOKPKAPKVLIVDASDLETGIPSRFSGSGGTDFILTISSLPEDATYCCQSDY 239
Qy 240 STAVFGTGTCLTV 252
Db 240 LPLTFGGGTKVDI 252
```

```
RESULT 8
US-10-072-301-31
; Sequence 31, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 31
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24 Variant
US-10-072-301-31
```

```
Query Match 58.8%; Score 794; DB 14; Length 253;
Best Local Similarity 62.8%; Pred. No. 3.5e-48;
Matches 159; Conservative 24; Mismatches 68; Indels 2; Gaps 2;

Qy 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINWDDKC 60
Db 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSRTTGEVGVWVRQPPGKALEWLLALYWDDEKR 60
Qy 61 YSPSLKSRLLITTKDTPKNQVVLAMSNMPPADTATYSCALDMPHDSGPFQSFASDVWGP 120
Db 61 YSPSLKSRLLITTKDTSKKQVLLMTNVDPADTATYCTHEQYYYDTSQPY-YFDWGGG 119
Qy 121 TMTVSSGGGGSGGGSGGGSSYELMQLP-SVSVSPGQTASITCSGDNLGDKYA 179
Db 120 TLVTVSSGGGGSGGGSGGGSSNIQVTSPLSASVGDRTMTCRASQDIRKNL 179
Qy 180 CMYQOKPGRSPVLVIYGDNRKPSGIPERFSGNSGNTATLTISGTQAMDEADYCCQAMDY 239
Db 180 NMWQOKPKAPKVLIVDASDLETGIPSRFSGSGGTDFILTISSLPEDATYCCQSDY 239
Qy 240 STAVFGTGTCLTV 252
Db 240 LPLTFGGGTKVDI 252
```

```
RESULT 9
US-10-071-866-23
; Sequence 23, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST H
```

```
; TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 23
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24
US-10-071-866-23
```

```
Query Match 58.8%; Score 794; DB 14; Length 253;
Best Local Similarity 62.8%; Pred. No. 3.5e-48;
Matches 159; Conservative 24; Mismatches 68; Indels 2; Gaps 2;

Qy 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINWDDKC 60
Db 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSRTTGEVGVWVRQPPGKALEWLLALYWDDEKR 60
Qy 61 YSPSLKSRLLITTKDTPKNQVVLAMSNMPPADTATYSCALDMPHDSGPFQSFASDVWGP 120
Db 61 YSPSLKSRLLITTKDTSKKQVLLMTNVDPADTATYCTHEQYYYDTSQPY-YFDWGGG 119
Qy 121 TMTVSSGGGGSGGGSGGGSSYELMQLP-SVSVSPGQTASITCSGDNLGDKYA 179
Db 120 TLVTVSSGGGGSGGGSGGGSSNIQVTSPLSASVGDRTMTCRASQDIRKNL 179
Qy 180 CMYQOKPGRSPVLVIYGDNRKPSGIPERFSGNSGNTATLTISGTQAMDEADYCCQAMDY 239
Db 180 NMWQOKPKAPKVLIVDASDLETGIPSRFSGSGGTDFILTISSLPEDATYCCQSDY 239
Qy 240 STAVFGTGTCLTV 252
Db 240 LPLTFGGGTKVDI 252
```

```
RESULT 10
US-10-071-866-31
; Sequence 31, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST F
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 31
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24 Variant
US-10-071-866-31
```

```
Query Match 58.8%; Score 794; DB 14; Length 253;
Best Local Similarity 62.8%; Pred. No. 3.5e-48;
Matches 159; Conservative 24; Mismatches 68; Indels 2; Gaps 2;

Qy 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRPPGKALEWLASINWDDKC 60
Db 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSRTTGEVGVWVRQPPGKALEWLLALYWDDEKR 60
Qy 61 YSPSLKSRLLITTKDTPKNQVVLAMSNMPPADTATYSCALDMPHDSGPFQSFASDVWGP 120
Db 61 YSPSLKSRLLITTKDTSKKQVLLMTNVDPADTATYCTHEQYYYDTSQPY-YFDWGGG 119
```

```

OY      121 TMVTVSSGGGSGGGGSGGGGSGGGSSSYELMQLP-SVSVSPGQTASITCSGDLGDKYA 179
         ||||||| ||||||| ||||||| ||| : : ||| : : ||| |
Db      120 TLVTVSSGGGSGGGGSGGGGSGGGGSGGSGNQTQPSSSLASVGDVRTMTCRASQDIRKNL 179
         ||||||| ||||||| ||||||| ||| : : ||| : : ||| |
OY      180 CMYQOKPGRSPVLVIYGNKRPSCGIPERPSGNSNGNTATLTISGTQAMDEADYYCQAMDT 239
         ||||||| : : ||| : : ||| ||||| ||| | ||||| |
Db      180 NMYQOKPKAPKVLIVDASDLETGIPSRFGSGSGTDFILTISSLQPEDIAIYYCQOSDY 239
         ||||||| : : ||| : : ||| ||||| ||| | ||||| |
OY      240 STAVFGTGTCLTV 252
         || ||||| : :
Db      240 LPLTFGGGTKVDI 252

```

```

RESULT 11
US-10-360-828-23
; Sequence 23, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24
US-10-360-828-23

```

	Query Match	58.8%;	Score 794;	DB 15;	Length 253;	
	Best Local Similarity	62.8%;	Pred. No. 3.5e-48;			
	Matches 159;	Conservative 24;	Mismatches 68;	Indels 2;	Gaps 2;	
QY	1 QVTLKESGPTLVKPQTCTLLTCTLSGSFSLSTSGSVSGWTRQPFGKALEWLASINWNDDKC	60				
	:					
Db	1 QVTLKESGPTLVKPFQCTLLTCTFSGSFLRRTGEGVGWRQPPGKALEWLALIIYWDDDKR	60				
QY	61 YSPSLKSRLTITKTDPKNQVVLAMSNMDPADTATYSCALDMPHDSGPQSFDAVDWPGP	120				
	:					
Db	61 YSPSLKSRLTITKTDTSKQOVLTMTNVPADTATYYCTHEQYYYDTSGQPY-YFDPMWGQG	119				
QY	121 TMTVTSSGGGSGGGSGGGSGGGSSGYELMQLP-SVSYSVPGQTASITCSGDNLGDKYA	179				
	:                                 : :					
Db	120 TLVTVSSGGGSGGGSGGGSGGGSGGGSNIQVTPSSLSASVGDVRTMTCRASQDIRKNL	179				
QY	180 CWYQQKPGRSPLVIYDGNNKRPSGIPERFSGSNSGNATALLISGTQAMDEADYYCQAWDT	239				
	: :					
Db	180 NMWQQKPGKAPKVLIVDASDLLETGIPSRFSGSGSDTFILTISSLQPEDIATYYCCQSDY	239				
QY	240 STAVFGTGKTLTV	252				
	: :					
Db	240 LP LTFGGGTKVDI	252				

RESULT 12  
US-10-360-828-31  
; Sequence 31, Application US/10360828  
; Publication No. US20030206909A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shaobing

```

; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24 Variant
US-10-360-828-31

```

[illegible]

```

RESULT 13
US-09-880-748-1548
; Sequence 1548, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1548
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens

```

US-09-880-748-1548

Query Match 58.0%; Score 783; DB 10; Length 250;  
Best Local Similarity 63.5%; Pred. No. 2e-47;  
Matches 162; Conservative 29; Mismatches 56; Indels 8; Gaps 4;

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QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLASINWDDKC 60
Db 1 QVQLQESGPGLVKPSSETLSLTCAVSGYSIS-SGYWGMIRQPPGKLEWIGSIYHSGSTY 59
QY 61 YSPSLKSRLLTITKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGPQSPDASDVWGP 120
Db 60 YNPSLKSRTVTSVDTSKNQFSLKLSSTVTAADTAVYYCA--RVHYDILTGYLEWAFDIWGG 117
QY 121 TMVTVSSGGGGGGGGGGGGSSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 180
Db 118 TMVTVSSGGGGGGGGGGGGSSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 180
QY 181 WYQKPGKSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYCCQAMDTS 240
Db 175 WYQKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGTQAEDEADYCNRSRDS 234
QY 241 --TAVFGTGKLTVL 253
Db 235 GNHVVFGGGTQLTVL 249
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## RESULT 14

```
US-10-293-418-1548
; Sequence 1548, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1548
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1548
```

Query Match 58.0%; Score 783; DB 12; Length 250;  
Best Local Similarity 63.5%; Pred. No. 2e-47;  
Matches 162; Conservative 29; Mismatches 56; Indels 8; Gaps 4;

```
QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLASINWDDKC 60
Db 1 QVQLQESGPGLVKPSSETLSLTCAVSGYSIS-SGYWGMIRQPPGKLEWIGSIYHSGSTY 59
QY 61 YSPSLKSRLLTITKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGPQSPDASDVWGP 120
Db 60 YNPSLKSRTVTSVDTSKNQFSLKLSSTVTAADTAVYYCA--RVHYDILTGYLEWAFDIWGG 117
QY 121 TMVTVSSGGGGGGGGGGGGSSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 180
```

```
Db 118 TMVTVSSGGGGGGGGGGGGSSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 174
QY 181 WYQKPGKSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYCCQAMDTS 240
Db 175 WYQKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGTQAEDEADYCNRSRDS 234
QY 241 --TAVFGTGKLTVL 253
Db 235 GNHVVFGGGTQLTVL 249
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## RESULT 15

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US-09-880-748-1651
; Sequence 1651, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1651
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1651
```

Query Match 57.7%; Score 779.5; DB 10; Length 247;  
Best Local Similarity 60.5%; Pred. No. 3.5e-47;  
Matches 161; Conservative 28; Mismatches 44; Indels 33; Gaps 5;

```
QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLASINWDDKC 60
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSNYSIS-SGYWGMIRQPPGKLEWIGSIYHSGSTY 59
QY 61 YSPSLKSRLLTITKDTPKNQVVLAMSNMDDPADTATYSCA-----LDMPPHDSGPQ 109
Db 60 YNPSLKSRTVTSVDTSKNQFSLKLSSTVTAADTAVYYCARFRYDILTGYYDM----- 111
QY 110 SFDASDVWGPMTMTVSSGGGGGGGGGGGGSSSYELMQLPSVSVSPGQTASITC 169
Db 112 -----DVMGRTLVTVSSGGGGGGGGGGGGSS-----ELTQDPASVALGQTVRITC 160
QY 170 SGDNLGDKYACWYQKPGKSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDE 229
Db 161 QGDSLRSYASWYQKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDE 220
QY 230 ADYCCQAMDTS--TAVFGTGKLTVL 253
Db 221 ADYCCNSRDSGSHNVFGGGTQLTVL 246
```

Search completed: May 13, 2004, 15:43:30  
Job time : 38.4587 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:50:27 ; Search time 11.4218 Seconds  
(without alignments)  
2130.694 Million cell updates/sec

Title: US-10-072-301-17  
Perfect score: 1351  
Sequence: 1 QVTLKESGPTLVKPTQTTLT.....CQAWDTSTAVFGTGTKLTVL 253

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pirl:\*  
2: pirl2:\*  
3: pirl3:\*  
4: pirl4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	516	38.2	231	2 S25738	Ig lambda chain -
2	494.5	36.6	120	2 S30525	Ig lambda chain V
3	486.5	36.0	249	2 S41374	single chain Fv an
4	485	35.9	107	2 PC4283	anti-SS-A/Ro 60K p
5	483.5	35.8	124	2 A49002	Ig heavy chain V r
6	483	35.8	268	2 A56446	Ig heavy chain V r
7	479	35.5	151	2 S25739	Ig lambda chain -
8	478	35.4	231	2 S25751	Ig lambda chain -
9	474	35.1	106	1 L4HUBU	Ig lambda chain V-
10	474	35.1	114	2 S16440	Ig lambda chain -
11	472	34.9	231	2 S25753	Ig lambda chain -
12	470	34.8	95	2 S36065	Ig lambda chain -
13	470	34.8	106	1 L4HUX	Ig lambda chain V-
14	469	34.7	138	2 S31513	Ig heavy chain - h
15	466	34.5	374	2 S69339	Ig heavy chain V r
16	462.5	34.2	105	2 S44124	Ig lambda chain V
17	457	33.8	125	1 MHUMC	Ig heavy chain V-I
18	455	33.7	119	2 S18555	Ig heavy chain V r
19	451	33.4	121	2 A36005	Ig heavy chain V r
20	441	32.6	106	1 L4HUMU	Ig heavy chain V-
21	436	32.3	121	1 G1HUME	Ig heavy chain V-I
22	427.5	31.6	233	2 JCS322	p53 specific singl
23	423.5	31.3	120	1 G1HUCO	Ig heavy chain V-I
24	419.5	31.1	118	2 S18556	Ig heavy chain V r
25	418	30.9	107	1 L4HUMU	Ig lambda chain V-
26	417	30.9	119	2 S30526	Ig lambda chain V
27	415.5	30.8	232	2 S25756	Ig lambda chain -
28	415	30.7	96	2 S26924	Ig heavy chain V r
29	412	30.5	120	2 S30527	Ig lambda chain V

30	411	30.4	96	2 S26923	Ig heavy chain V r
31	403.5	29.9	106	2 S38495	Ig lambda chain -
32	403	29.8	106	1 L4HUX	Ig lambda chain V-
33	400	29.6	132	2 S09713	Ig lambda chain V
34	398.5	29.5	143	2 PT0174	Ig heavy chain pre
35	398.5	29.5	147	1 G2HUCS	Ig heavy chain pre
36	395	29.2	128	2 S24319	Ig lambda chain pr
37	393	29.1	108	1 L5HUDL	Ig lambda chain V-
38	389	28.8	233	2 S25747	Ig lambda chain -
39	388	28.7	105	2 S49533	anti-5m antibody V
40	386.5	28.6	122	2 S11740	Ig heavy chain pre
41	384	28.4	119	1 G1HUMU	Ig heavy chain V-I
42	380	28.1	96	2 S26922	Ig heavy chain V r
43	378	28.0	127	2 S70444	Ig lambda chain pr
44	375	27.8	108	2 S47184	Ig lambda chain -
45	375	27.8	109	2 S19663	Ig lambda chain V

ALIGNMENTS

RESULT 1					
S25738					
Ig lambda chain - human					
C:Species: Homo sapiens (man)					
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000					
C:Accession: S25738					
R:Combriato, G.; Klobeck, H.G.					
Eur. J. Immunol. 21, 1513-1522, 1991					
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam					
A:Reference number: S16439; MUID:91257162; PMID:1904362					
A:Accession: S25738					
A:Status: preliminary; translation not shown					
A:Molecule type: mRNA					
A:Residues: 1-231 <COM>					
A:Cross-references: EMBL:X57802; NID:g33701; PIDN:CAA40940.1; PID:g33702					
C:Superfamily: immunoglobulin V region; immunoglobulin homology					
C:Keywords: heterotetramer; immunoglobulin					
F:146-214/Domain: immunoglobulin homology <IMM>					
Query Match					
Best Local Similarity 38.2%; Score 516; DB 2; Length 231;					
Matches 98; Conservative 89.1%; Pred. No. 1.1e-27;					
Matches 98; Conservative 4; Mismatches 8; Indels 0; Gaps 0;					
Qy	144	GGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYACWYQOKRGRSPVLVIYGDNRPSG	203		
Db	16	GSVASYEITQPPSVSVSPGQTASITCSGDTLGDKYACWYQOKRGRSPVLVIFQDSKRPSG	75		
Qy	204	IPERFSGNSGNTATLTISGTQAMDEADYYCQAWDTSTAVFGTGTKLTVL	253		
Db	76	IPERFSGNSGNTATLTISGTQAMDEADYYCQAWDSTAVFGGTGTKLTVL	125		
RESULT 2					
S30525					
Ig lambda chain V region - human					
C:Species: Homo sapiens (man)					
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000					
C:Accession: S30525					
R:Marlette, X.					
submitted to the EMBL Data Library, October 1992					
A:Reference number: S30520					
A:Accession: S30525					
A:Status: preliminary					
A:Molecule type: mRNA					
A:Residues: 1-120 <MAR>					
A:Cross-references: EMBL:Z18331					
C:Superfamily: immunoglobulin V region; immunoglobulin homology					
C:Keywords: heterotetramer; immunoglobulin					
F:15-89/Domain: immunoglobulin homology <IMM>					
Query Match					
Best Local Similarity 36.6%; Score 494.5; DB 2; Length 120;					
Matches 88.8%; Pred. No. 1.6e-26;					

Matches 95; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 148 SYELMQLPSVSVSPGQTASITCSGDNLGDKYACWYQOKPGRSPVLVIYGDNKRPSGIPER 207  
Db 1 SYELTPPSVSVSPGQTASITCSGDKLGKRYACWYQOKPGRSPVLVIYGDNKRPSGIPER 60  
QY 208 FSGNSGNTATLTISGTQAMDEADYCCQAWDST-AVFGTGTXTVL 253  
Db 61 FSGNSGNTATLTISGTQAMDEADYCCQAWDSTVVFGGTGTXTVL 107

## RESULT 3

S41374  
Single chain Fv antibody - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C/Accession: S41374  
R/Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.  
Submitted to the EMBL Data Library, January 1994  
A/Description: Construction and functional characterization of a single chain Fv antibody  
A/Reference number: S41374  
A/Accession: S41374  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-249 <ART>  
A/Cross-references: EMBL:Z29480

Query Match 36.0%; Score 486.5; DB 2; Length 249;  
Best Local Similarity 43.6%; Pred. No. 1.1e-25;  
Matches 112; Conservative 34; Mismatches 90; Indels 21; Gaps 7;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSGVSVMIRPPKALEWLASI-NMNDK 59  
Db 1 QVQLQSGAELVIRPGASVYKLSCTASGFNFKD--YIMWVKQRPKGLWIAIAPASGNV 58  
QY 60 CYSPLKSRLLTTTKDTPKQVVLAMSNMPPADTATYSCALDMPHDSGPQSFASDVWG 119  
Db 59 KYVPRFQDKATITADTSNTAYLLSLTSEDVAVYCA-----RRDTLYTSLGYWQ 111  
QY 120 GTMVTVSSGGGGSGGGSGGGSSYELMQL-PSVSVSPGQTASITC-SGDNL--- 174  
Db 112 GSTVTVS-----SRGGSGGGSGGGSGGSDIELTQSPSVVVIPEGESVISCSSKSLYS 166  
QY 175 -GDKYACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADY 233  
Db 167 DGDSTLFWELQRPQSPQLLIRMSNLSAGVPRFSGSGSGTSTFLIRSRVEADVGVY 226  
QY 234 CQAWDSTAVFGTGTXTL 250  
Db 227 CMQHREYPLTFGAGTKL 243

## RESULT 4

PC4283  
anti-SS-A/Ro 60K peptide light chain E-60 - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 07-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 16-Jul-1999  
C/Accession: PC4283  
R/Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.  
Biochem. Biophys. Res. Commun. 232, 101-106, 1997  
A/Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltratin  
A/Reference number: PC4279; MUID:97236289; PMID:9125110  
A/Accession: PC4283  
A/Molecule type: protein  
A/Residues: 1-107 <SUZ>  
C/Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjog  
F,13-87/Domain: immunoglobulin homology <IMM>

Query Match 35.9%; Score 485; DB 2; Length 107;  
Best Local Similarity 87.7%; Pred. No. 6e-26;  
Matches 93; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 150 ELMQLPSVSVSPGQTASITCSGDNLGDKYACWYQOKPGRSPVLVIYGDNKRPSGIPER 209  
Db 1 ELLQPPSVSVSPGQTASITCSGDKLGDKYTCWYQOKPGRSPVLVIYGDNKRPSGIPER 60  
QY 210 GNSGNTATLTISGTQAMDEADYCCQAWDST-AVFGTGTXTVL 253  
Db 61 GNSGNTATLTISGTQAMDEADYCCQAWDSTVVFGGTGTXTVL 106

## RESULT 5

A49002  
Ig heavy chain V region, rheumatoid factor RF antibody - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999  
C/Accession: A49002  
R/Stuber, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, H.W.J.; Gaskin,  
Arthritis Rheum. 35, 900-904, 1992  
A/Title: A rheumatoid factor from a normal individual encoded by VH2 and V kappa II g-  
A/Reference number: A49002; MUID:92352481; PMID:1322670  
A/Accession: A49002  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-124 <STU>  
A/Cross-references: GB:M90808; NID:G185515; PIDN:AAA52989.1; PID:G567176  
A/Experimental source: EBV-transformed lymphoblastoid cell line GSH23  
A/Note: sequence extracted from NCBI backbone (NCBIN:110261, NCBIPI:110262)  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F,15-99/Domain: immunoglobulin homology <IMM>

Query Match 35.8%; Score 483.5; DB 2; Length 124;  
Best Local Similarity 74.6%; Pred. No. 8.8e-26;  
Matches 97; Conservative 7; Mismatches 17; Indels 9; Gaps 2;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSGVSVMIRPPKALEWLASI-NMNDK 60  
Db 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSGVSVMIRPPKALEWLASI-NMNDK 60  
QY 61 YSPSLKSRLLTTTKDTPKQVVLAMSNMPPADTATYSCA---LDMPPHDSGPQSFASDVW 117  
Db 61 YSPSLKSRLLTTTKDTPKQVVLAMSNMPPADTATYSCA---LDMPPHDSGPQSFASDVW 117  
QY 118 GPGTMTVSS 127  
Db 115 GQGTLVTVSS 124

## RESULT 6

A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996  
C/Accession: A56446  
R/Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.  
J. Biol. Chem. 270, 7829-7835, 1995  
A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally identit  
A/Reference number: A56446; MUID:95229583; PMID:7713873  
A/Accession: A56446  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-268 <TAN>  
A/Cross-references: GB:U20617  
C/Keywords: heterotetramer; immunoglobulin

Query Match 35.8%; Score 483; DB 2; Length 268;  
Best Local Similarity 42.0%; Pred. No. 2.1e-25;  
Matches 108; Conservative 38; Mismatches 87; Indels 24; Gaps 7;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSGVSVMIRPPKALEWLASI-NMNDK 59  
Db 3 QVQLQSGAELVIRPGASVYKLSCTASGFNFKD--YIMWVKQRPKGLWIAIAPASGNV 60  
QY 60 CYSPLKSRLLTTTKDTPKQVVLAMSNMPPADTATYSCALDMPHDSGPQSFAS---DV 116

Db 61 KYDPKFGKATIAADTSSNTAYLQLSLTSEDYAVYYCA-----SYLLTRYENY 109  
Qy 117 WPGTMYTVSSGGGGSGGGSSGYELMQLPSV-SVSPGQTASITCSGDNIG 175  
Db 110 WGGCTTVTVS-----SGGGSGGGSDSGGSDIELTQSPAIMSASLGEKVTMSCRASS-S 163  
Qy 176 DKYACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQ 235  
Db 164 VNFYWYQOKSDASPKLMVYTTSHLPQVPARFSGSGSGNSYSLTISMEGEDAATYYCQ 223  
Qy 236 AWDSTAVFGTGKLTIV 252  
Db 224 QFTSSPFTFGSGTKLEI 240

RESULT 7  
S25739  
Ig lambda chain - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S25739  
R:Combriato, G.; Klobeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam  
A:Reference number: S16439; MUID:91257162; PMID:1904362  
A:Accession: S25739  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-151 <COM>  
A:Cross-references: EMBL:X57803; NID:g33703; PIDN:CAA40941.1; PID:g33704  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-108/Domain: immunoglobulin homology <IMM>

Query Match 35.5%; Score 479; DB 2; Length 151;  
Best Local Similarity 84.5%; Pred. No. 2.2e-25;  
Matches 93; Conservative 3; Mismatches 14; Indels 0; Gaps 0;  
Qy 144 GGGSSYELMQLPSVSVSPGQTASITCSGDNIGDKYACWYQOKPGRSPVLVIYGDNKRPSG 203  
Db 16 GSVASYELTQPPSVSVSPGQTASITCSGDTLGDKYACWYQOKPGRSPVLVIYQDSKRPSG 75  
Qy 204 IPERFSGNSGNTATLTISGTQAMDEADYYCQAWDSTAVFGTGKLTIVL 253  
Db 76 IPERFSGNSGNTATLTISGTQAMDEADYYCQALGQHCVFGGTGKLTIVL 125

RESULT 8  
S25751  
Ig lambda chain - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S25751  
R:Combriato, G.; Klobeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam  
A:Reference number: S16439; MUID:91257162; PMID:1904362  
A:Accession: S25751  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-231 <COM>  
A:Cross-references: EMBL:X57816; NID:g33731; PIDN:CAA40953.1; PID:g33732  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:146-214/Domain: immunoglobulin homology <IMM>

Query Match 35.4%; Score 478; DB 2; Length 231;  
Best Local Similarity 83.6%; Pred. No. 3.9e-25;  
Matches 92; Conservative 5; Mismatches 13; Indels 0; Gaps 0;  
Qy 144 GGGSSYELMQLPSVSVSPGQTASITCSGDNIGDKYACWYQOKPGRSPVLVIYGDNKRPSG 203  
Db 16 GSVASYELTQPPSVSVSPGQTASITCSGDKLGDKYACWYQOKPGRSPVLVIYQDSKRPSG 75

Db 16 GSVASYELTQPPSVSVSPGKTASITCSGDKLGDKYASWYQOKAGQSPVLVIYRHSKRPSG 75  
Qy 204 IPERFSGNSGNTATLTISGTQAMDEADYYCQAWDSTAVFGTGKLTIVL 253  
Db 76 IPERFSGNSGNTATLTISGTQVMEADYYCQAWDSIVVFGGTGKLTIVL 125

RESULT 9  
L4HUBU  
Ig lambda chain V-IV region (Bau) - human  
C:Species: Homo sapiens (man)  
C:Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 02-Sep-1997  
C:Accession: A01981  
R:Baczko, K.; Braun, D.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 355, 131-154, 1974  
A:Title: Pattern of antibody structure. The primary structure of a monoclonal immunoglo  
A:Reference number: A01981; MUID:75059189; PMID:4435717  
A:Accession: A01981  
A:Molecule type: protein  
A:Residues: 1-106 <BAC>  
C:Comment: This is a Bence Jones protein.  
C:Genetics:  
A:Gene: GDB:IGLV@  
A:Cross-references: GDB:119342; OMIM:147240  
A:Map position: 22q11.2-22q11.2  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:14-88/Domain: immunoglobulin homology <IMM>  
F:21-86/Disulfide bonds: #status predicted

Query Match 35.1%; Score 474; DB 1; Length 106;  
Best Local Similarity 83.8%; Pred. No. 3.2e-25;  
Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;  
Qy 149 YELMQLPSVSVSPGQTASITCSGDNIGDKYACWYQOKPGRSPVLVIYGDNKRPSGIPERF 208  
Db 1 YGLTQPPSLSVSPGQTASITCSGDKLGEQYVCWYQOKPGRSPVLVIYHDSKRPSGIPERF 60  
Qy 209 SGSNSGNTATLTISGTQAMDEADYYCQAWDSTAVFGTGKLTIVL 253  
Db 61 SGSNSGNTATLTISGTQAMDEADYYCQAWDSYTVIFGGTGKLTIVL 105

RESULT 10  
S16440  
Ig lambda chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S16440  
R:Combriato, G.; Klobeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam  
A:Reference number: S16439; MUID:91257162; PMID:1904362  
A:Accession: S16440  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-114 <COM>  
A:Cross-references: EMBL:X57826  
C:Genetics:  
A:Introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-108/Domain: immunoglobulin homology <IMM>

Query Match 35.1%; Score 474; DB 2; Length 114;  
Best Local Similarity 89.9%; Pred. No. 3.5e-25;  
Matches 89; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
Qy 144 GGGSSYELMQLPSVSVSPGQTASITCSGDNIGDKYACWYQOKPGRSPVLVIYGDNKRPSG 203  
Db 16 GSVASYELTQPPSVSVSPGQTASITCSGDKLGDKYACWYQOKPGRSPVLVIYQDSKRPSG 75



OY 204 IPERFSGNSGNTATLTISGTQAMDEADYYCQAWDTSTA 242  
Db 76 IPERFSGNSGNTATLTISGTQAMDEADYYCQAWDSSTA 114

RESULT 11  
S25753  
Ig lambda chain - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C/Accession: S25753  
R/Combrato, G.; Klobbeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam  
A/Reference number: S16439; MUID:91257162; PMID:1904362  
A/Accession: S25753  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-231 <COM>  
A/Cross-references: EMBL:X57818; NID:G33735; PIDN:CAA40955.1; PID:G33736  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F,146-214/Domain: immunoglobulin homology <IMM>

Query Match 34.9%; Score 472; DB 2; Length 231;  
Best Local Similarity 80.9%; Pred. No. 9.8e-25;  
Matches 89; Conservative 7; Mismatches 14; Indels 0; Gaps 0;  
OY 144 GGGSYELMQLPSVSPGQTASITCSGDNLDKXACWYQOKPGRSPVLVIYGDNRKPSG 203  
Db 16 GSVASYELTPSPSVSPGQTASITCFGDKLDKXSWYQOKPQSPVLVIYQDNRPSG 75  
OY 204 IPERFSGNSGNTATLTISGTQAMDEADYYCQAWDTSTAVFGTGTCLTVL 253  
Db 76 IPERFSGNSGNTATLTISGTQAMDEADYYCQAWDSNTVVFGGGTCLTVL 125

RESULT 12  
S36065  
Ig lambda chain - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 01-Dec-1995 #text\_change 21-Jan-2000  
C/Accession: S36065  
R/Williams, S.C.  
Submitted to the EMBL Data Library, April 1993  
A/Reference number: S36046  
A/Accession: S36065  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-95 <WIL>  
A/Cross-references: EMBL:Z22208; NID:G312871; PIDN:CAA80216.1; PID:G312872  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F,15-89/Domain: immunoglobulin homology <IMM>

Query Match 34.8%; Score 470; DB 2; Length 95;  
Best Local Similarity 92.6%; Pred. No. 5.3e-25;  
Matches 88; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
OY 148 SYELMQLPSVSPGQTASITCSGDNLDKXACWYQOKPGRSPVLVIYGDNRKPSGIPER 207  
Db 1 SYELTPSPSVSPGQTASITSGDKLDKXACWYQOKPQSPVLVIYQDSKRPSGIPER 60  
OY 208 FSGNSGNTATLTISGTQAMDEADYYCQAWDTSTA 242  
Db 61 FSGNSGNTATLTISGTQAMDEADYYCQAWDSSTA 95

RESULT 13  
LAHUX  
Ig lambda chain V-IV region (X) - human  
C/Species: Homo sapiens (man)

C/Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 02-Sep-1997  
C/Accession: A01982  
R/Milstein, C.; Clegg, J.B.; Jarvis, J.M.  
Biochem. J. 110, 631-652, 1968  
A/Title: Immunoglobulin lambda-chains. The complete amino acid sequence of a Bence-Jone  
A/Reference number: A90243; MUID:69088380; PMID:4883841  
A/Accession: A01982  
A/Molecule type: protein  
A/Residues: 1-106 <MIL>  
C/Comment: This is a Bence Jones protein.  
C/Genetics:  
A/Gene: GDB:IGLV@  
A/Cross-references: GDB:119342; OMIM:147240  
A/Map position: 22q11.2-22q11.2  
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer  
F,14-88/Domain: immunoglobulin homology <IMM>  
F,21-86/Disulfide bonds: #status predicted

Query Match 34.8%; Score 470; DB 1; Length 106;  
Best Local Similarity 83.8%; Pred. No. 5.9e-25;  
Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;  
OY 149 YEIMQLPSVSPGQTASITCSGDNLDKXACWYQOKPGRSPVLVIYGDNRKPSGIPERF 208  
Db 1 YDLTPSPSVSPGQTASITCSGDKLDKXQKPCWYQQRPGSPVLVIYQDNRSGIPERF 60  
OY 209 SGSNSGNTATLTISGTQAMDEADYYCQAWDTSTAVFGTGTCLTVL 253  
Db 61 SGSNSGNTATLTISGTQAMDEADYYCQAWDSMSVVFGGGTCLTVL 105

RESULT 14  
S31513  
Ig heavy chain - human  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C/Accession: S31513  
R/Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
Submitted to the EMBL Data Library, December 1992  
A/Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autc  
A/Reference number: S31509  
A/Accession: S31513  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-138 <CHA>  
A/Cross-references: EMBL:X69861; NID:G33084; PIDN:CAA49495.1; PID:G33085  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F,30-114/Domain: immunoglobulin homology <IMM>

Query Match 34.7%; Score 469; DB 2; Length 138;  
Best Local Similarity 74.0%; Pred. No. 9.1e-25;  
Matches 94; Conservative 7; Mismatches 20; Indels 6; Gaps 2;  
OY 1 QVTLKESGPTLVKPTQTLTCTLSGFSLSSTSGVSGWIRQPPGKALEWLASINMDDKC 60  
Db 16 QITLKESGPTLVKPTQTLTCTLSGFSLSSTSGVSGWIRQPPGKLEWLASIYWDDBKR 75  
OY 61 YSPSLKRLTITKDTPRNQVLAAMSNMPPADTATYSCALDMPHDSGPQSFDA--DVWGP 119  
Db 76 YSPSLKRLTITKDTSQNQVLTMTNMDPVDATYYCA-----HRPGIAVTGNGFDYWGQ 130  
OY 120 GTMVTVS 126  
Db 131 GTLVTVS 137

RESULT 15  
S69339  
Ig heavy chain V region precursor - human



C;Species: Homo sapiens (man)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C;Accession: S69339; S72664  
R;Khamlchi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A;Reference number: S69339; MUID:95262687; PMID:7744049  
A;Accession: S69339  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-374 <KHA>  
R;Khamlchi, A.A.  
submitted to the EMBL Data Library, September 1994  
A;Reference number: S72664  
A;Accession: S72664  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-140,'C',142-374 <KH2>  
A;Cross-references: EMBL:X81695  
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 34.5%; Score 466; DB 2; Length 374;  
Best Local Similarity 71.7%; Pred. No. 4.1e-24;  
Matches 91; Conservative 11; Mismatches 21; Indels 4; Gaps 1;

QY 1 QVTLKESGPTLVKPTQTTLTLTCTLSGFSLSGVSVGWIRQPPGKALEWLASINWDDKC 60  
|:|||||  
DB 20 QITLKESGPTLVKPTQTTLTCTFSGFSLSKSGVGVGIRQPPGQALEWLASIFWDDDKR 79  
|:|||||

QY 61 YSPSLKSRITTKDTPKNQVVLAMSNMADPATYSCALDMPPHDSGPGSFDASDVWGP 120  
|:|||||  
DB 80 YSPSLRTRITTKDTSKNQVVLMTNVDPADPATYTCGYSVEGYGGYRPHS---WGQG 135  
|:|||||

QY 121 TMTVSS 127  
|:|||||  
DB 136 TLVTSS 142  
|:|||||

Search completed: May 13, 2004, 15:08:40  
Job time : 12.4218 secs

(0.288) NY 70 70 70 70 70  
THIS PAGE IS FOR THE

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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:01 ; Search time 7.1233 Seconds  
(without alignments)  
1849.388 Million cell updates/sec

Title: US-10-072-301-17

Perfect score: 1351

Sequence: 1 QVTLKESGPTLVKPTQTTLT.....CQAMDTSTAVFGTGTKLTVL 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	474	35.1	106	1 LV4A_HUMAN	P01715 homo sapien
2	470	34.8	106	1 LV4B_HUMAN	P01716 homo sapien
3	457	33.8	125	1 HV2D_HUMAN	P01817 homo sapien
4	441	32.6	106	1 LV4E_HUMAN	P06889 homo sapien
5	436	32.3	121	1 HV2E_HUMAN	P01818 homo sapien
6	423.5	31.3	120	1 HV2B_HUMAN	P01815 homo sapien
7	418	30.9	107	1 LV4C_HUMAN	P01717 homo sapien
8	403	29.8	106	1 LV4D_HUMAN	P01718 homo sapien
9	398.5	29.5	147	1 HV2H_HUMAN	P04338 homo sapien
10	393	29.1	108	1 LV5A_HUMAN	P01719 homo sapien
11	389	28.8	111	1 LV3B_HUMAN	P01748 homo sapien
12	384	28.4	119	1 HV2C_HUMAN	P01816 homo sapien
13	369.5	27.4	126	1 HV2A_HUMAN	P01814 homo sapien
14	351	26.0	108	1 LV3A_HUMAN	P01720 homo sapien
15	351	26.0	111	1 LV7A_HUMAN	P01720 homo sapien
16	337	24.9	111	1 LV1D_HUMAN	P01702 homo sapien
17	336	24.9	130	1 LV1G_HUMAN	P06316 homo sapien
18	325	24.1	109	1 LV1F_HUMAN	P04208 homo sapien
19	324	24.0	129	1 HV2F_HUMAN	P01824 homo sapien
20	324	24.0	144	1 HV43_MOUSE	P01819 mus musculu
21	320	23.7	109	1 LV1I_HUMAN	P06888 homo sapien
22	319	23.6	111	1 LV2G_HUMAN	P01710 homo sapien
23	317	23.5	111	1 LV1C_HUMAN	P01701 homo sapien
24	313.5	23.2	111	1 LV1B_HUMAN	P01700 homo sapien
25	312	23.1	111	1 LV2F_HUMAN	P01709 homo sapien
26	310	22.9	109	1 LV2E_HUMAN	P01708 homo sapien
27	309.5	22.9	110	1 LV2J_HUMAN	P01713 homo sapien
28	309	22.9	111	1 LV2C_HUMAN	P01706 homo sapien
29	308.5	22.8	112	1 LV2K_HUMAN	P04209 homo sapien
30	303.5	22.5	112	1 LV1H_HUMAN	P06887 homo sapien
31	303.5	22.5	112	1 LV6A_HUMAN	P01721 homo sapien
32	302	22.4	111	1 LV6C_HUMAN	P06317 homo sapien
33	301	22.3	111	1 LV2I_HUMAN	P01712 homo sapien

34	296.5	21.9	131	1 LV6E_HUMAN	P06319 homo sapien
35	294	21.8	111	1 LV2B_HUMAN	P01705 homo sapien
36	292.5	21.7	135	1 HV02_XENLA	P20957 xenopus lae
37	290	21.5	137	1 HV46_MOUSE	P01822 mus musculu
38	289	21.4	111	1 LV2A_HUMAN	P01704 homo sapien
39	283	20.9	111	1 LV1A_HUMAN	P01699 homo sapien
40	283	20.9	111	1 LV6D_HUMAN	P06318 homo sapien
41	280.5	20.8	116	1 HV6I_MOUSE	P18532 mus musculu
42	279	20.7	115	1 HV44_MOUSE	P01820 mus musculu
43	277	20.5	111	1 LV2H_HUMAN	P01711 homo sapien
44	275.5	20.4	112	1 LV6B_HUMAN	P01722 homo sapien
45	274	20.3	111	1 LV2D_HUMAN	P01707 homo sapien

ALIGNMENTS

RESULT 1					
LV4A_HUMAN					
ID LV4A_HUMAN	STANDARD;	PRT;	106 AA.		
AC P01715;					
DT 21-JUL-1986 (Rel. 01, Created)					
DT 21-JUL-1986 (Rel. 01, Last sequence update)					
DT 10-OCT-2003 (Rel. 42, Last annotation update)					
DE Ig lambda chain V-IV region Bau.					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
OX NCBI_Taxid=9606;					
RN [1]					
RP SEQUENCE.					
RX MEDLINE=75059189; PubMed=4435717;					
RA Baczko K., Braun D., Hilschmann N.;					
RT "Pattern of antibody structure, the primary structure of monoclonal					
RT immunoglobulin L-chain of the lambda-type, subgroup IV (Bence-Jones					
RT protein Bau.)."					
RL Hoppe-Seyler's Z. Physiol. Chem. 355:131-154(1974).					
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.					
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.					
DR PIR; A01981; L4HUB.					
DR HSSP; P80748; ZLOT.					
DR GO; GO:0005576; C:extracellular; NAS.					
DR GO; GO:0003823; F:antigen binding; NAS.					
DR GO; GO:0006955; P:immune response; NAS.					
DR InterPro; IPR007110; Ig-like.					
DR InterPro; IPR003596; Ig_v.					
DR Pfam; PF00047; Ig_1.					
DR SMART; SM00406; IGV; 1.					
DR PROSITE; PS50835; IG LIKE; 1.					
KW Immunoglobulin V region; Bence-Jones protein.					
FT DOMAIN 1 102 . IG-LIKE.					
FT NON TER 106 106					
SQ SEQUENCE 106 AA; 11305 MW; 4B6A688E0EC46571 CRC64;					
Query Match					
Best Local Similarity 35.1%; Score 474; DB 1; Length 106;					
Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;					
QY	149	YELMQLPSVSPGQTASITCSGDNLGKACWYQOKPGRSPVLYIGDNKRPSPGIPERF	208		
DB	1	YGLTOPPSLSVSPGQTASITCSGDKLGEQYVCWYQOKPGQSPVLVIYHDSKRPSPGIPERF	60		
QY	209	SGSNSGNTATLTISGTQAMDEADYYCQAMDTSTAVFGTGTKLTVL	253		
DB	61	SGSNSGNTATLTISGTQAMDEADYYCQAMDSYTVIFGGGTKLTVL	105		
RESULT 2					
LV4B_HUMAN					
ID LV4B_HUMAN	STANDARD;	PRT;	106 AA.		
AC P01716;					
DT 21-JUL-1986 (Rel. 01, Created)					
DT 21-JUL-1986 (Rel. 01, Last sequence update)					

DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-IV region X.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP  
RX MEDLINE=69088380; PubMed=4833841;  
RA Milstein C., Clegg J.B., Jarvis J.M.;  
RT "Immunoglobulin lambda-chains. The complete amino acid sequence of a  
RT Bence-Jones protein.";  
RL Biochem. J. 110:631-652(1968).  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01982; L4HUX.  
DR HSSP; P80748; 2LOI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00447; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 102 IG-LIKE.  
FT NON\_TER 106  
SQ SEQUENCE 106 AA; 11334 MW; 24D04344AA812855 CRC64;

Query Match 34.8%; Score 470; DB 1; Length 106;  
Best Local Similarity 83.8%; Pred. No. 1.4e-27;  
Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

OY 149 YELMQLPSVSVSPGQTASITCSGDNLGDKYACWYQOKPGKSPVLVIYGDNKRPSGIPERF 208  
DB 1 YDLTOPPSVSVSPGQTASITCSGDKLGDKDCWYQOKPGKSPVLVIYQDNQRSSGIPERF 60  
OY 209 SGSNSGNTATLTISGTQAMDEADYVQAWDTSTAVFGTGTXTLTVL 253  
DB 61 SGSNSGNTATLTISGTQAMDEADYVQAWDSMSVVFSGTTRLTVL 105

RESULT 3  
HV2D\_HUMAN  
ID HV2D\_HUMAN STANDARD; PRT; 125 AA.  
AC P01817;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-II region MCE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP  
RX MEDLINE=8118242; PubMed=6780622;  
RA Gerber-Jenson B., Kazin A., Kehoe J.M., Scheffell C., Erickson B.W.,  
RA Litman G.W.;  
RT "Molecular basis for the temperature-dependent insolubility of  
RT cryoglobulins. X. The amino acid sequence of the heavy chain variable  
RT region of MCE.";  
RL J. Immunol. 126:1212-1216(1981).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM  
CC CRYOIMMUNOGLOBULIN.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A02092; MHUMC.  
DR HSSP; P01825; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Pyrrrolidone carboxylic acid.  
FT DOMAIN 1 113  
FT MOD\_RES 1 113  
FT NON\_TER 125 125  
SQ SEQUENCE 125 AA; 13783 MW; 7A1ADFC40F47BB5 CRC64;

Query Match 33.8%; Score 457; DB 1; Length 125;  
Best Local Similarity 70.9%; Pred. No. 1.5e-26;  
Matches 90; Conservative 11; Mismatches 24; Indels 2; Gaps 1;

OY 1 QVTLKESGPTLVKPTOTLTCTLSGFSLSGVSIGWIRPPGKALEWLASINMDDKC 60  
DB 1 QITLKESGPTLVKPTETTLTCTFSGFSLSGVSIGWIRPPGKALEWLASINMDDNR 60  
OY 61 YSPSLKSRLLTTTKDTPKQVVLAMSNMPPADATYSCALDMPHDSGQSFSDASDVWGP 120  
DB 61 YSPSLKSRLLTTTKDTSRQVVLITNMDPVSIGTYFCAHRPPWRTG--NLGFDXWGG 118  
OY 121 TMVTIVSS 127  
DB 119 TLVTIVSS 125

## RESULT 4

LVAE\_HUMAN  
ID LVAE\_HUMAN STANDARD; PRT; 106 AA.  
AC P06889;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-IV region MOL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP  
RX MEDLINE=87156515; PubMed=3103603;  
RA Holm E., Sletten K., Huby G.;  
RT "Structural studies of a carbohydrate-containing  
RT immunoglobulin-lambda-light-chain amyloid-fibril protein (AL) of  
RT variable subgroup III.";  
RL Biochem. J. 239:545-551(1986).  
CC -1- MISCELLANEOUS: RESIDUES 29-30 AND 56-58 WERE POSITIONED BY  
CC HOMOLOGY.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A26019; L4HUM.  
DR HSSP; P80748; 2LOI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00447; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Amyloid; Glycoprotein.  
FT DOMAIN 1 103  
FT DISULFID 21 86  
FT CARBOHYD 90 90  
FT NON\_TER 106 106  
SQ SEQUENCE 106 AA; 11272 MW; D9BB77D4797D2123 CRC64;

Query Match 32.6%; Score 441; DB 1; Length 106;  
Best Local Similarity 77.1%; Pred. No. 1.7e-25;  
Matches 81; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

OY 149 YELMQLPSVSVSPGQTASITCSGDNLGDKYACWYQOKPGKSPVLVIYGDNKRPSGIPERF 208  
DB 1 YDLTOPPSVSVSPGQTASITCSGDKLGDKDCWYQOKPGKSPVLVIYQDNQRSSGIPERF 60



Db 1 YELTPPSVSVSPGQTATISCSGDKLGESYYDMYQSPGSPPLVIYEGDKRPSGIPZRF 60

QY 209 SGNSNGNTATLTISGTOAMDEADYVYCOAMDSTAVFGTGTCLTVL 253  
|||||:|||||:|||||  
61 SGNSNGNTATLTISGTESMDEADYVYCOAMNSSSVLFGGGTCLTVL 105

```

RESULT 5
HV2E_HUMAN
ID HV2E_HUMAN STANDARD; PRT; 121 AA.
AC P01818;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE 1g heavy chain V-II region HE.
OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

```

RK	MEDLINE=70114712; PubMed=5264153;
RA	Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.;
RT	"Subgroups of amino acid sequences in the variable regions of
RT	immunoglobulin heavy chains.",
RL	Proc. Natl. Acad. Sci. U.S.A. 64:997-1003(1969).
CC	-1- MISCELLANEOUS: THIS GAMMA-1 CHAIN WAS ISOLATED FROM A MYELOMA
CC	PROTEIN.
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR	PIR; A02093; GIHQHE.
DR	HSSP; P01825; 7FAB.
DR	GO; GO:0005576; C:extracellular; NAS.
DR	GO; GO:0003823; F:antigen binding; NAS.
DR	GO; GO:0006955; P:immune response; NAS.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig_1.
DR	SMART; SM00406; IGv_1.
DR	PROSITE; PSS0835; IG LIKE; 1.
KW	Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT	DOMAIN 1 120 IG-LIKE.
FT	MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT	NON_TER 121 121
SQ	SEQUENCE 121 AA; 13483 MW; 88A5082C273753B4 CRC64;

Query Match	32.3%	Score 436;	DB 1;	Length 121;
Best Local Similarity	68.8%	Pred. No. 4.6e-25;		
Matches	88;	Conservative	13;	Mismatches 19;
			Indels	8;
			Gaps	3;

```

QY      1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSSTGVSVGWIRQPPGKALEWLA-SINWDDK 59
      |||||:|||||:|||||:|:|:|||||:|||||:|:|:|
Db      1 QVTLKENGPTLVKPTETLLTCTLSGSLTJTDGVAVGWIRQPGRALEWLAWLLYDDDK 60
QY      60 CYSPLKSRLTITKDTPKQNVVLA MSNNDPADTATYSCALDMPHDSGPGQSFASDVWGP 119
      :|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 RFSPLKSRLTIVTRDTSKNQVVLMTWINDPVDATATYYCV-----HRHPRTL-AFDVWGQ 113
QY      120 GTMVTVSS 127
      ||| |||
Db      114 GTKVAVSS 121

```

RESULT 6		
HV2B_HUMAN		
ID	HV2B_HUMAN	STANDARD; PRT; 120 AA.
AC	P01815;	
DT	21-JUL-1986 (Rel. 01, Created)	
DT	21-JUL-1986 (Rel. 01, Last sequence update)	
DT	10-OCT-2003 (Rel. 42, Last annotation update)	
DE	Ig heavy chain V-II region COR.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	

```

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;
RA Press E.M., Hogg N.M.;
RT "The amino acid sequences of the Fd fragments of two human gamma-1
RT heavy chains.";
RL Biochem. J. 117:641-660(1970).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02089; GHIHCO.
DR HSSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.
FT DOMAIN 1 110 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 94
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .).
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13226 MW; 158A8B29AE7EEB98 CRC64;

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Query Match	31.3%;	Score 423.5;	DB 1;	Length 120;
Best Local Similarity	67.2%;	Pred. No. 3.6e-24;		
Matches	86;	Conservative	14;	Mismatches 19;
			Indels	9;
			Gaps	3;

```

OY      1 QVTLKESGPTLVKPTQTLLTCTCTSGFSLSTGVSVGWIRQPPGKALEWIASINWDDKC 60
        ||||:||||| ||||| |||||:|: ||||| ||||| |||||:|: |||
Db      1 QVTLRESGPALVKPTQTLLTCTCTSGFSLSTGMCVGMIRQPPGKLEWILARIDWDDKY 60
OY      61 YSPSLKSRLLTITKDTPKNOVLAMSNMDDPADTATYSCA-LDMPPHDSGPOSFDAADVWGP 119
        |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 YNTSLETRLTISKDTSRNQVVL---TMDPVDATATYCARITVIPAPAG-----YMDVWGR 112

```

QY	120	GTMTVSS	127
Db	113	GTPTVSS	120

```

RESULT 7
LV4C_HUMAN
ID LV4C_HUMAN STANDARD; PRT; 107 AA.
AC P01717;
DC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-IV region H11.
OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

```

RA Lopez de Castro J.A., Chiu Y.-Y.H., Poljak R.J.;  
 RT "Amino acid sequence of the variable region of the light (lambda)  
 chain from human myeloma cryoimmunoglobulin IgG H1.",  
 RL Biochemistry 17:1718-1723 (1978).  
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS APPARENTLY  
 CC IDENTICAL WITH THAT OF HUMAN SH LAMBDA CHAIN EXCEPT IN HAVING  
 CC 155-116 (H1L NUMBERING) INSTEAD OF VAL.  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A01983; L4HUHL.  
 DR HSSP; P80748; 2LOI.  
 DR GO; GO:0005576; C:extracellular; NAS.

DR GO:0003823; F:antigen binding; NAS.  
DR GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 97  
FT NON TER 107 107 IG-LIKE.  
SQ SEQUENCE 107 AA; 11517 MW; A5C8AFBE0C0C590A CRC64;

Query Match 30.9%; Score 418; DB 1; Length 107;  
Best Local Similarity 74.5%; Pred. No. 7.9e-24;  
Matches 79; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 148 YEIMQLPSVSPGQTASITCSGDNLGKACWYQOKPGRSPVLVIYGDNKRPSGIPER 207  
Db 1 SYELTOPPSVSPGQTARITCSANALPNQAYWYQKPRAPVMVIYKDTQRPSPGIPOR 60  
QY 208 FSGNSGNTATLTISGTQAMDEADYCCQAMDSTAVFGTGTCLTVL 253  
Db 61 FSSSTSGTITLTISGVAEDADYCCQAMDNSASITGGGTCLTVL 106

RESULT 8  
LV4D\_HUMAN  
ID LV4D\_HUMAN STANDARD; PRT; 106 AA.  
AC P01718;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-IV region Kern.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71150336; PubMed=5549568;  
RA Ponscigl H., Hess M., Hilschmann N.;  
RT "Structural rule of antibodies. Primary structure of a monoclonal  
RT immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-  
RT protein Kern). V. The complete amino acid sequence and its genetic  
RT interpretation.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ MARKER.  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR: A01984; L4HUKN.  
DR HSSP: P80748; 2LOI.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003823; F:antigen binding; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 102  
FT DISULFID 21 86 IG-LIKE.  
FT NON TER 106 106 BY SIMILARITY.  
SQ SEQUENCE 106 AA; 11277 MW; C8B4A05B9CB43CBE CRC64;

Query Match 29.8%; Score 403; DB 1; Length 106;  
Best Local Similarity 72.4%; Pred. No. 9.4e-23;  
Matches 76; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 149 YEIMQLPSVSPGQTASITCSGDNLGKACWYQOKPGRSPVLVIYGDNKRPSGIPER 208  
Db 1 YALTQPPSVSPGQTAVITCSGDNLEKTFVSWFOQRPQSPPLVIYHTSRSPSEIPERF 60

QY 209 SGNSTGNTATLTISGTQAMDEADYCCQAMDSTAVFGTGTCLTVL 253  
Db 61 SSSSGATATLTISGAQSVDEADYFCQTDWDTITTAIFGGGTCLTVL 105

RESULT 9  
HV2H\_HUMAN  
ID HV2H\_HUMAN STANDARD; PRT; 147 AA.  
AC P0438;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V-II region SESS precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84298107; PubMed=6089186;  
RA Takahashi N., Noma T., Honjo T.;  
RT "Rearranged immunoglobulin heavy chain variable region (VH)  
RT pseudogene that deletes the second complementarity-determining  
RT region.";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).  
DR PIR: A02090; G2HUCS.  
DR HSSP: P01825; 7FAB.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003823; F:antigen binding; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 147 IG HEAVY CHAIN V-II REGION SESS.  
FT DOMAIN 20 118 V SEGMENT.  
FT FT 119 132 D SEGMENT.  
FT DOMAIN 133 147 J SEGMENT.  
FT NON TER 147 147  
SQ SEQUENCE 147 AA; 16323 MW; FCBCDB3D00FB6666 CRC64;

Query Match 29.5%; Score 398.5; DB 1; Length 147;  
Best Local Similarity 63.9%; Pred. No. 2.8e-22;  
Matches 78; Conservative 16; Mismatches 27; Indels 1; Gaps 1;

QY 1 QVTLKESGPTLVPTQTTLTCTLSGFSLSGVSQVGTROPKGALEWLASINWDDKC 60  
Db 20 QVNLRESGPALVATHTLTCTFSGLSVNTRGMSVSWTRQPPKALEWLASINWDDKY 79  
QY 61 YSPSLKSRITTKDTPKNQVVLAMSNMDPADTATYSCA-LDMPPHDSGPOSFDAQDVWGP 119  
Db 80 YGTSLETSLTSLKSDTSKNQVVLKVTNMDPADTATYCCARMQVTMVRVWITSNAFDIMGQ 139  
QY 120 GT 121  
Db 140 GT 141

RESULT 10  
LV5A\_HUMAN  
ID LV5A\_HUMAN STANDARD; PRT; 108 AA.  
AC P01719;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-V region DEL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
RP SEQUENCE.  
RX MEDLINE=75112179; PubMed=4452363;  
RA Eulitz M.;  
RT "A new subgroup of human I-chains of the lambda-type. Primary  
structure of Bence-Jones protein DEL.";  
RL Eur. J. Biochem. 50:49-69(1974).  
CC -1- MISCELLANEOUS: THIS IS THE FIRST SEQUENCED V REGION OF LAMBDA  
CHAIN SUBGROUP V.  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01985; LSHUDL.  
DR HSSP; P80748; 2LOI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 97 IG-LIKE.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11342 MW; B8E8ED9C09C9E451 CRC64;  
  
Query Match 29.1%; Score 393; DB 1; Length 108;  
Best Local Similarity 71.0%; Pred. No. 5e-22;  
Matches 76; Conservative 9; Mismatches 20; Indels 2; Gaps 1;  
  
Qy 149 YELMQLPSVSVSPGQTASITCSGDNLDKRYACWYQOKPGRSPVLVIYGDNKRPSGIPERF 208  
Db 1 YVLSQPPSVSVAPGQTARITCGGDIIGKSVHWYQOKPGQAPVLVHEDNDRPAGIPERF 60  
209 SGSNSGNTATLTISGTQAMDEADYYCOAWDTSTA--VFGTGTLTVL 253  
61 SGSNSGNTATLTISRVEAGDEADYYCEWDDRTAHVVFGGTGLTVL 107  
  
RESULT 11  
LV3B\_HUMAN  
ID LV3B\_HUMAN STANDARD; PRT; 111 AA.  
AC P80748;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-III region LOI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE, SUBUNIT, DISEASE, AND 3D-STRUCTURE MODELLING.  
RC TISSUE=Urine;  
RX MEDLINE=99441384; PubMed=10510403;  
RA Jokiranta T.S., Solomon A., Pangburn M.K., Zipfel P.F., Meri S.;  
RT "Nephritogenic lambda light chain dimer: a unique human  
mini-autoantibody against complement factor H.";  
RL J. Immunol. 163:4590-4596(1999).  
CC -1- FUNCTION: ACTIVATES THE ALTERNATIVE COMPLEMENT PATHWAY BY BINDING  
TO THE SHORT CONSENSUS REPEAT DOMAIN 3 (SCR3) OF FACTOR H.  
CC -1- SUBUNIT: Homodimer.  
CC -1- DISEASE: The blocking of factor H by LOI protein leads to the  
developmental of membranoproliferative glomerulonephritis (MPGN).  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PDB; 2LOI; 29-DEC-99.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Ig; 1.

DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; 3D-structure.  
FT DOMAIN 1 97 IG-LIKE.  
FT BINDING 15 15 SCR3.  
FT BINDING 25 25 SCR3.  
FT BINDING 29 29 SCR3.  
FT BINDING 48 51 SCR3.  
FT BINDING 94 94 SCR3.  
FT DISULFID 21 86 BY SIMILARITY.  
FT STRAND 4 4  
FT STRAND 8 8  
FT TURN 13 14  
FT STRAND 16 22  
FT STRAND 32 37  
FT TURN 38 40  
FT STRAND 41 46  
FT TURN 49 50  
FT STRAND 54 54  
FT TURN 55 55  
FT TURN 58 59  
FT STRAND 60 61  
FT STRAND 64 65  
FT TURN 66 67  
FT STRAND 68 74  
FT TURN 78 79  
FT STRAND 82 88  
FT TURN 91 93  
FT STRAND 97 98  
FT STRAND 102 104  
FT TURN 107 108  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11935 MW; 69498EBEFD82053 CRC64;  
  
Query Match 28.8%; Score 389; DB 1; Length 111;  
Best Local Similarity 70.1%; Pred. No. 1e-21;  
Matches 75; Conservative 12; Mismatches 18; Indels 2; Gaps 1;  
  
Qy 149 YELMQLPSVSVSPGQTASITCSGDNLDKRYACWYQOKPGRSPVLVIYGDNKRPSGIPERF 208  
Db 1 YVLTQPPSVSVAPGETARLTTCGNDIGSESVHWYQOKPGQAPVLVIYFDRDRPSGIPERF 60  
209 SGSNSGNTATLTISGTQAMDEADYYCOAWDTST--AVFGTGLTVL 253  
61 SGSNSGNTATLTISRVEAGDEADYYCQLWDSSEHVFVGGTGLTVL 107  
  
RESULT 12  
HV2C\_HUMAN  
ID HV2C\_HUMAN STANDARD; PRT; 119 AA.  
AC P01816;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-II region DAW.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=70258837; PubMed=5449120;  
RA Press E.M., Hogg N.M.;  
RT "The amino acid sequences of the Fd fragments of two human gamma-1  
heavy chains.";  
RL Biochem. J. 117:641-660(1970).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE  
SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A02091; GHUDW.  
DR HSSP; P01789; 1MCP.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.



DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Pyroliadone carboxylic acid.  
FT DOMAIN 1 113  
FT MOD\_RES 1 113  
FT NON\_TER 1 113  
SQ SEQUENCE 119 AA; 13045 MW; 4E13E0214BAD789 CRC64;

Query Match  
Best Local Similarity 28.4%; Score 384; DB 1; Length 119;  
Matches 79; Conservative 12; Mismatches 28; Indels 8; Gaps 2;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSGVSVGWIRPPGKALEWLASINWDDKC 60  
DB 1 QVTLRESGPALVPRPTQTLTLTCTFSGFSLSGETMCVAMIRPPGEALWLASINWDDKC 60  
QY 61 YSPSLKSLRTITKDTPKQVVLAMSNMDDPADTATYSCALDMPHDSGQSFDSADVWGP 60  
DB 61 YGASLETRLAVSKDTSKNQVLSMNTVGPGLATYCA-----RSCGSQYF---DYMGG 120  
QY 121 TMVTVSS 127  
DB 113 ILVTVSS 119

RESULT 13  
HV2A\_HUMAN STANDARD; PRT; 126 AA.  
ID HV2A\_HUMAN  
AC P01814;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-II region OU.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=74005511; PubMed=4742735;  
RA Putnam F.W., Florent G., Paul C., Shinoda T., Shimizu A.;  
RT "Complete amino acid sequence of the Mu heavy chain of a human IgM  
RT Immunoglobulin.";  
RL Science 182:287-291(1973).  
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S  
CC MACROGLOBULIN.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A02088; MHUOU.  
DR HSSP; P01825; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Pyroliadone carboxylic acid.  
FT DOMAIN 1 113  
FT MOD\_RES 1 113  
FT NON\_TER 1 113  
SQ SEQUENCE 126 AA; 14276 MW; A85C0BE0DABC296F CRC64;

Query Match  
Best Local Similarity 27.4%; Score 369.5; DB 1; Length 126;  
Matches 80; Conservative 15; Mismatches 30; Indels 3; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSGVSVGWIRPPGKALEWLASINWDDKC 60  
DB 1 QVTLRESGPALVPRPTQTLTLTCTFSGFSLSGETMCVAMIRPPGEALWLASINWDDKC 60

DB 1 QVTLRESGPALVPRPTQTLTLTCTFSGFSLSGRNRVSWIRPPGKALEWLASINWDDKC 60  
QY 61 Y-SPSLKSLRTITKDTPKQVVLAMSNMDDPADTATYSCALDMPHDSGQSFDSADVWGP 119  
DB 60 YWSTSLRTRLSISKNDKSNQVLLIMINVPVDTATYCCARVNSVMAG-YYYYYNDVWGP 118  
QY 120 GIMVTVSS 127  
DB 119 GTTVTVSS 126

RESULT 14  
LV3A\_HUMAN STANDARD; PRT; 108 AA.  
ID LV3A\_HUMAN  
AC P01714;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-II region SH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=70166723; PubMed=4909564;  
RA Tiltani K., Wikler M., Shinoda T., Putnam F.W.;  
RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The  
RT complete amino acid sequence and the location of the disulfide  
RT bridges.";  
RL J. Biol. Chem. 245:2171-2176(1970).  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01980; L3HUSH.  
DR HSSP; P80748; 2LOI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 97  
FT DISULFID 21 86  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;

Query Match  
Best Local Similarity 26.0%; Score 351; DB 1; Length 108;  
Matches 70; Conservative 14; Mismatches 20; Indels 2; Gaps 1;

QY 150 ELMQPLSVSPGQATASITSGDNLGDKYACWYQOKPGRSPVLVYGDNRPSGIPERFS 209  
DB 2 ELTQDPVAVSVALGQTVRLITCGDSLRLGYDAWYQOKPQAPLVLVYGRNRPSPGIPERFS 61  
QY 210 GSNQNTATLTISGTQAMDEADYCCQAWDT--TAVFGTGTCLTVL 253  
DB 62 GSSSGHTASLTITGAQAEDEADYCCNSRDSGKVLFGGGLTLTVL 107

RESULT 15  
LV7A\_HUMAN STANDARD; PRT; 111 AA.  
ID LV7A\_HUMAN  
AC P01720;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-VII region MOT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.



OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81122740, PubMed=6780787;  
RA Kojima M., Odani S., Ikenaka T.;  
RT "Amino acid sequence of the lambda type light chain of a human IgG1  
RT myeloma protein (MOP) with unusual antigenicity: a possible new  
RT subgroup of lambda chain having a unique N-terminal sequence.";  
RL Mol. Immunol. 17:1407-1414(1980).  
CC -1- MISCELLANEOUS: THIS SEQUENCE REPRESENTS A NEW LAMBDA CHAIN  
CC SUBGROUP. IT HAS AN AMINO-TERMINAL EXTENSION OF THREE RESIDUES  
CC COMPARED WITH OTHER HUMAN LAMBDA CHAINS.  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+  
CC MARKERS.  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR, A01986; L7HUMT.  
DR HSSP, P80748; 2LOI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IgV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 105 IG-LIKE.  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11942 MW; 140A28A2F86A6911 CRC64;  
  
Query Match 26.0%; Score 351; DB 1; Length 111;  
Best Local Similarity 61.7%; Pred. No. 5.4e-19;  
Matches 66; Conservative 17; Mismatches 22; Indels 2; Gaps 1;  
  
QY 149 YELMQLPSVSVPGQTASITCSGDNLGDKYACWYQOKPGRSPVLVIYGDNKRPSGIPERF 208  
DB 4 YELTQPPSVSLAAGQTAMITCEGNDIGERSVHWYQOKPGQAPVPVIYDDADRPSPGVPARF 63  
  
QY 209 SGSNSGNTATLTISGTQAMDEADYYCQAMDST--AVFGTGKLTVL 253  
DB 64 SGYNSGNSAILTINRVEAGDEADYFCQSWDNGSYEVVEGTGTMTVL 110

Search completed: May 13, 2004, 15:02:03  
Job time : 7.1233 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:31 ; Search time 34.0199 Seconds  
(without alignments)  
2346.453 Million cell updates/sec

Title: US-10-072-301-17  
Perfect score: 1351  
Sequence: 1 QVTLKESGPTLVKPTQTTLT.....CQAWDTSTAVFGTGTKLTVL 253

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	528.5	39.1	298	11	Q9QYF0	Q9QYF0 mus musculu
2	472	34.9	241	11	Q921A6	Q921A6 mus musculu
3	460	34.0	121	4	Q9UL96	Q9UL96 homo sapien
4	454	33.6	243	11	Q7TQM2	Q7TQM2 mus musculu
5	419.5	31.1	218	11	Q925S1	Q925S1 mus musculu
6	417	30.9	233	4	Q8TBC9	Q8TBC9 homo sapien
7	410.5	30.4	234	4	Q8N3S5	Q8N3S5 homo sapien
8	390.5	28.9	118	11	Q811U5	Q811U5 mus musculu
9	389	28.8	233	4	Q8N5F4	Q8N5F4 homo sapien
10	382.5	28.3	107	4	Q9UL82	Q9UL82 homo sapien
11	376	27.8	97	4	Q43234	Q43234 homo sapien
12	374	27.7	107	4	Q9NSD6	Q9NSD6 homo sapien
13	368.5	27.3	234	4	Q7Z2U7	Q7Z2U7 homo sapien
14	353	26.1	233	4	Q961E9	Q961E9 homo sapien
15	346	25.6	492	4	Q7Z374	Q7Z374 homo sapien
16	335	24.8	110	4	Q8TE63	Q8TE63 homo sapien

17	328.5	24.3	150	4	Q95973	Q95973 homo sapien
18	327.5	24.2	236	4	Q8NEJ1	Q8NEJ1 homo sapien
19	324.5	24.0	496	4	Q96KX8	Q96KX8 homo sapien
20	320	23.7	613	4	Q96EY0	Q96EY0 homo sapien
21	319.5	23.6	588	4	Q8WUX4	Q8WUX4 homo sapien
22	319.5	23.6	597	4	Q9BU10	Q9BU10 homo sapien
23	319.5	23.6	618	4	Q96AA6	Q96AA6 homo sapien
24	318.5	23.6	236	4	Q96E61	Q96E61 homo sapien
25	317	23.5	237	4	Q8WUK4	Q8WUK4 homo sapien
26	316.5	23.4	597	4	Q9BQ88	Q9BQ88 homo sapien
27	315.5	23.4	478	4	Q7Z379	Q7Z379 homo sapien
28	315	23.3	237	4	Q8WTU6	Q8WTU6 homo sapien
29	314.5	23.3	130	4	Q81ZD7	Q81ZD7 homo sapien
30	312	23.1	101	4	Q81ZD8	Q81ZD8 homo sapien
31	310.5	23.0	121	11	Q99NG4	Q99NG4 mus musculu
32	310.5	23.0	479	11	Q99M22	Q99M22 mus musculu
33	310.5	23.0	482	11	Q91X92	Q91X92 mus musculu
34	307	22.7	116	4	Q96JD0	Q96JD0 homo sapien
35	305.5	22.6	112	4	Q96JD1	Q96JD1 homo sapien
36	305	22.6	119	4	Q9UL73	Q9UL73 homo sapien
37	301	22.3	613	4	Q8WUK1	Q8WUK1 homo sapien
38	295.5	21.9	122	4	Q9UL75	Q9UL75 homo sapien
39	295	21.8	112	4	Q96JD2	Q96JD2 homo sapien
40	294	21.8	235	11	Q99M11	Q99M11 mus musculu
41	293	21.7	81	4	Q7Z2E8	Q7Z2E8 homo sapien
42	291.5	21.6	473	4	Q8TC63	Q8TC63 homo sapien
43	291	21.5	108	4	Q96SB0	Q96SB0 homo sapien
44	290	21.5	499	4	Q8N5K4	Q8N5K4 homo sapien
45	282	20.9	139	4	Q86SX2	Q86SX2 homo sapien

ALIGNMENTS

RESULT 1  
ID Q9QYF0 PRELIMINARY; PRT; 298 AA.  
AC Q9QYF0;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE CN 8 scfv.  
GN CN 8.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Balb/c; TISSUE=Spleen;  
RX MEDLINE=20183931; PubMed=10706631;  
RA Shinohara N., Demura T., Fukuda H.;  
RT "Isolation of a vascular cell wall-specific monoclonal antibody  
RT recognizing a cell polarity by using a phage display subtraction  
RT method."  
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).  
DR EMBL; AB036341; BAA8633.1; .  
DR PIR; A33933; A33933.  
DR PIR; S19112; S19112.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_2.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PSS0835; IG\_LIKE; 2.  
SQ SEQUENCE 298 AA; 31867 MW; E0F96BBA17004317 CRC64;

Query Match 39.1%; Score 528.5; DB 11; Length 298;  
Best local similarity 46.1%; Pred. No. 7.9e-35;  
Matches 117; Conservative 27; Mismatches 93; Indels 17; Gaps 5;  
QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVGWIRQPPGKALEWLASINMNDKC 60  
|||::||| ||||:|:|:| |||:|:|:| |||:|:|:| |||:|:|:|

Db 40 QVKLQSGGGLVKGPGSLKLSGASGDSFRRYMS--WVRQAPGKGLWIGELINPDSTI 97  
QY 61 -YSPSLKRLTTTKDTPKNOVVLAMSNMADPATATYSCALDMPPHDSGPGQSFASDVWGP 119  
Db 98 NYTPSLKDKFIISRDNAKNTLLYLQMSKVRSEDTALYYCA-----RASYYGHSAYWQ 149  
QY 120 GTMTVTVSSGGGGGGGGGGGGGGSSSYELMQLP-SVSVSPGQTASITCSGDNLDGKY 178  
Db 150 GTTVTVS-----SGGGSGGGGGGGGGGGSDIELTQSPASLSASVGETVITCRASGNINHY 204  
QY 179 ACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYCOAMD 238  
Db 205 LAMYQOKQKSPQLLVYNNAKTLADGVPSRFSGSGSGTQYSLKINSLOPEDFGSYCCQHF 264  
QY 239 TSTAVFGTGTXTLV 252  
Db 265 TTPYTFGGGTKEI 278

RESULT 2  
Q921A6 PRELIMINARY; PRT; 241 AA.  
AC Q921A6; 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98170165; PubMed=9509426;  
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,  
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;  
RT "Cloning and characterization of cDNAs encoding VH and VL of a  
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and  
RL generation of a single-chain Fv molecule (scFv).";  
RL Mol. Cells 7:816-819(1997).  
DR EMBL; U88067; AAB48044.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_2.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
FT NON\_TER 1  
FT NON\_TER 241  
SQ SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

Query Match 34.9%; Score 472; DB 11; Length 241;  
Best Local Similarity 42.4%; Pred. No. 2.2e-30;  
Matches 109; Conservative 35; Mismatches 85; Indels 28; Gaps 9;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTSGSVGWIRQPPGKALEWLASIN-WNDK 59  
Db 1 QVKLQSGPELKKPGFTVKISCKASGYFTDYGMN--WVQAQPGKGLKMMGWINTYTGEP 58  
QY 60 CYSPLKSLRLTTKDTPKNOVVLAMSNMADPATATYSCA-LDMPPHDSGPGQSFASDVWG 118  
Db 59 TYADDFKGRFAPSLETSASTAVLQINLNKNEATATYFCARKDLRY-----FDYWG 109  
QY 119 PGTMVTVSSGGGGGGGGGGGGGGSSSYELMQLP-SVSVSPGQTASITCSGDNLDGDK 177  
Db 110 QGTVTVS-----SGGGSGGGGGGGGGGGSDIELTQSPASLSASVGETVITCRASGNINHY 204  
QY 178 YACWYQOKPGRSP---VLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADY 233  
Db 165 YIAMYQHKPGKGRPSAHTLIY---IQPGISRFSGSGSGRDYSPSISNLEPEDATY 220  
QY 234 COAMDSTAVFGTGTXL 250  
Db 221 CLHYD-NLHTFGGGTXL 236

RESULT 3  
Q9UL96 PRELIMINARY; PRT; 121 AA.  
AC Q9UL96; 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035018; AAD56254.1; -.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 121  
SQ SEQUENCE 121 AA; 13695 MW; D582D450596BDD35 CRC64;

Query Match 34.0%; Score 460; DB 4; Length 121;  
Best Local Similarity 73.2%; Pred. No. 9.1e-30;  
Matches 93; Conservative 7; Mismatches 21; Indels 6; Gaps 2;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTSGSVGWIRQPPGKALEWLASINWDDK 60  
Db 1 QITLKESGPTLVKPTQTLTLTCTLSGFSLSSTSGMDVGMIRQPPGKALEWLASIYDDDKR 60  
QY 61 YSPSLKSLRLTTKDTPKNOVVLAMSNMADPATATYSCALDMPPHDSGPGQSFASDVWGP 120  
Db 61 YSPSLKSLRLTTKDTSPKNOVDLTMTFMDPMDPATATYYCA-----HRSKGDGY-YFDYWG 114  
QY 121 TWTVSS 127  
Db 115 TLTVSS 121

RESULT 4  
Q7TQM2 PRELIMINARY; PRT; 243 AA.  
AC Q7TQM2; 01-OCT-2003 (Tremblrel. 25, Created)  
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE scFv 6H8 protein (Fragment).  
GN scFv 6H8.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=Balb/C;  
RA Peter J.C., Effekhari P., Billfield P., Wallukat G.;  
RT "scFv single chain antibody variable fragment as inverse agonist for  
RT the beta-2 adrenergic receptor.";  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AU574851; CAB00495.1; -.  
FT NON\_TER 1



SQ SEQUENCE 243 AA; 25976 MW; BEFF64D2DCF4F76 CRC64;  
Query Match 33.6%; Score 454; DB 11; Length 243;  
Best Local Similarity 40.5%; Pred. No. 6.5e-29;  
Matches 106; Conservative 42; Mismatches 78; Indels 36; Gaps 10;  
QY 1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSGVSVMIRQPPGKALEWLASI----- 53  
Db 1 QVQLQSGSELVVRPGASVKLSCKASGYTFITYMH--WVKQRHGGGLEWIGNIYRPGSGIT 58  
QY 54 NMNDKCYSPSLKSRLLTTKDTPKNQVVLAMSNMDPADTATYSCALDMPHDSGQSFDA 113  
Db 59 N-----YDEKFKNKGILTVDTSSSTAYMHLSLASEDSAVYYCA-----RGRG 102  
QY 114 SDVWGPETMTVTVSSGGGGSGGGSGGGSSSYELMQ-LPSVSVSPGQTASITC-SG 171  
Db 103 LDVWGAGTTLTVS-----SGGGSGGGGGSGGGGSDIQMTQSSSSFSVSLGDRVTTTCKAS 157  
QY 172 DNLGDKYACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEAD 231  
Db 158 EDIYNRLA-WYQOKPGNAPRLISGATSLGTGVPSPRFSGSGSKDYTLTISLTQTEDEVAT 216  
QY 232 YYCQA-WDTSTAVFGTGKTLTV 252  
Db 217 YYCQYWSSTRT--FGGGTKLEI 236

## RESULT 5

ID Q925S1 PRELIMINARY; PRT; 218 AA.  
AC Q925S1;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE MRPS (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX PubMed=11819679;  
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,  
RA Su C.;  
RT "Mechanism of exogenous nucleic acids and their precursors improving  
RT the repair of intestinal epithelium after irradiation in mice.";  
RL World J. Gastroenterol. 6:709-717(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Cui D., Zeng G., Yan X., Li X., Su C.;  
RT "Cloning of mouse genes related to repairing of intestinal epithelium  
RT of the irradiated mice by treatment with the intestinal RNA of mice of  
RT the same strain.";  
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
DR EMBL; AF240168; AAK43733.1; -.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig\_2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
FT NON TER 218  
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 31.1%; Score 419.5; DB 11; Length 218;  
Best Local Similarity 41.9%; Pred. No. 3.5e-26;  
Matches 95; Conservative 37; Mismatches 74; Indels 21; Gaps 7;

QY 1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSGVSVMIRQPPGKALEWLASINMND-K 59  
Db 3 QVTLQSGSELVVRPGASVKLSCKASGYTFITYAGM--WVKQMPGKGLKWIWINTHSGVP 60

QY 60 CYSPSLKSRLLTTKDTPKNQVVLAMSNMDPADTATYSCALDMPHDSGQSFDAVDWGP 119  
Db 61 KYAEFPKGRPAFSLFETASAVYLQISNLKNEDTATYFCM--RWDYDGG-----PAYWQG 112  
QY 120 GTMTVTVSSGGGGSGGGSGGGSGGGSSSYELMQLP-SVSVSPGQTASITC---SGDNL 174  
Db 113 GTTVTVS-----SGGGSGGGSGGGSGGSDIVLTQSPASLAVSLGQRATISCRASESDNI 167  
QY 175 GDKYACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLT 221  
Db 168 GISFMMWFOQKPGQPPLKLLIYASKGSGVPAGLLASGSGTDFSLNI 214

## RESULT 6

ID Q8TBC9 PRELIMINARY; PRT; 233 AA.  
AC Q8TBC9;  
DT 01-JUN-2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell;  
RA Strausberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC022823; AAH22823.1; -.  
DR PIR; S12442; S12442.  
DR PIR; S30526; S30526.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;

Query Match 30.9%; Score 417; DB 4; Length 233;  
Best Local Similarity 75.0%; Pred. No. 6e-26;  
Matches 84; Conservative 8; Mismatches 18; Indels 2; Gaps 1;

QY 144 GGGSSYELMQLPSVSPGQTASITCSGDNLGDKYACWYQOKPGRSPVLVIYGDNKRPSG 203  
Db 16 GSEASYELTQPPSVSPGQTARITCSGDALPKQYAWYQOKPGQAPVLVIYKDNERPSPG 75  
QY 204 IPRFSGNSGNTATLTISGTQAMDEADYYCOAMDSTA--VFGTGKTLTVL 253  
Db 76 IPRFSGSSSGTTVTTLTISGVQADEADYYCQADSSGTYWVFGGKTLTVL 127

## RESULT 7

ID Q8N355 PRELIMINARY; PRT; 234 AA.  
AC Q8N355;  
DT 01-OCT-2002 (Tremblrel. 22, Created)  
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC028090; AAH28090.1; --  
DR PIR; S12441; S12441.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG\_2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
DR Hypothetical protein.  
KW  
SQ SEQUENCE 234 AA; 24792 MW; CC848CAEBA4A9D63 CRC64;

Query Match 30.4%; Score 410.5; DB 4; Length 234;  
Best Local Similarity 70.8%; Pred. No. 2e-25;  
Matches 80; Conservative 10; Mismatches 20; Indels 3; Gaps 1;

QY 144 GGGSSYLEMQLPSVSPGQTASITCSGDNLGDKYACWYQKPGRSPVLVYGDNRKPSG 203  
DB 16 GSVTSYLTQPPSVSAPGQTARITCGANNIGSKSVHWYQKPGQAPLVYDDSDRPSG 75  
QY 204 IPRFSGSNGNTATLTISGTQAMDEADYCCQAWDTST--AVFGTGTKLTVL 253  
DB 76 IPRFSGSNGNTATLTISRVDAGDEADYCCQAWDTST--AVFGTGTKLTVL 128

RESULT 8  
Q811U5 PRELIMINARY; PRT; 118 AA.  
ID Q811U5  
AC Q811U5  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Anti-human Fc gamma receptor III 3G8 gamma heavy chain variable region (Fragment).  
DE Mus musculus (Mouse).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Bruenke J., Valerius T., Repp R., Fey G.H.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY173025; AA018227.1; --  
DR GO; GO:0004872; F\_receptor activity; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
DR Receptor.  
KW Receptor.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 118 AA; 12979 MW; F57BB07033742E99 CRC64;

Query Match 28.9%; Score 390.5; DB 11; Length 118;  
Best Local Similarity 61.4%; Pred. No. 3.7e-24;  
Matches 78; Conservative 17; Mismatches 23; Indels 9; Gaps 2;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGSLSTSGSVGWIRQPGKALEWIASINWDDKC 60  
DB 1 QVTLKESGPTLVKPTQTLTLTCTLSGSLSTSGSVGWIRQPGKALEWIASINWDDKC 60  
QY 61 YSPSLKSLTLTKDTPPKQVVLAMSNMDDADATATYSCALDMPHDSGPGSFDASDVWGP 120  
DB 61 YNPALKSLTLTKDTSSNQVFLKIASVDTADTATYYCA-----QINPAWF--AYWGQG 111

QY 121 TMVTVSS 127  
DB 112 TLVTVSA 118

RESULT 9  
Q8N5F4 PRELIMINARY; PRT; 233 AA.  
ID Q8N5F4  
AC Q8N5F4  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain, and Lung;  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC032452; AAH32452.1; --  
DR PIR; S12441; S12441.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 233 AA; 24961 MW; F092CFB6A6E3A9A CRC64;

Query Match 28.8%; Score 389; DB 4; Length 233;  
Best Local Similarity 72.5%; Pred. No. 1.1e-23;  
Matches 79; Conservative 8; Mismatches 20; Indels 2; Gaps 1;

QY 147 SSYELMQLPSVSPGQTASITCSGDNLGDKYACWYQKPGRSPVLVYGDNRKPSG 206  
DB 19 ASYELTQPPSVSAPGQTARITCSGDNLPKYAYWYQKSGQTPVLVYDTERPSG 78  
QY 207 RFSGSGSNGNTATLTISGTQAMDEADYCCQAWDTST--VFGTGTKLTVL 253  
DB 79 RFSGSGSNGNTATLTLSGAQVEDADYCCYSSDSSGHWVFGGTGTKLTVL 127

RESULT 10  
Q9UL82 PRELIMINARY; PRT; 107 AA.  
ID Q9UL82  
AC Q9UL82  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035032; AAD56268.1; --

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DR HSSP; P01703; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11445 MW; 52F0CC1AB26821DC CRC64;

Query Match          28.3%; Score 382.5; DB 4; Length 107;
Best Local Similarity 72.0%; Pred. No. 1.4e-23;
Matches 77; Conservative 8; Mismatches 21; Indels 1; Gaps 1;

QY 148 SYELMQLPSVSPGQTASITCSGDNIGDKYACWYQOKPGRSPVLVIYGDNKRPSGIPER 207
DB 1 SYELTQPSSVSPGQTARITCSGDLAKKYARWFQOKPGQAPILVIFKTERPSGIPER 60

QY 208 FSGNSGNATLTISGTQAMDEADYYC-QAWDTSTAVFGTGTCLTVL 253
DB 61 FSGSSSGTIVTLTISGAQVEADYYCYASBDNNGRVFGGTTCLTVL 107

RESULT 11
ID 043234 PRELIMINARY; PRT; 97 AA.
AC 043234;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Rheumatoid factor RF-ET13 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Borretzen M., Natvig J.B., Thompson K.M.;
RT "Heterogenous RF structures between and within healthy individuals are
RT not related to HLA DRB1*0401.";
RL Mol. Immunol. 0:0-0(1997).
DR EMBL; AF035802; AAB88534.1; -.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 97
SQ SEQUENCE 97 AA; 10748 MW; DDC0BF47B9AA812D CRC64;

Query Match          27.8%; Score 376; DB 4; Length 97;
Best Local Similarity 76.0%; Pred. No. 4.3e-23;
Matches 73; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 3 TLKESGPTLVKPTQLTLTCTLSGFSLSGVSVMIRQPPGKALEWLASINWDDKCY 62
DB 1 TLKESGPALVKTETLTCTVSGFSLSNRMGVSWIRQPPGKAVENLAHIFANDEKSYS 60

QY 63 PSLKSRLLTKDTPKNQVVLAMSNMPPADTATYSCA 98
DB 61 TSLKSRLLTISKDTSKSQVVLTMNMDPMDTATYCYCA 96

RESULT 12
ID 09NSD6 PRELIMINARY; PRT; 107 AA.
AC 09NSD6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
```

```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RA Hohmann A.;
RT "Autoimmunity.";
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; L43092; AAA69746.2; -.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match          27.7%; Score 374; DB 4; Length 107;
Best Local Similarity 70.8%; Pred. No. 7e-23;
Matches 75; Conservative 10; Mismatches 19; Indels 2; Gaps 1;

QY 150 ELMQLPSVSPGQTASITCSGDNIGDKYACWYQOKPGRSPVLVIYGDNKRPSGIPERFS 209
DB 1 ELTQDPVSVALGQTVRITCGDLSRSYASWYQOKPGQAPVLYIGKNRPSGIPDRFS 60

QY 210 GSNSGNATLTISGTQAMDEADYYCQAWDTS--TAVFGTGTCLTVL 253
DB 61 GSSSGNATLTITGAQAEADYYCNSRDSSGNHNAVFGGTTCLTVL 106

RESULT 13
ID 0722U7 PRELIMINARY; PRT; 234 AA.
AC 0722U7;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalius D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
```





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:48:56 ; Search time 52.2796 Seconds  
(without alignments)  
1372.754 Million cell updates/sec

Title: US-10-072-301-19

Perfect score: 1359

Sequence: 1 QVQLQESGPGLVKPSSETLSL.....YYCAWDESLNGVFGGGPR 254

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: geneseqp19808:\*  
2: geneseqp19908:\*  
3: geneseqp20008:\*  
4: geneseqp20018:\*  
5: geneseqp20028:\*  
6: geneseqp20038a:\*  
7: geneseqp20038b:\*  
8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1000.5	73.6	252	5	ABP45212	Abp45212 Human Bly
2	993.5	73.1	246	3	AAy15126	AAy15126 Anti-muri
3	981.5	72.2	240	4	AAAB46058	AAAB46058 Human TF
4	975.5	71.8	244	6	AAE36248	AAE36248 TRAIL rec
5	975	71.7	241	4	AAAB46061	AAAB46061 Human TF
6	975	71.7	255	5	ABP45631	ABP45631 Human Bly
7	974.5	71.7	244	4	AAAB46060	AAAB46060 Human TF
8	970.5	71.4	244	2	AAy21883	AAy21883 Amino aci
9	963.5	70.9	252	5	ABP45983	ABP45983 Human Bly
10	960.5	70.7	250	6	AAE36254	AAE36254 TRAIL rec
11	960	70.6	255	5	ABP45586	ABP45586 Human Bly
12	959	70.6	251	5	ABP45499	ABP45499 Human Bly
13	957	70.4	239	4	AAAB46059	AAAB46059 Human TF
14	951	70.0	251	5	ABP45535	ABP45535 Human Bly
15	938	69.0	247	5	ABP45970	ABP45970 Human Bly
16	936	68.9	243	4	AAAB46056	AAAB46056 Human TF
17	920	67.7	242	4	AAAB46057	AAAB46057 Human TF
18	917	67.5	247	5	ABP45982	ABP45982 Human Bly
19	912.5	67.1	254	5	ABP45648	ABP45648 Human Bly
20	904	66.5	249	5	ABP45951	ABP45951 Human Bly
21	904	66.5	251	6	ABJ19829	ABJ19829 Human VEG
22	899	66.2	247	5	ABP45987	ABP45987 Human Bly
23	898.5	66.1	256	5	ABP45596	ABP45596 Human Bly
24	893	65.7	251	5	ABP45527	ABP45527 Human Bly
25	888.5	65.4	244	2	AAy06718	AAy06718 Antibody

26	888.5	65.4	266	5	ABG97835	Abg97835 Single ch
27	888.5	65.4	266	5	ABG35336	Abg35336 Thrombopo
28	887.5	65.3	258	5	ABP46072	ABP46072 Human Bly
29	878	64.6	251	5	ABP44979	ABP44979 Human Bly
30	870	64.0	245	5	ABP45853	ABP45853 Human Bly
31	869	63.9	253	5	ABP45608	ABP45608 Human Bly
32	862.5	63.5	254	5	ABP45947	ABP45947 Human Bly
33	861.5	63.4	248	5	ABP45879	ABP45879 Human Bly
34	861.5	63.4	254	5	ABP45567	ABP45567 Human Bly
35	859	63.2	247	5	ABP45182	ABP45182 Human Bly
36	856	63.0	247	5	ABP45755	ABP45755 Human Bly
37	854.5	62.9	256	5	ABP45734	ABP45734 Human Bly
38	853.5	62.8	252	5	ABP45318	ABP45318 Human Bly
39	853	62.8	251	5	ABP45531	ABP45531 Human Bly
40	852.5	62.7	250	5	ABP45402	ABP45402 Human Bly
41	847	62.3	253	5	ABP45328	ABP45328 Human Bly
42	847	62.3	253	5	ABP44943	ABP44943 Human Bly
43	846	62.3	253	6	ABJ19830	ABJ19830 Human VEG
44	845	62.2	255	5	ABP44830	ABP44830 Human Bly
45	844	62.1	247	5	ABP45389	ABP45389 Human Bly

ALIGNMENTS

RESULT 1	ABP45212	standard; protein; 252 AA.
ID	ABP45212	
XX	AC	ABP45212;
XX	DT	19-AUG-2002 (first entry)
XX	DE	Human Blys binding scFv SEQ ID 1223.
XX	KW	Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
XX	OS	Homo sapiens.
XX	PN	WO200202641-A1.
XX	PD	10-JAN-2002.
XX	PF	15-JUN-2001; 2001WO-US019110.
XX	PR	16-JUN-2000; 2000US-0212210P.
XX	PR	17-OCT-2000; 2000US-0240816P.
XX	PR	16-MAR-2001; 2001US-0276248P.
XX	PR	21-MAR-2001; 2001US-0277379P.
XX	PR	25-MAY-2001; 2001US-0293499P.
XX	PA	(HUMA-) HUMAN GENOME SCI INC.
XX	PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX	PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX	PT	WPI; 2002-114799/15.
XX	PT	Antibodies against B lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
XX	PS	Claim 1; Page 1861-1862; 3148pp; English.
XX	CC	This invention describes novel antibodies that immunospecifically bind to B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
XX the invention  
SQ Sequence 252 AA;

Query Match 73.6%; Score 1000.5; DB 5; Length 252;  
Best Local Similarity 76.6%; Pred. No. 4.4e-53;  
Matches 196; Conservative 16; Mismatches 33; Indels 11; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGIGH--DYMSWIRQPPGEGLEWIGFIFFDSTN 58  
Db 1 QVQLQESGPGVAVPESETLSLTCTVSGGFISRTSYMGWIRQPPGKLEWIGNIYYTGKTY 60  
QY 59 YNPISLNGRVITISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVW 118  
Db 61 YSPSLKSRVTISADTSKNQLSLRLTSVTAADTAVYFCARAGYDLTGYPFYF-----DSW 115  
QY 119 GGGTIVTVPSGGGGSGGGGGSGGGGSGNFMLTQPPSASGTPGQRVVISCSGSSSDIG 178  
Db 116 GKGTMVTYSSGGGGSGGGGGSGGGGSGNFMLTQPPSASGTPGQRVVISCSGSSSDIG 171  
QY 179 SNTVMWYQQLPGTAPKLLIYNNQRPSPGVDPDRFSGFSGTSASLVISGLQSEDEADYYCA 238  
Db 172 SNTVMWYQQLPGTAPKLLIYNNQRPSPGVDPDRFSGFSGTSASLVISGLQSEDEADYYCA 231  
QY 239 AWDESLNGVVFEGGPR 254  
Db 232 TWDDSLNGVPVFGGGTK 247

RESULT 2  
AA15126  
ID AA15126 standard; protein; 246 AA.  
XX  
AC AA15126;  
XX  
DT 07-FEB-2000 (first entry)  
XX  
DE Anti-murine CTLA-4 M3 sFv.  
XX  
KW Anti-murine CTLA-4 sFv; M3 sFv; single chain antibody; murine CTLA4;  
KW membrane-associated protein; chimeric construct; extracellular domain;  
KW human CD8; ligand; activated T-cell; co-stimulatory signal; donor B7;  
KW xenograft-specific immunosuppression.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
PN WO9557266-A2.  
XX  
PD 11-NOV-1999.  
XX  
PF 30-APR-1999; 99WO-GB001350.  
XX  
PR 30-APR-1998; 98GB-00009280.  
XX  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX  
PI Lechler IR, Dorling A;  
XX  
DR WPI; 2000-038615/03.  
DR N-PSDB; AA228998.

XX  
PT Inhibiting T-cell mediated rejection of xenotransplanted organs.  
XX  
PS Claim 9; Fig 11; 43pp; English.  
XX

XX The present sequence is the anti-murine CTLA-4 sFv (M3 sFv). This is a  
CC membrane-associated protein which binds to CTLA-4. Chimeric constructs  
CC comprising DNA sequences encoding the extracellular domain of murine  
CC CTLA4 and human CD8 were used for the study of anti-CTLA4-sFv protein.  
CC The anti-hCTLA4 sFv functions as a ligand binding to CTLA-4 on activated  
CC T-cells and antagonises the co-stimulatory signal provided by the  
CC interaction between donor B7 and recipient CD28. Cells expressing the  
CC anti-hCTLA4 sFv failed to stimulate T-cell proliferation. This is used in  
CC xenograft-specific immunosuppression  
XX  
SQ Sequence 246 AA;

Query Match 73.1%; Score 993.5; DB 3; Length 246;  
Best Local Similarity 75.8%; Pred. No. 1.1e-52;  
Matches 194; Conservative 17; Mismatches 24; Indels 21; Gaps 4;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSI--GHDYMSWIRQPPGEGLEWIGFIFFDSTN 58  
Db 3 QVQLQESGPGLVKPSSETLSLTCTVSGSVSGSYWMSWIRQPPGKLEWIGIYYSGSTN 62  
QY 59 YNPISLNGRVITISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVW 118  
Db 63 YNPISLKSRTVISVTSKNQPSLKLSSVTAADTAVYFCARMR-----KDFDYW 110  
QY 119 GGGTIVTVPSGGGGSGGGGGSGGGGSGNFMLTQPPSASGTPGQRVVISCSGSSSDIG 178  
Db 111 GGGTLVTV-----SSGGGGSGGGGGSGGSLAQSVLTQPPSASGTPGQRVVISCSGSSSDIG 165  
QY 179 SNTVMWYQQLPGTAPKLLIYNNQRPSPGVDPDRFSGFSGTSASLVISGLQSEDEADYYCA 238  
Db 166 SNTVMWYQQLPGTAPKLLIYNNQRPSPGVDPDRFSGFSGTSASLVISGLQSEDEADYYCA 225  
QY 239 AWDESLNGVVFEGGPR 254  
Db 226 AWDDSL--FVFGGGTK 239

RESULT 3  
AAB46058  
ID AAB46058 standard; peptide; 240 AA.  
XX  
AC AAB46058;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Human TF anti-idiotypic antibody fragment ZA4.  
XX  
KW MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer;  
KW anti-idiotypic antibody; cytosolic; virucidal; antibacterial; TF antigen;  
KW antiparasitic; infectious disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200073430-A2.  
XX  
PD 07-DEC-2000.  
XX  
PF 29-MAY-2000; 2000WO-DE001809.  
XX  
PR 27-MAY-1999; 99DE-01024405.  
XX  
PR 09-SEP-1999; 99DE-01043016.  
XX  
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.  
XX  
PI Goletz S, Karsten U;  
XX  
DR WPI; 2001-049937/06.  
XX

PT Vaccines against conformation-dependent or non-peptide antigens, based on  
PT DNA encoding peptide which mimics the antigen, useful e.g. as antitumor  
PT vaccines.  
XX  
PS Disclosure; Page 13; 36pp; German.  
XX  
CC This invention describes a novel vaccine (V1) against conformation-  
CC dependent antigens (CDA) comprising DNA (I) and/or an antibody, or  
CC peptide which immunologically imitates CDA, is new. (I) encodes a region  
CC of an antidiotypic antibody (Ab2) or another peptide which: (a)  
CC specifically binds to the binding site of an antibody (Ab1) or an antigen  
CC binding molecule; and (b) immunologically mimics the initial antigen. The  
CC epitope is partially or completely conformation-dependent, and has an  
CC immunogenic structure defined by a specific spatial conformation of amino  
CC acids. (I) is used in the form of linear or circular naked DNA and/or  
CC with a viral vector and/or adjuvants. The products of the invention have  
CC cytosstatic, virucidal, antibacterial and antiparasitic. The invention  
CC also describes (1) a corresponding vaccine (V2) against antigens which  
CC are not proteins or peptides, as defined above but which have epitopes  
CC which show an immunogenic structure; (2) preparing (V1) and (V2); (3)  
CC human antidiotypic antibody fragments against the MUC1-conformation  
CC epitope having one of 31 approximately 60 residue amino acids sequences,  
CC all fully defined in the specification; (4) MUC1-conformation epitope  
CC mimics having one of 16 9-17 residue amino acid sequences, all fully in  
CC the specification; (5) antidiotypic antibody fragments against the TF  
CC antigen having one of 24 approximately 200 residue amino acid sequences,  
CC fully defined in the specification; (6) TF carbohydrate epitope mimetics  
CC having one of 25 7-13 residue amino acid sequences, all fully defined in  
CC the specification; and (7) DNA sequences encoding the fragments and  
CC derivatives defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat  
CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria  
CC and parasites. The vaccines are effective in cases where vaccination has  
CC previously not been possible  
XX  
SQ Sequence 240 AA;  
  
Query Match 72.2%; Score 981.5; DB 4; Length 240;  
Best Local Similarity 75.3%; Pred. No. 5.9e-52;  
Matches 192; Conservative 15; Mismatches 27; Indels 21; Gaps 3;  
  
QY 1 QVQLQESGPGLVKPSETLSLTCTVSGGSF-GHDYWSMIRQPPGEGLEWIGFIFPDGSTNY 59  
Db 1 QVQLQESGPGLVKPSGTLSTLTCAVSGGSISSSNMWSWVRQPPGKGLEWIGEITYHSGSTNY 60  
  
QY 60 NPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEBPYFSSDGMVWG 119  
Db 61 NPSLKSRYTISVDKSKNQFSLKLSVTADTAVYCAR-----DDKGGWG 105  
  
QY 120 QGTTVTVPSSGGSGSGSGSGSGGSNFMLTQPPSASGTPGGRVVISCSGSSSDIGS 179  
Db 106 QGTLVTV-----SSGGGGSGSGSGSGSALQSVLTQPPSASGTPGGRVTISCSGSSSNIGS 160  
  
QY 180 NTVMNMYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVTISGLQSEDEADYYCAA 239  
Db 161 NTVMNMYQQLPGTAPKLLIYSNNQRPSPGVDRFSGSKSGTSASLVTISGLQSEDEADYYCAA 220  
  
QY 240 WDESLNGVVFEGGPR 254  
Db 221 WDDSLRSLVFGGGTK 235  
  
RESULT 4  
AAE36248  
ID AAE36248 standard; protein; 244 AA.  
XX  
AC AAE36248;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE TRAIL receptor protein binding scFv protein, T1014A02.  
XX  
KW TRAIL receptor; TR4; cancer; Kaposi's sarcoma; cerebellar degeneration;  
KW hyperproliferative disorder; neurodegenerative disorder; immune disorder;

KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
KW retinitis pigmentosa; Huntington's disease; Hashimoto's thyroiditis;  
KW rheumatoid arthritis; multiple sclerosis; Sjogren's syndrome; asthma;  
KW biliary cirrhosis; Behcet's disease; Crohn's disease; allergic disorder;  
KW glomerulonephritis; immune deficiency syndrome; myasthenia gravis;  
KW polymyositis; inflammatory disorder; rheumatoid arthritis; septic shock;  
KW infectious disease; acquired immunodeficiency syndrome; viral infection;  
KW AIDS; proliferative disorder; myelodysplastic syndrome; aplastic anaemia;  
KW ischaemic injury; myocardial infarction; reperfusion injury; cachexia;  
KW anorexia; stroke; cardiovascular disorder; peripheral artery disease;  
KW limb ischaemia; arrhythmia; congestive heart failure; neovascularisation;  
KW ocular disorder; wound healing; angiogenesis; transplantation.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Domain 1. .118  
FT /note= "VH domain"  
FT 26. .35  
FT /note= "VH domain complementarity determining region 1  
FT (CDR1) "  
FT 50. .65  
FT /note= "VH domain complementarity determining region 2  
FT (CDR2) "  
FT 98. .105  
FT /note= "VH domain complementarity determining region 3  
FT (CDR3) "  
FT 134. .244  
FT /note= "VL domain"  
FT 156. .168  
FT /note= "VL domain complementarity determining region 1  
FT (CDR1) "  
FT 184. .190  
FT /note= "VL domain complementarity determining region 2  
FT (CDR2) "  
FT 223. .233  
FT /note= "VL domain complementarity determining region 3  
FT (CDR3) "  
XX  
PN WO200297033-A2.  
XX  
PD 05-DEC-2002.  
XX  
PF 07-MAY-2002; 2002WO-US014268.  
XX  
PR 25-MAY-2001; 2001US-0293473P.  
PR 04-JUN-2001; 2001US-0294981P.  
PR 02-AUG-2001; 2001US-0309176P.  
PR 21-SEP-2001; 2001US-0323807P.  
PR 09-OCT-2001; 2001US-0327364P.  
PR 07-NOV-2001; 2001US-0331044P.  
PR 14-NOV-2001; 2001US-0331310P.  
PR 20-DEC-2001; 2001US-0341237P.  
PR 05-APR-2002; 2002US-0369860P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Salcedo T, Ruben SM, Rosen CA, Albert VR, Dobson CL, Vaughan TJ;  
XX WPI; 2003-140454/13.  
DR N-PSDB; AAD54849.  
DR  
XX  
XX Novel antibody useful for treating cancers and other hyperproliferative  
PT disorders, immunospecifically binds to TRAIL receptor and comprises  
PT variable heavy or light chain complementarity determining regions.  
XX  
PS Claim 1; Page 285-286; 301pp; English.  
XX  
CC The present invention relates to novel antibodies that immunospecifically  
CC bind to TRAIL receptor (TR4). Sequences of the invention are useful for  
CC treating, preventing or ameliorating cancer (e.g. colon, breast, uterine,  
CC pancreatic, lung, gastrointestinal or central nervous system cancer e.g.  
CC medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in







RESULT 6  
ABP45631  
ID ABP45631 standard; protein; 255 AA.  
XX  
AC ABP45631;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scFv SEQ ID 1642.  
XX  
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US019110.  
XX  
PR 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-027379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX  
XX WPI; 2002-114799/15.  
DR  
XX  
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.  
XX  
PS Claim 1; Page 2362-2363; 3148pp; English.  
XX  
XX This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 255 AA;  
  
Query Match 71.7%; Score 975; DB 5; Length 255;  
Best Local Similarity 74.5%; Pred. No. 1.5e-51;  
Matches 190; Conservative 23; Mismatches 36; Indels 6; Gaps 2;

Db 61 PSLKSRVTISVDASKNQFSLKSSVTADTAIVYFCARERSYDILTGYSPRSKYGMDVWG 120  
QY 120 QGTTVTVPSGGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRVISICSGSSSDIGS 179  
Db 121 RGTLVTV-----SSGGGSGGGGSGGGSGGSQSVLTQPPSASGTPGQRVITISCSGSSSNIGS 175  
QY 180 NTVANVTQQLPGTAPKLLIYSNNQRPSPVDRFSGFKSGTSASLVISGLQSEDEADYYCAA 239  
Db 176 NTVANVTQRLPGAAPOLLITNNQRPSPGIDPRFSGSKSGTSGSLVISGLQSEDEADYYCAS 235  
QY 240 WDESINGVVEGGGPR 254  
Db 236 WDDSLNGRVFEGGK 250  
  
RESULT 7  
AAB46060  
ID AAB46060 standard; peptide; 244 AA.  
XX  
AC AAB46060;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Human TP anti-idiotype antibody fragment ZA14.  
XX  
KW MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer;  
KW antidiotypic antibody; cytostatic; virucidal; antibacterial; TF antigen;  
KW antiparasitic; infectious disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200073430-A2.  
XX  
PD 07-DEC-2000.  
XX  
PF 29-MAY-2000; 2000WO-DE001809.  
XX  
PR 27-MAY-1999; 99DE-01024405.  
PR 09-SEP-1999; 99DE-01043016.  
XX  
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.  
XX  
PI Goletz S, Karsten U;  
XX  
XX WPI; 2001-049937/06.  
DR  
XX  
XX Vaccines against conformation-dependent or non-peptide antigens, based on  
PT DNA encoding peptide which mimics the antigen, useful e.g. as antitumor  
PT vaccines.  
XX  
PS Disclosure; Page 14; 36pp; German.  
XX  
CC This invention describes a novel vaccine (V1) against conformation-  
CC dependent antigens (CDA) comprising DNA (I) and/or an antibody, or  
CC peptide which immunologically imitates CDA, is new. (I) encodes a region  
CC of an antidiotypic antibody (Ab2) or another peptide which: (a)  
CC specifically binds to the binding site of an antibody (Ab1) or an antigen  
CC binding molecule; and (b) immunologically mimics the initial antigen. The  
CC epitope is partially or completely conformation-dependent, and has an  
CC immunogenic structure defined by a specific spatial conformation of amino  
CC acids. (I) is used in the form of linear or circular naked DNA and/or  
CC with a viral vector and/or adjuvants. The products of the invention have  
CC cytostatic, virucidal, antibacterial and antiparasitic. The invention  
CC also describes (1) a corresponding vaccine (V2) against antigens which  
CC are not proteins or peptides, as defined above but which have epitopes  
CC which show an immunogenic structure; (2) preparing (V1) and (V2); (3)  
CC human antidiotypic antibody fragments against the MUC1-conformation  
CC epitope having one of 31 approximately 60 residue amino acid sequences,  
CC all fully defined in the specification; (4) MUC1-conformation epitope  
CC mimics having one of 16 9-17 residue amino acid sequences, all fully in  
CC the specification; (5) antidiotypic antibody fragments against the TP  
CC antigen having one of 24 approximately 200 residue amino acid sequences,

CC fully defined in the specification; (6) TF carbohydrate epitope mimetics  
CC having one of 25 7-13 residue amino acid sequences, all fully defined in  
CC the specification; and (7) DNA sequences encoding the fragments and  
CC derivatives defined in (3, 4, 5, or 6). (VI) and (V2) are used to treat  
CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria  
CC and parasites. The vaccines are effective in cases where vaccination has  
CC previously not been possible  
XX  
SQ Sequence 244 AA;

Query Match 71.7%; Score 974.5; DB 4; Length 244;  
Best Local Similarity 74.9%; Pred. No. 1.6e-51;  
Matches 191; Conservative 17; Mismatches 30; Indels 17; Gaps 4;

QY 1 QVQLQESGPGGLVLPSETLSLTCTVSGGSI-GHDYMSWIRQPPGEGLEWIGFIFFDGSSTNY 59  
DB 1 QVQLQESGPGGLVLPSETLSLTCAVSGSISSNMWSWVRQPPGKLEWIGFIHSGSTNY 60  
QY 60 NPSLNGRVTISLDTSKNQSLRLTSVTADTAVYFCARLKAWLLSEPPYFSSDGMVWG 119  
DB 61 NPSLKRVTISVXKSKNQFSLKLSVTAXDTAVYCAR-----PSHNA--GTHTWG 109  
QY 120 QGTVTVPSSGGSGGGSGGGSGGSGSNFMLTQPPSASGTPGQRVISICSGSSSDIGS 179  
DB 110 QGTLVTV-----SSGGSGGGSGGGSGGSALQSVLTQPPSASGTPGQRVITISCGSSSNIGS 164  
QY 180 NTVNMYQQLPGTAPKLLIYSNNORPSGVDPDRFSGFKSGTASLVISGLQSEDEADYYCA 239  
DB 165 NTVNMYQQLPGTAPKLLIYSNNORPSGVDPDRFSGSKSGTASLVISGLQSEDEADYYCA 224  
QY 240 WDESLNGVVFSGGPR 254  
DB 225 WDSLRLALVFGGGRK 239

RESULT 8  
AAY21883  
ID AAY21883 standard; protein, 244 AA.

AC AAY21883;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
DE Amino acid sequence of antibody BIOA8.  
XX  
KM Prostate-specific antigen; PSA; anti-chymotrypsin; ACT; antibody;  
XX KM diagnostic assay; PSA-ACT; prostate cancer; tumour; immunotherapy; BIOA8.  
OS Homo sapiens.

Key Location/Qualifiers  
FT Misc-difference 201  
FT /label= unknown  
FT /note= "encoded by TST"

PN EP934953-A2.  
XX  
PD 11-AUG-1999.  
XX  
PF 01-DEC-1998; 98EP-00122546.  
XX  
PR 03-DEC-1997; 97US-0067428P.

PA (BOEF ) BOEHRINGER MANNHEIM CORP.  
XX  
PI Winter GP, Mahoney W, Sawyer JR;  
XX  
DR WPI; 1999-432068/37.  
DR N-PSDB; AAX86940.  
XX

PT New anti-complex antibody useful for diagnosing prostate cancer.  
XX  
PS Claim 28; Page 25-27; 42pp; English.

XX  
CC The invention relates to an antibody that binds a complex between  
CC prostate-specific antigen (PSA) and anti-chymotrypsin (ACT), and has an  
CC affinity for the complex which is at least 10 fold higher than the  
CC affinity for either PSA or ACT alone. The antibody is used in diagnostic  
CC assays to detect PSA-ACT in serum samples from patients. The levels of  
CC PSA-ACT complex increase in patients suffering from prostate cancer  
CC compared to the levels in patients with benign or no growths in the  
CC prostate. Therefore detection of PSA in complex with ACT is useful for  
CC the early detection of prostate tumours, by distinguishing between benign  
CC and malignant conditions of the prostate as well as for the management of  
CC patients with prostate cancer, such as the disclosure of metastasis and  
CC the monitoring of the PSA levels after treatment. The antibodies may also  
CC be used in immunotherapy, affinity chromatography and isolation or  
CC purification of PSA-ACT. Unlike prior art antibodies which bind to PSA-  
CC ACT complexes but may also bind PSA or ACT alone, the present antibody is  
CC specific for PSA-ACT alone. Diagnostic assays using the antibodies are  
CC more accurate in diagnosing prostate cancer as they only detect the  
CC intact complex of PSA-ACT. Sequences AAY21880-884 represent specific  
CC examples of antibodies directed against PSA-ACT. The present sequence  
XX represents the amino acid sequence of antibody BIOA8  
SQ Sequence 244 AA;

Query Match 71.4%; Score 970.5; DB 2; Length 244;  
Best Local Similarity 74.8%; Pred. No. 2.8e-51;  
Matches 190; Conservative 14; Mismatches 33; Indels 17; Gaps 3;

QY 1 QVQLQESGPGGLVLPSETLSLTCTVSGGSI-GHDYMSWIRQPPGEGLEWIGFIFFDGSSTNY 60  
DB 3 QVQLQESGAGLLKPSETLSLTCAVYGSFSGYIWSWIRQPPGKLEWIGFIHSGSTNY 62  
QY 61 PSLNGRVTISLDTSKNQSLRLTSVTADTAVYFCARLKAWLLSEPPYFSSDGMVWG 120  
DB 63 PSLKRVTISVDTSKNQFSLKLSVTADTAVYCARM--WSLK-----FDYWGQ 110  
QY 121 GTVTVPSSGGSGGGSGGGSGGSGSNFMLTQPPSASGTPGQRVISICSGSSSDIGS 180  
DB 111 GTLVTV-----SSGGSGGGSGGGSGGSALQSVLTQPPSASGTPGQRVITISCGSSSNIGS 165  
QY 181 TVNMYQQLPGTAPKLLIYSNNORPSGVDPDRFSGFKSGTASLVISGLQSEDEADYYCA 240  
DB 166 VYVWYQQLPGTAPKLLIYSNNORPSGVDPDRFSGSKSGTASLVISGLQSEDEADYYCA 225  
QY 241 DESLNGVVFSGGPR 254  
DB 226 DDSLRLGIVFGGGRK 239

RESULT 9  
ABP45983  
ID ABP45983 standard; protein, 252 AA.

AC ABP45983;  
XX  
DT 19-AUG-2002 (first entry)  
XX

DE Human Blys binding scFv SEQ ID 1994.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; anti-rheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
OS Homo sapiens.

PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US019110.

```

XX 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
DR WPI; 2002-114799/15.
XX
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2779-2780; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumor necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAids activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 252 AA;
XX
Query Match 70.9%; Score 963.5; DB 5; Length 252;
Best Local Similarity 73.0%; Pred. No. 7.5e-51;
Matches 187; Conservative 22; Mismatches 36; Indels 11; Gaps 3,
QY 1 QVQLQESGPGGLVPSSETISLTCTVSGGSI--GHDYMSWIRQPPGEGLEWIGFIFPDGSTN 58
DB 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 1
1 QQLQESGPGLVKPSQTLSTLTCTVSGGSISSGDYMSWIRQHPGEGLEWIGYIYHSGSTY 60
QY 59 YNPSLNGRVTISLDTSKNQLSRLTSVTAADTAVVFCARLKGAWLSEPPYFSSDGMVDVW 118
DB 61 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 1
1 YNPSLKSRVSMVSVDTSKNQYSLKLSVTAADTAVVYCARLR-----PDADYGDYGFDPW 114
QY 119 GQGTITVTVPSSGGGSGGGGSGGGGSGGGGSGNFMLTQPPSASGTPQQRVSISSCGSSSDIG 178
DB 115 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 1
1 GQGTMTVTSSGGGSGGGGSGGGGSGGGGSG--ALSIVLTQPPSASATPCQRTVITSCSGSRNIG 171
QY 179 SNTVNWYQQLPGTAPKLLIYSNNORPSGVPDRFSGFGKSGTSASLVISGLQSEDEADYYCA 238
DB 172 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 1
1 SNTVNWYQQLPGTAPKLLIYSNNORPSGVPDRFSGFGKSGTSASLVISGLRSEDEADYYCA 231
QY 239 AWDESLNGVVFSGGPR 254
DB 232 :||:|||||: 1
1 TWDDRLRGLVFGGGTK 247
RESULT 10
AAE36254 ID AAE36254 standard; protein; 250 AA.
AC AAE36254;
XX
XX 26-JUN-2003 (first entry)
XX
DE TRAIL receptor protein binding scFv protein, T1015A02.

```

XX	TRAIL receptor; TR4; cancer; Kaposi's sarcoma; cerebellar degeneration;
KW	hyperproliferative disorder; neurodegenerative disorder; immune disorder;
KW	Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW	retinitis pigmentosa; Huntington's disease; Hashimoto's thyroiditis;
KW	rheumatoid arthritis; multiple sclerosis; Sjogren's syndrome; asthma;
KW	biliary cirrhosis; Behcet's disease; Crohn's disease; allergic disorder;
KW	glomerulonephritis; immune deficiency syndrome; myasthenia gravis;
KW	polymyositis; inflammatory disorder; rheumatoid arthritis; septic shock;
KW	infectious disease; acquired immunodeficiency syndrome; viral infection;
KW	AIDS; proliferative disorder; myelodysplastic syndrome; aplastic anaemia;
KW	ischaemic injury; myocardial infarction; reperfusion injury; cachexia;
KW	anorexia; stroke; cardiovascular disorder; peripheral artery disease;
KW	limb ischaemia; arrhythmia; congestive heart failure; neovascularisation;
KW	ocular disorder; wound healing; angiogenesis; transplantation.
XX	
OS	Unidentified.
XX	
FH	Key
FT	Location/Qualifiers
FT	1. .123
FT	/note= "VH domain"
FT	Misc-difference 23
FT	/label= Unknown
FT	/note= "Encoded by RGT"
FT	26. .37
FT	/note= "VH domain complementarity determining region 1
FT	(CDR1) "
FT	52. .67
FT	/note= "VH domain complementarity determining region 2
FT	(CDR2) "
FT	100. .112
FT	/note= "VH domain complementarity determining region 3
FT	(CDR3) "
FT	140. .250
FT	/note= "VL domain"
FT	162. .174
FT	/note= "VL domain complementarity determining region 1
FT	(CDR1) "
FT	190. .196
FT	/note= "VL domain complementarity determining region 2
FT	(CDR2) "
FT	229. .239
FT	/note= "VL domain complementarity determining region 3
FT	(CDR3) "
XX	
PN	WO200297033-A2.
XX	
PD	05-DEC-2002.
XX	
PF	07-MAY-2002; 2002WO-US014268.
XX	
PR	25-MAY-2001; 2001US-0293473P.
PR	04-JUN-2001; 2001US-0294981P.
PR	02-AUG-2001; 2001US-0309176P.
PR	21-SEP-2001; 2001US-0323807P.
PR	09-OCT-2001; 2001US-0327364P.
PR	07-NOV-2001; 2001US-0331044P.
PR	14-NOV-2001; 2001US-0331310P.
PR	20-DEC-2001; 2001US-0341237P.
PR	05-APR-2002; 2002US-0369860P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Salcedo T, Ruben SM, Rosen CA, Albert VR, Dobson CL, Vaughan TJ;
XX	
DR	WPI; 2003-140454/13.
XX	
DR	N-PSDB; AAD54855.
XX	
PT	Novel antibody useful for treating cancers and other hyperproliferative
PT	disorders, immunospecifically binds to TRAIL receptor and comprises
PT	variable heavy or light chain complementarity determining regions.
XX	
PS	Claim 1; Page 291-292; 301PP; English.



XX The present invention relates to novel antibodies that immunospecifically  
CC bind to TRAIL receptor (TR4). Sequences of the invention are useful for  
CC treating, preventing or ameliorating cancer (e.g. colon, breast, uterine,  
CC pancreatic, lung, gastrointestinal or central nervous system cancer e.g.  
CC medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in  
CC human. They are useful for detecting expression of TR4 polypeptide and  
CC detecting, diagnosing, prognosis or monitoring cancers and other hyper-  
CC proliferative disorders. Antibodies of the invention are useful for  
CC treating, preventing or ameliorating neurodegenerative disorders (e.g.  
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,  
CC retinitis pigmentosa, cerebellar degeneration and Huntington's disease),  
CC immune disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis,  
CC Sjogren's syndrome, biliary cirrhosis, Behcet's disease, Crohn's disease,  
CC polymyositis, immune-related glomerulonephritis, myasthenia gravis,  
CC Hashimoto's thyroiditis and immune deficiency syndrome), inflammatory  
CC disorders (e.g. asthma, allergic disorders and rheumatoid arthritis),  
CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS),  
CC herpes viral infections and other viral infections) and proliferative  
CC disorders. They are also useful for treating myelodysplastic syndromes  
CC (e.g. aplastic anaemia), ischaemic injury (such as that caused by stroke,  
CC myocardial infarction and reperfusion injury), septic shock, cachexia,  
CC anorexia and toxin-induced liver diseases (such as alcohol). They are  
CC also useful for treating cardiovascular disorders including peripheral  
CC artery diseases such as limb ischaemia, arrhythmia, congestive heart  
CC failure and cardiovascular tuberculosis, diseases or disorders associated  
CC with neovascularisation and ocular disorders, for wound healing, for  
CC promoting angiogenesis and as adjuvants to enhance immune responsiveness  
CC to specific antigen e.g. viral antigen. They are also useful in the  
CC preparation or recovery from surgery, trauma, radiation therapy and  
CC transplantation. The present sequence is T1015A02 single chain Fv (scFv)  
CC antibody that immunospecifically bind to TR4 protein. This sequence is  
XX used in the invention

SQ Sequence 250 AA;

Query Match 70.7%; Score 960.5; DB 6; Length 250;  
Best Local Similarity 74.0%; Pred. No. 1.1e-50;  
Matches 188; Conservative 22; Mismatches 31; Indels 13; Gaps 5;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIGHD--YMSWIRQPPGEGLEWIGFIFFDGSTN 58  
Db 1 QVQLQESGPGLVKPSQTLSTLKNVSGSIGTGYWSWIRQPPGKLEWIGIYHSGSTY 60  
QY 59 YNPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGDVW 118  
Db 61 YKPSLRSLTLVSMDSLRNPSLKLTSVTADTALYCVR--EW--ANGDHWSA--FDLW 113  
QY 119 GGGTWTVPSSGGSGSGSGSGSGSGSGSGSNFMLTOPPSASGTPGQRVVISCSGSSSDIG 178  
Db 114 GGGTLVTVSSGGSG 169  
QY 179 SNTVMWYQQLPGTAPKLLIYSNNORPSGVDFRFSGFKSGTSASLVISGLQSDADYCA 238  
Db 170 GNTVMWYQQLPGTAPKLLIYGNDRPSGVDFRFSGSKSGTSASLAITGLQSEDEADYCA 229  
QY 239 AWDESLNGVVFSGG 252  
Db 230 AWDSLIGYVFGTG 243

RESULT 11  
ABP45586  
ID ABP45586 standard; protein; 255 AA.  
XX ABP45586;  
AC  
DT 19-AUG-2002 (first entry)  
XX  
DE Human BlyS binding scFv SEQ ID 1597.  
XX  
KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;

KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US019110.  
XX  
PR 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
DR  
XX  
PT Antibodies against B lymphocyte stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.  
XX  
PS Claim 1; Page 2308-2309; 3148pp; English.  
XX

This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of BlyS. They may also be  
CC administered to treat diseases associated with aberrant BlyS expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
XX the invention

SQ Sequence 255 AA;

Query Match 70.6%; Score 960; DB 5; Length 255;  
Best Local Similarity 72.2%; Pred. No. 1.2e-50;  
Matches 190; Conservative 20; Mismatches 31; Indels 22; Gaps 4;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSI--GHDYMSWIRQPPGEGLEWIGFIFFDGSTN 58  
Db 1 QVQLQESGPGLVKSSGTLSTLCSVSGASILEGDIYFTWIRQPPGKLEWIGEINRGDIN 60  
QY 59 YNPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCAR-----LKGAWLSEPPYFS 111  
Db 61 YNPSLSKRVTLIVDTSKNQLSLKLNSTVTAADTAVYFCARHYRDYDILTG-----YYR 112  
QY 112 SDGMDVWGCGTWTVPSSGGSGSGSGSGSGSGSGSNFMLTOPPSASGTPGQRVVISCS 171  
Db 113 GHYFDYWGKGLVTV-----SSGGSGSGSGSGSGSGSGSVLTQPPSASGTPGQRTVISCS 167  
QY 172 GSSSDIGSNTVMWYQQLPGTAPKLLIYSNNORPSGVDFRFSGFKSGTSASLVISGLQSED 231  
Db 168 GSSSNIGSNTVMWYQRLPGAAPQDLIYNNDRPSGIPDRFSGSKSGTSGLVISGLQSED 227  
QY 232 EADYYCAWDESLNGVVFSGGPR 254



Db 228 EADYYCASWDDSLNGRVFGGTX 250

RESULT 12

ABP45499

ID ABP45499 standard; protein; 251 AA.

XX

AC ABP45499;

XX

DT 19-AUG-2002 (first entry)

XX

DE Human Blys binding scFv SEQ ID 1510.

XX

KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

XX

OS Homo sapiens.

XX

PN WO200202641-A1.

XX

PD 10-JAN-2002.

XX

PF 15-JUN-2001; 2001WO-US019110.

XX

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX

DR WPI; 2002-114799/15.

XX

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.

PT

XX

PS Claim 1; Page 2205-2206; 3148pp; English.

XX

CC This invention describes novel antibodies that immunospecifically bind to B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of Blys. The antibodies bind to Blys and so may be used to detect and quantitate the presence of Blys in biological samples and may be used in this way to diagnose disease associated with aberrant expression of Blys. They may also be administered to treat diseases associated with aberrant Blys expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention

CC

XX

SQ Sequence 251 AA;

Query Match 70.6%; Score 959; DB 5; Length 251;

Best Local Similarity 74.6%; Pred. No. 1.4e-50;

Matches 191; Conservative 20; Mismatches 33; Indels 12; Gaps 4;

QY 1 QVQLQESGPGLVKPSETLSLTCTVSGSGSIQH--DYMSWIRQPPGSGLEWIGFIFDGSTN 58

DB 1 QVQLQESGPGLVKPSETLSLTCTVSGSGSISSRTSYGMWIRQPPGKLEWIGNITYYTKTY 60

QY 59 YNPSLNGRVTTISLDTSKNQLSLRLTSVTADTAVYFCARLKGMWLLSEPPYSSSDGMDVW 118

DB 61 YSPSLKSRVTISADTSKNQLSLKLSVTAADTAVYCCARAGYDLLTGYPFYF-----DSW 115

QY 119 GGGTTVTVPSSGGGSGGGGSGGGGSGGGSNFMLTQPPSASGTPGQRVVISCSGSSSDIG 178

DB 116 GRGTLVTVSSGGGSGGGGSGGGGS----AQAVLTQPPSASGTPGQRVVISCSGSSSNIG 171

QY 179 SNTVWVYQQLPGTAPKLLIYSNNQRPSCVDPDRFSGFKSGTSASLVISGLQSEDEADYYCA 238

DB 172 STTVAWYQQVPGTAPKLLIYSNDRRPSGVDPDRFSGSKGTSASLAIISGLQSEDEADYYCA 231

QY 239 AWDESLNGVVEGGGPR 254

DB 232 SWDDSPH-VVEGGGTX 246

RESULT 13

AAB46059

ID AAB46059 standard; peptide; 239 AA.

XX

AC AAB46059;

XX

DT 23-MAR-2001 (first entry)

XX

DE Human TF anti-idiotypic antibody fragment ZA36.

XX

KW MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer; antidiotypic antibody; cytostatic; virucidal; antibacterial; TF antigen; antiparasitic; infectious disease.

XX

OS Homo sapiens.

XX

PN WO200073430-A2.

XX

PD 07-DEC-2000.

XX

PF 29-MAY-2000; 2000WO-DE001809.

XX

PR 27-MAY-1999; 99DE-01024405.

PR 09-SEP-1999; 99DE-01043016.

XX

PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

XX

PI Goletz S, Karsten U;

XX

DR WPI; 2001-049937/06.

XX

PT Vaccines against conformation-dependent or non-peptide antigens, based on DNA encoding peptide which mimics the antigen, useful e.g. as antitumor vaccines.

PT

XX

PS Disclosure; Page 14; 36pp; German.

XX

CC This invention describes a novel vaccine (V1) against conformation-dependent antigens (CDA) comprising DNA (I) and/or an antibody, or peptide which immunologically imitates CDA, is new. (I) encodes a region of an antidiotypic antibody (Ab2) or another peptide which: (a) specifically binds to the binding site of an antibody (Ab1) or an antigen binding molecule; and (b) immunologically mimics the initial antigen. The epitope is partially or completely conformation-dependent, and has an immunogenic structure defined by a specific spatial conformation of amino acids. (I) is used in the form of linear or circular naked DNA and/or with a viral vector and/or adjuvants. The products of the invention have cytostatic, virucidal, antibacterial and antiparasitic. The invention also describes (1) a corresponding vaccine (V2) against antigens which are not proteins or peptides, as defined above but which have epitopes which show an immunogenic structure; (2) preparing (V1) and (V2); (3) human antidiotypic antibody fragments against the MUC1-conformation CC epitope having one of 31 approximately 60 residue amino acids sequences, all fully defined in the specification; (4) MUC1-conformation epitope CC mimics having one of 16 9-17 residue amino acid sequences, all fully in

CC the specification; (5) anti-idiotypic antibody fragments against the TF  
CC antigen having one of 24 approximately 200 residue amino acid sequences,  
CC fully defined in the specification; (6) TF carbohydrate epitope mimetics,  
CC having one of 25 7-13 residue amino acid sequences, all fully defined in  
CC the specification; and (7) DNA sequences encoding the fragments and  
CC derivatives defined in (3, 4, 5, or 6). (VI) and (V2) are used to treat  
CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria  
CC and parasites. The vaccines are effective in cases where vaccination has  
CC previously not been possible  
XX  
SQ Sequence 239 AA;

Query Match 70.4%; Score 957; DB 4; Length 239;  
Best Local Similarity 73.3%; Pred. No. 1.8e-50;  
Matches 187; Conservative 17; Mismatches 29; Indels 22; Gaps 3;

QY 1 QVQLQESGPGIIVKPSSETLSLTCTVSGGSI-GHDYMSWIRQPPGEGLEWIGFIFDSTNY 59  
Db 1 QVQLQESGPGIIVKPSGTLSTCAVSGGSISSSNMWSMVRQPPGKLEWIGIYHSGSTNY 60  
QY 60 NPSLNGRVTISLDTSKNQLSLRLTSVTADTAVYFCARLKGAWLSEPPYFSSDGMVNG 119  
Db 61 NPSLKSRTVISVDKSKNQFSLKLSVTADTAVYFCAR-----PSSIMG 104  
QY 120 QGTVTVPSGGSGGGSGGGSGGGSNFMLTQPPSASGTPGQRVVISCSGSSSDIGS 179  
Db 105 QGTVTV-----SSGGGGSGGGSGGGSALQSVLTQPPSASGTPGQRTVISCSGSSSNGS 159  
QY 180 NTYVNWYQQLPGTAPKLLIYSNNORPSGVDRFSGFKSGTSASLVISGLQSEDEADYCAA 239  
Db 160 NYVYVYQQLPGTAPKLLIYRNQRPSPGVDRFSGSKSGTSASLAIISGLRSEADYCAA 219  
QY 240 WDESINGVVFEGGPR 254  
Db 220 WDDSLRSLVFGGTRK 234

RESULT 14  
ABP45535  
ID ABP45535 standard; protein; 251 AA.  
XX

AC ABP45535;  
XX  
DT 19-AUG-2002 (first entry)  
XX

DE Human Blys binding scFv SEQ ID 1546.  
XX

KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX

OS Homo sapiens.  
XX

PN WO200202641-A1.  
XX

PD 10-JAN-2002.  
XX

PF 15-JUN-2001; 2001WO-US019110.  
XX

PR 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX

PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX

DR WPI; 2002-114799/15.

XX Antibodies against B lymphocyte stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.  
XX  
PS Claim 1; Page 2247-2249; 3148pp; English.  
XX

CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX

SQ Sequence 251 AA;

Query Match 70.0%; Score 951; DB 5; Length 251;  
Best Local Similarity 72.7%; Pred. No. 4.3e-50;  
Matches 189; Conservative 19; Mismatches 32; Indels 20; Gaps 5;

QY 1 QVQLQESGPGIIVKPSSETLSLTCTVSGGSI-GHDYMSWIRQPPGEGLEWIGFIFDSTNY 59  
Db 1 QVQLQESGPGIIVKPSGTLSTCAVSGDSIRGCHWNVVRQPPGKLEWIGIYHSGSTNS 60  
QY 60 NPSLNGRVTISLDTSKNQLSLRLTSVTADTAVYFCAR-----LKGAWLSEPPYFSSDG 114  
Db 61 NPSLKSRTVISLADKSKNPSLSISVTADTAVYFCARGDYDVLTG-----YLK-- 110  
QY 115 MDVWGCGTTVTPPSGGSGGGSGGGSGGGSNFMLTQPPSASGTPGQRVVISCSGSS 174  
Db 111 LDYWGKGLTVTVSSGGSGGGSGGGSGGGS-----AQVLTQPPSASGTPGQRTVISCSGSS 166  
QY 175 SDIGSNTVNWYQQLPGTAPKLLIYSNNORPSGVDRFSGFKSGTSASLVISGLQSEDEAD 234  
Db 167 SNIGSRTVNWYQQLPGTAPKLLVSTNLRPSGVDRFSGSKSGTSASLAIISGLRSEDEAD 226  
QY 235 YYCAWDESINGVVFEGGPR 254  
Db 227 YYCSAWDDSLNGVPVFGGTRK 246

RESULT 15  
ABP45970  
ID ABP45970 standard; protein; 247 AA.  
XX

AC ABP45970;  
XX

DT 19-AUG-2002 (first entry)  
XX

DE Human Blys binding scFv SEQ ID 1981.  
XX

KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX

OS Homo sapiens.  
XX

PN WO200202641-A1.  
XX

PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US019110.  
XX  
PR 16-JUN-2000; 2000US-0212210P.  
XX  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
DR  
XX  
XX  
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
XX diagnosis and treatment of cancers and immune disorders.  
XX  
PS Claim 1; Page 2764-2765; 3148pp; English.  
XX  
XX This invention describes novel antibodies that immunospecifically bind to  
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 247 AA;  
  
Query Match 69.0%; Score 938; DB 5; Length 247;  
Best Local Similarity 71.5%; Pred. No. 2.6e-49;  
Matches 183; Conservative 22; Mismatches 35; Indels 16; Gaps 4;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGIG--HDYMSWIRQPPGEGLEWIGFIFPDGSTN 58  
Db 1 QLQLQESGPGLVKPLETSLTCTVSGSGVSGRTHYWGWI RLPKGMIEWIASLSFDGTPF 60  
  
QY 59 YNP SLNGRYTISLDTSKNQLSLRLTSYTAADTAVYFCARLKGAWLSEPPYFSSDGMVW 118  
Db 61 YNP SLKSRYSVS RDTSKNQFSLKVTSTYAADTAVYYCAR-----HDVY--GDLFDYW 110  
  
QY 119 GGGTIVTVPSGGGGSGGGSGGGSGGSGNFM LTOPPSASGTPGQRVVISCSGSSSDIG 178  
Db 111 GGGTIVTVSSGGGGSGGGSGGGSGGGS-----AQS VLTQPPSASGTPGQRVVISCSGSGSNIG 166  
  
QY 179 SNTVNMVYQQLPGTAPKLLIYSNNQRPSPGVDRPFGFKSGTSASLVISGLQSEDEADYYCA 238  
Db 167 SNSVSWYQOVPGTAPKLLIYNNNRPSGVDRFSASKSGTSASLAISGLQSEDEADYYCA 226  
  
QY 239 AWDESLNGVVFEGGPR 254  
Db 227 SWDDSLTVPVFEGGGTK 242

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FEATURE:  
OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected  
OTHER INFORMATION: from a naive phage display library known as the  
OTHER INFORMATION: Synthetic scFv Library (#1) from the Centre for  
OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK  
US-09-260-527-3

Query Match 57.9%; Score 787; DB 3; Length 278;  
Best Local Similarity 62.0%; Pred. No. 4.2e-50;  
Matches 158; Conservative 24; Mismatches 51; Indels 22; Gaps 5;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSI-GHDYMSWIRQPPGEGLEWIGFIFPDSTNY 59  
DB 23 QVQLQESGPGLVKPSDTLSLTCAVSGYSISSNMWGWIRQPPGKLEWIGYIYSGSTYY 82  
QY 60 NPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWG 119  
DB 83 NPSLKSRTVMSVDTSKNQFSLKSSVTAVDTAVYYCARF-----HPRVYD-----WG 129  
QY 120 QGTTVTVPSSGGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRVISCSGSSSDIGS 179  
DB 130 QGTLVTVSRGGGSGGGSGGGSGGGSS-----ELTQDPAVSVALGQIVRITCGDS--LRS 181  
QY 180 NTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYCA 239  
DB 182 YYASWYQQRPGQAPVLVIYKNNRPSGIPDRFSGSSSGNTASTLTGCAQAEDEADYYCNS 241  
QY 240 WDESLNGVFGGPR 254  
DB 242 RDSSGNHVFGGGTK 256

RESULT 5  
US-09-079-029-11

; Sequence 11, Application US/09079029  
; Patent No. 6342369  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camilia W.  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Chuntharapai, Anan  
; APPLICANT: Kim, Kyung J.  
; TITLE OF INVENTION: Apo-2 Receptor  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079, 029  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1101R2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 310 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-079-029-11

Query Match 57.2%; Score 778; DB 4; Length 310;  
Best Local Similarity 60.2%; Pred. No. 2.1e-49;  
Matches 154; Conservative 32; Mismatches 52; Indels 18; Gaps 4;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIGHDYMSWIRQPPGEGLEWIGFIFPDGSTN-Y 59  
DB 40 QVQLVQSGGVVQPGRSRLRSCASGFISSYGMHWVRQAPGKLEWVAGIFYDGKNKY 99  
QY 60 NPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWG 119  
DB 100 ADSVKGRFTISRDNKNTLYQWNSLRADTAVYYCARDRGYY-----MDVWG 148  
QY 120 QGTTVTVPSSGGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRVISCSGSSSDIGS 179  
DB 149 KGTIVTV-----SSGGGSGGGSGGGSGGSQSVLTQPPSVSGAFGQRTVISTGRSSNIGA 203  
QY 180 -NTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYCA 238  
DB 204 GHVHWYQQLPGTAPKLLIYDSDNRPSPGVDRFSGSRSGTSASLAITGLQAEDEADYYCQ 263  
QY 239 AWDESLNGVFGGPR 254  
DB 264 SYDSSLRGSVFGGGTK 279

RESULT 6  
US-08-665-202-5

; Sequence 5, Application US/08665202  
; Patent No. 5977322  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D.  
; APPLICANT: Schier, Robert  
; TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to  
; TITLE OF INVENTION: Tumor Antigens  
; NUMBER OF SEQUENCES: 141  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/665, 202  
; FILING DATE: 13-JUN-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000, 238  
; FILING DATE: 14-JUN-1995  
; APPLICATION NUMBER: US 60/000, 250  
; FILING DATE: 15-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 02307E-061410  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 258 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-665-202-5

Query Match 56.9%; Score 773; DB 2; Length 258;

Best Local Similarity 60.2%; Pred. No. 4e-49;  
Matches 157; Conservative 32; Mismatches 54; Indels 18; Gaps 6;

QY 1 QVQLQESGPGELVKPSETLSLTCTVSGSGSIGHDYW-SWIRQPPGEGLEWIGFIF-FDGSTN 58  
Db 1 QVQLQESGAELEKPKESLTKISCKSGYSF-TSYWIAWVRQMPGKGLIYMGILYPGDSDTK 59  
QY 59 YNPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSE-----PPYFSSD 113  
Db 60 YSPSFGQGVTVISVDKSVSTAYLQWSSLKPSDSAVYFCARHDVGYCSSSNCAKMPYFQH- 118  
QY 114 GMDVWGQGTITVTPSPSGGGSGGGSGGGSGGSGNFMLTQPPSASGTPGQRVISICSGS 173  
Db 119 ----WGQGLVTV-----SSGGGGSGGGSGGGSGGSGSVLTQPPSVSAAPGQKVTISCSGS 169  
QY 174 SSDIGSNTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEA 233  
Db 170 SSNIGNNVSWYQQLPGTAPKLLIYGHTRPAGVDRFSGSKSGTSASLAIISGFRSEDEA 229  
QY 234 DYCCAAMDESLNGVVFSGGPR 254  
Db 230 DYCCAAMWDSLSGWFVGGGTK 250

RESULT 7

US-09-315-574-5  
; Sequence 5, Application US/09315574  
; Patent No. 6512097

GENERAL INFORMATION:

APPLICANT: Marks, James D.  
APPLICANT: Schier, Robert  
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to  
NUMBER OF SEQUENCES: 141  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.  
STREET: Four Embarcadero Center, Suite 1100  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4106

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/315,574  
FILING DATE: 20-MAY-99  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,238  
FILING DATE: 14-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,250  
FILING DATE: 15-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/665,202  
FILING DATE: 13-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 02307E-061411  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-315-574-5

Query Match  
Best Local Similarity 56.9%; Score 773; DB 4; Length 258;  
Matches 157; Conservative 32; Mismatches 54; Indels 18; Gaps 6;

QY 1 QVQLQESGPGELVKPSETLSLTCTVSGSGSIGHDYW-SWIRQPPGEGLEWIGFIF-FDGSTN 58  
Db 1 QVQLQESGAELEKPKESLTKISCKSGYSF-TSYWIAWVRQMPGKGLIYMGILYPGDSDTK 59  
QY 59 YNPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSE-----PPYFSSD 113  
Db 60 YSPSFGQGVTVISVDKSVSTAYLQWSSLKPSDSAVYFCARHDVGYCSSSNCAKMPYFQH- 118  
QY 114 GMDVWGQGTITVTPSPSGGGSGGGSGGGSGGSGNFMLTQPPSASGTPGQRVISICSGS 173  
Db 119 ----WGQGLVTV-----SSGGGGSGGGSGGGSGGSGSVLTQPPSVSAAPGQKVTISCSGS 169  
QY 174 SSDIGSNTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEA 233  
Db 170 SSNIGNNVSWYQQLPGTAPKLLIYGHTRPAGVDRFSGSKSGTSASLAIISGFRSEDEA 229  
QY 234 DYCCAAMDESLNGVVFSGGPR 254  
Db 230 DYCCAAMWDSLSGWFVGGGTK 250

RESULT 8

US-09-646-028-53  
; Sequence 53, Application US/09646028  
; Patent No. 6562347

GENERAL INFORMATION:

APPLICANT: Kwak, Larry  
APPLICANT: Biragyn, Arya  
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF  
FILE REFERENCE: 14014.0316/P  
CURRENT FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: 60/077,745  
PRIOR FILING DATE: 1998-03-12  
SOFTWARE: FaesSeq for Windows Version 3.0  
SEQ ID NO 53  
LENGTH: 334  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct  
US-09-646-028-53

Query Match  
Best Local Similarity 51.5%; Score 700; DB 4; Length 334;  
Matches 146; Conservative 30; Mismatches 62; Indels 22; Gaps 6;

QY 1 QVQLQESGPGELVKPSETLSLTCTVSGSGSIGHDYW-SWIRQPPGEGLEWIGFIF-FDGSTN-Y 59  
Db 80 EVQLLESGGGLVQSGSLRLSCVSAAGLTFSASAITWVROAPGKGLIYSGISFGSDITYY 139  
QY 60 NPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDG---MD 116  
Db 140 ADSVKGFRFSASRDNSKNTVYLLQMNLRPNDAVYFCAN-----NQTGNFCLD 186  
QY 117 VMGQGTITVTPS-GGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRVISICSGSS 175  
Db 187 NMGQGLVTVSSRGGSGGGSGGGSGGGS---GSQSVLTQPPSVSAAPGQKVTISCTGSR 243  
QY 176 DIGSN-TVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEA 234  
Db 244 NIGAGYDVNWYQKFPETAPKVLIIYSNNRPSGVDRFSGSKSGTSASLAIITGLQLEDEGT 303  
QY 235 YCCAAMDESLNGVVFSGGPR 254  
Db 304 YCCQCNDSLSGLWLFVGGGTK 323





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RESULT 12
US-08-918-148-74
; Sequence 74, Application US/06918148A
; Patent No. 6342220
GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 74
; LENGTH: 249
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-74

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RESULT 13
US-10-039-785-42
; Sequence 42, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PFS50

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Query Match	48.9%;	Score 665;	DB 4;	Length 245;
Best Local Similarity	52.0%;	Pred. NO. 2.8e-41;		
Matches 133;	Conservative	43;	Mismatch	10;

RESULT 14  
 US-09-079-029-9  
 ; Sequence 9, Application US/09079029  
 ; Patent No. 6342369  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Adams, Camilla W.  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Chuntcharapal, Anan  
 ; APPLICANT: Kim, Kyung J.  
 ; TITLE OF INVENTION: Apo-2 Receptor  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ;  
 ; ZIP: 94080

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,029  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-079-029-9

## Query Match

Best Local Similarity 48.7%; Score 661.5; DB 4; Length 309;  
Matches 138; Conservative 32; Mismatches 65; Indels 23; Gaps 6;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYWSWIRQPPGEGLEWI-GFIFPDGSTNY 59  
DB 40 EVQLVQSGGVERPGSGLRSLSCAASGFTPDYGMWVRQAPGKLEWVSGINWNGSTGY 99  
QY 60 NPSLNGRYTISLDTSKNQLSLRLTSVTADTAVYFCARLKA---WLSEPPYFSSDGM 116  
DB 100 ADSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCAKILGAGRW-----YF-----D 148  
QY 117 VMGQGTITVTPSSGGSGSGSGSGSGSGSNFMLTQPPSASGTPGQRVVISCSGSSSD 176  
DB 149 LMGKGTITVTPSSGGSGSGSGSGSGSGSS-----ELTQDPAVSVALGQTVRITCQGDS-- 200  
QY 177 IGSNTVNWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYY 236  
DB 201 LRSYYASWYQOKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY 260  
QY 237 CAAMDESINGVFGGPR 254  
DB 261 CNSRDSSGNHVFGGGTK 278

## RESULT 15

US-09-079-029-10  
Sequence 10, Application US/09079029  
Patent No. 6342369  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilla W.  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Chuncharapai, Anan  
APPLICANT: Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,029

## FILING DATE:

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 312 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-079-029-10

## Query Match

Best Local Similarity 48.6%; Score 661; DB 4; Length 312;  
Matches 140; Conservative 28; Mismatches 68; Indels 22; Gaps 5;

QY 2 VQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYWSWIRQPPGEGLEWIGFIFPDGSTNYN- 60  
DB 41 VQLVESGGGLVQPGSGLRSLSCAASGFTFSYMWVRQAPGKLEWVANIKQDSEKYYV 100  
QY 61 PSLNGRYTISLDTSKNQLSLRLTSVTADTAVYFCAR---LKGAWLSEPPYFSSDGM 116  
DB 101 DSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCARDLKYGS-----SSGWFD 151  
QY 117 VMGQGTITVTPSSGGSGSGSGSGSGSGSNFMLTQPPSASGTPGQRVVISCSGSSSD 176  
DB 152 PMGRGTITVTPSSGGSGSGSGSGSGSS-----ELTQDPAVSVALGQTVRITCQGDS-- 203  
QY 177 IGSNTVNWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYY 236  
DB 204 LRSYYASWYQOKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY 263  
QY 237 CAAMDESINGVFGGPR 254  
DB 264 CNSRDSSGNHVFGGGTK 281

Search completed: May 13, 2004, 15:10:46  
Job time : 14.933 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 15:07:07 ; Search time 37.6068 Seconds  
(without alignments)  
1879.405 Million cell updates/sec

Title: US-10-072-301-19  
Perfect score: 1359  
Sequence: 1 QVQLQESGPGLVKPSSETLSL.....YYCAWDESLNGVVFGGGPR 254

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
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10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
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14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1359	100.0	254	14	US-10-072-301-19 Sequence 19, Appl
2	1359	100.0	254	14	US-10-071-866-19 Sequence 19, Appl
3	1359	100.0	254	15	US-10-360-828-19 Sequence 19, Appl
4	1340	98.6	258	14	US-10-072-301-27 Sequence 27, Appl
5	1340	98.6	258	14	US-10-071-866-27 Sequence 27, Appl
6	1340	98.6	258	15	US-10-360-828-27 Sequence 27, Appl
7	1000.5	73.6	252	10	US-09-880-748-1223 Sequence 1223, Ap
8	1000.5	73.6	252	12	US-10-293-418-1223 Sequence 1223, Ap
9	975.5	71.8	244	13	US-10-039-785-44 Sequence 44, Appl
10	975.5	71.8	244	14	US-10-139-785-44 Sequence 44, Appl
11	975	71.7	255	10	US-09-880-748-1642 Sequence 1642, Ap
12	975	71.7	255	12	US-10-293-418-1642 Sequence 1642, Ap
13	963.5	70.9	252	10	US-09-880-748-1994 Sequence 1994, Ap
14	963.5	70.9	252	12	US-10-293-418-1994 Sequence 1994, Ap
15	960.5	70.7	250	13	US-10-039-785-50 Sequence 50, Appl

16	960.5	70.7	250	14	US-10-139-785-50 Sequence 50, Appl
17	960	70.6	255	10	US-09-880-748-1597 Sequence 1597, Ap
18	960	70.6	255	12	US-10-293-418-1597 Sequence 1597, Ap
19	959	70.6	251	10	US-09-880-748-1510 Sequence 1510, Ap
20	959	70.6	251	12	US-10-293-418-1510 Sequence 1510, Ap
21	951	70.0	251	10	US-09-880-748-1546 Sequence 1546, Ap
22	951	70.0	251	12	US-10-293-418-1546 Sequence 1546, Ap
23	938	69.0	247	10	US-09-880-748-1981 Sequence 1981, Ap
24	938	69.0	247	12	US-10-293-418-1981 Sequence 1981, Ap
25	917	67.5	247	10	US-09-880-748-1993 Sequence 1993, Ap
26	917	67.5	247	12	US-10-293-418-1993 Sequence 1993, Ap
27	912.5	67.1	254	10	US-09-880-748-1659 Sequence 1659, Ap
28	912.5	67.1	254	12	US-10-293-418-1659 Sequence 1659, Ap
29	904	66.5	249	10	US-09-880-748-1962 Sequence 1962, Ap
30	904	66.5	249	12	US-10-293-418-1962 Sequence 1962, Ap
31	904	66.5	251	14	US-10-120-414-75 Sequence 75, Appl
32	899	66.2	247	10	US-09-880-748-1998 Sequence 1998, Ap
33	899	66.2	247	12	US-10-293-418-1998 Sequence 1998, Ap
34	898.5	66.1	256	10	US-09-880-748-1607 Sequence 1607, Ap
35	898.5	66.1	256	12	US-10-293-418-1607 Sequence 1607, Ap
36	893	65.7	251	10	US-09-880-748-1538 Sequence 1538, Ap
37	893	65.7	251	12	US-10-293-418-1538 Sequence 1538, Ap
38	887.5	65.3	258	10	US-09-880-748-2083 Sequence 2083, Ap
39	887.5	65.3	258	12	US-10-293-418-2083 Sequence 2083, Ap
40	878	64.6	251	10	US-09-880-748-990 Sequence 990, App
41	878	64.6	251	12	US-10-293-418-990 Sequence 990, App
42	870	64.0	245	10	US-09-880-748-1864 Sequence 1864, Ap
43	870	64.0	245	12	US-10-293-418-1864 Sequence 1864, Ap
44	869	63.9	253	10	US-09-880-748-1619 Sequence 1619, Ap
45	869	63.9	253	12	US-10-293-418-1619 Sequence 1619, Ap

ALIGNMENTS

RESULT 1  
US-10-072-301-19  
; Sequence 19, Application US/10072301  
; Publication No. US20030152913A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF  
; FILE REFERENCE: 25636-718  
; CURRENT APPLICATION NUMBER: US/10/072,301  
; CURRENT FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.11  
US-10-072-301-19

Query Match	100.0%;	Score 1359;	DB 14;	Length 254;
Best Local Similarity	100.0%;	Pred. No. 1.9e-86;		
Matches	254;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;
QY	1	QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGIFFDGSTNN	60	
DB	1	QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGIFFDGSTNN	60	
QY	61	PSLNGRYTISLDTSKNQLSLRTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ	120	
DB	61	PSLNGRYTISLDTSKNQLSLRTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ	120	
QY	121	GTIVTVPSGGGSGGGSGGGSGGGSGNFMLTQPPSASGTGQRVVISCSGSSSDIGSN	180	
DB	121	GTIVTVPSGGGSGGGSGGGSGGGSGNFMLTQPPSASGTGQRVVISCSGSSSDIGSN	180	

QY 181 TVNMWQQLPGTAPKLLIYSNNORPSGVPDRFSGFKSGTSASLVISGLQSEDEADYCAAW 240  
Db 181 TVNMWQQLPGTAPKLLIYSNNORPSGVPDRFSGFKSGTSASLVISGLQSEDEADYCAAW 240  
QY 241 DESLNGVVFEGGPR 254  
Db 241 DESLNGVVFEGGPR 254

RESULT 2

US-10-071-866-19  
; Sequence 19, Application US/10071866  
; Publication No. US20030165988A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST F  
; FILE REFERENCE: 25636-717  
; CURRENT APPLICATION NUMBER: US/10/071,866  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.11  
US-10-071-866-19

Query Match  
Best Local Similarity 100.0%; Score 1359; DB 14; Length 254;  
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVOLOESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGFIFDGTSTNN 60  
Db 1 QVOLOESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGFIFDGTSTNN 60  
QY 61 PSINGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWQ 120  
Db 61 PSINGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWQ 120  
QY 121 GTTVTPSGGGSGGGSGGGSGGGSGGNFMLTOPPSASGTPGQRVISICSGSSSDIGSN 180  
Db 121 GTTVTPSGGGSGGGSGGGSGGGSGGNFMLTOPPSASGTPGQRVISICSGSSSDIGSN 180  
QY 181 TVNMWQQLPGTAPKLLIYSNNORPSGVPDRFSGFKSGTSASLVISGLQSEDEADYCAAW 240  
Db 181 TVNMWQQLPGTAPKLLIYSNNORPSGVPDRFSGFKSGTSASLVISGLQSEDEADYCAAW 240  
QY 241 DESLNGVVFEGGPR 254  
Db 241 DESLNGVVFEGGPR 254

RESULT 3

US-10-360-828-19  
; Sequence 19, Application US/10360828  
; Publication No. US20030206909A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS  
; FILE REFERENCE: 25636-727  
; CURRENT APPLICATION NUMBER: US/10/360,828  
; PRIOR FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: US 10/071,866  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/072,301

; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/133,978  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.11  
US-10-360-828-19

Query Match  
Best Local Similarity 100.0%; Score 1359; DB 15; Length 254;  
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVOLOESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGFIFDGTSTNN 60  
Db 1 QVOLOESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGFIFDGTSTNN 60  
QY 61 PSINGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWQ 120  
Db 61 PSINGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWQ 120  
QY 121 GTTVTPSGGGSGGGSGGGSGGGSGGNFMLTOPPSASGTPGQRVISICSGSSSDIGSN 180  
Db 121 GTTVTPSGGGSGGGSGGGSGGGSGGNFMLTOPPSASGTPGQRVISICSGSSSDIGSN 180  
QY 181 TVNMWQQLPGTAPKLLIYSNNORPSGVPDRFSGFKSGTSASLVISGLQSEDEADYCAAW 240  
Db 181 TVNMWQQLPGTAPKLLIYSNNORPSGVPDRFSGFKSGTSASLVISGLQSEDEADYCAAW 240  
QY 241 DESLNGVVFEGGPR 254  
Db 241 DESLNGVVFEGGPR 254

RESULT 4

US-10-072-301-27  
; Sequence 27, Application US/10072301  
; Publication No. US20030152913A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF  
; FILE REFERENCE: 25636-718  
; CURRENT APPLICATION NUMBER: US/10/072,301  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 27  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.11  
US-10-072-301-27

Query Match  
Best Local Similarity 98.8%; Score 1340; DB 14; Length 258;  
Matches 251; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVOLOESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGFIFDGTSTNN 60  
Db 1 QVOLOESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGFIFDGTSTNN 60  
QY 61 PSINGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWQ 120  
Db 61 PSINGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWQ 120

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QY      121 GTTVPSSGGGSGGGSGGGSGGGSNFMLTQPPSASGTPGQRVISICSGSSSDIGSN 180
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Db      121 GTTVPSSGGGSGGGSGGGSGGGSNFMLTQPPSASGTPGQRVISICSGSSSDIGSN 180

QY      181 TVNMWQQLPGTAPKLLIYSNNORPSGVPDFRFSGFKSGTSASLVISGLQSEDEADYYCAAW 240
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Db      181 TVNMWQQLPGTAPKLLIYSNNORPSGVPDFRFSGFKSGTSASLVISGLQSEDEADYYCAAW 240

QY      241 DESLNGVVFEGGPR 254
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Db      241 DESLNGVVFEGGPR 254
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; Sequence 27, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST F
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.11
US-10-071-866-27
```

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Query Match      98.6%; Score 1340; DB 14; Length 258;
Best Local Similarity 98.8%; Pred. No. 4e-85;
Matches 251; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYN 60
        |||||
Db      1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYN 60

QY      61 PSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ 120
        |||||
Db      61 PSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ 120

QY      121 GTTVPSSGGGSGGGSGGGSGGGSNFMLTQPPSASGTPGQRVISICSGSSSDIGSN 180
        |||||
Db      121 GTTVPSSGGGSGGGSGGGSGGGSNFMLTQPPSASGTPGQRVISICSGSSSDIGSN 180

QY      181 TVNMWQQLPGTAPKLLIYSNNORPSGVPDFRFSGFKSGTSASLVISGLQSEDEADYYCAAW 240
        |||||
Db      181 TVNMWQQLPGTAPKLLIYSNNORPSGVPDFRFSGFKSGTSASLVISGLQSEDEADYYCAAW 240

QY      241 DESLNGVVFEGGPR 254
        |||||
Db      241 DESLNGVVFEGGPR 254
```

```
RESULT 6
US-10-360-828-27
; Sequence 27, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07
```

```
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.11 Variant
US-10-360-828-27
```

```
Query Match      98.6%; Score 1340; DB 15; Length 258;
Best Local Similarity 98.8%; Pred. No. 4e-85;
Matches 251; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYN 60
        |||||
Db      1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYN 60

QY      61 PSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ 120
        |||||
Db      61 PSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ 120

QY      121 GTTVPSSGGGSGGGSGGGSGGGSNFMLTQPPSASGTPGQRVISICSGSSSDIGSN 180
        |||||
Db      121 GTTVPSSGGGSGGGSGGGSGGGSNFMLTQPPSASGTPGQRVISICSGSSSDIGSN 180

QY      181 TVNMWQQLPGTAPKLLIYSNNORPSGVPDFRFSGFKSGTSASLVISGLQSEDEADYYCAAW 240
        |||||
Db      181 TVNMWQQLPGTAPKLLIYSNNORPSGVPDFRFSGFKSGTSASLVISGLQSEDEADYYCAAW 240

QY      241 DESLNGVVFEGGPR 254
        |||||
Db      241 DESLNGVVFEGGPR 254
```

```
RESULT 7
US-09-880-748-1223
; Sequence 1223, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1223
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1223
```

```
Query Match      73.6%; Score 1000.5; DB 10; Length 252;
Best Local Similarity 76.6%; Pred. No. 1.2e-61;
Matches 196; Conservative 16; Mismatches 33; Indels 11; Gaps 3;
```



```
QY      1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIQH--DYMSWIRQPPGEGLEWIGFIFFDGSTN 58
Db      1 QVQLQESGPGVVKPSETLSLTCTVSGGFISSRTSYMGWIRQPPGKLEWIGNITYTGKTY 60
QY      59 YNPSLNGRVYITSLDTSKNQSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVW 118
Db      61 YSPSLKSRVTISADTSKNQSLRLTSVTAADTAVYFCARAGYDLTLGYPFYF-----DSW 115
QY      119 GQGTITVTPSGGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRYVISCSGSSSDIG 178
Db      116 GKGTMTVTVSSGGSGGGSGGGSGGGSG---AQSVLTQPPSASGTPGQRTVISCSGSSSNIG 171
QY      179 SNTVNMVYQQLPGTAPKLLIYSNNORPSGVDPDRFSGFKSGTSASLVISGLQSEDEADYYCA 238
Db      172 SNTVNMVYQQLPGTAPKLLIYLNORPSGVDPDRFSGSKSGTSASLAISGLQSEDEADYYCL 231
QY      239 AMDESLNGVVFEGGPR 254
Db      232 TWDDSLNGPVFEGGTK 247
```

```
RESULT 8
US-10-293-418-1223
; Sequence 1223, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1223
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1223
```

```
Query Match
Best Local Similarity 73.6%; Score 1000.5; DB 12; Length 252;
Matches 196; Conservative 16; Mismatches 33; Indels 11; Gaps 3;
```

```
QY      1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIQH--DYMSWIRQPPGEGLEWIGFIFFDGSTN 58
Db      1 QVQLQESGPGVVKPSETLSLTCTVSGGFISSRTSYMGWIRQPPGKLEWIGNITYTGKTY 60
QY      59 YNPSLNGRVYITSLDTSKNQSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVW 118
Db      61 YSPSLKSRVTISADTSKNQSLRLTSVTAADTAVYFCARAGYDLTLGYPFYF-----DSW 115
QY      119 GQGTITVTPSGGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRYVISCSGSSSDIG 178
Db      116 GKGTMTVTVSSGGSGGGSGGGSGGGSG---AQSVLTQPPSASGTPGQRTVISCSGSSSNIG 171
QY      179 SNTVNMVYQQLPGTAPKLLIYSNNORPSGVDPDRFSGFKSGTSASLVISGLQSEDEADYYCA 238
Db      172 SNTVNMVYQQLPGTAPKLLIYLNORPSGVDPDRFSGSKSGTSASLAISGLQSEDEADYYCL 231
```

```
QY      239 AMDESLNGVVFEGGPR 254
Db      232 TWDDSLNGPVFEGGTK 247
```

```
RESULT 9
US-10-039-785-44
; Sequence 44, Application US/10039785
; Publication No. US20020067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T101AA02 bCFv
US-10-039-785-44
```

```
Query Match
Best Local Similarity 71.8%; Score 975.5; DB 13; Length 244;
Matches 188; Conservative 18; Mismatches 33; Indels 15; Gaps 2;
```

```
QY      1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIQHDYMSWIRQPPGEGLEWIGFIFFDGSTNYN 60
Db      1 QVQLQESGPGLVKPSSETLSLTCTVSGGISDYMSWVRQSPGKLEWIGSIDYAGSTNYN 60
QY      61 PSLNGRVYITSLDTSKNQSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWQ 120
Db      61 PSLKSRVTITIDSKSKQEPPLKIDSVTAADTAVYFCARQLGRI-----SDYWGQ 108
QY      121 GTTIVTPSGGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRYVISCSGSSSDIGSN 180
Db      109 GTIVTVSSGGSGGGSGGGSGGGSG---ALSYVLTQPPSASGTPGQRTVISCSGSSSNIGN 165
QY      181 TVNMVYQQLPGTAPKLLIYSNNORPSGVDPDRFSGFKSGTSASLVISGLQSEDEADYYCAW 240
Db      166 TVNMVYQQLPATAPKLLIYSNNORPSGVDPDRFSGSKSGTSASLAISGLQSEDEADYYCATW 225
QY      241 DESLNGVVFEGGPR 254
Db      226 DDSRGWVFGGTK 239
```

```
RESULT 10
US-10-139-785-44
; Sequence 44, Application US/10139785
```



```

; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014A02 scFv
US-10-139-785-44

```

```

Query Match          71.8%; Score 975.5; DB 14; Length 244;
Best Local Similarity 74.0%; Pred. No. 66-60;
Matches 188; Conservative 18; Mismatches 33; Indels 15; Gaps 2;

```

```

QY      1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIQHDYMSWIRQPPGEGLEWIGIFFDGSTNYN 60
DB      1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSISDYMSWVRQSPGKLEWIGSIDYAGSTNYN 60
QY      61 PSLNGRVTISLDTSKNQSLRLTSVTADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ 120
DB      61 PSLKSRVTWTIDSKKQPLKIDSVTADTAVYCARQLGRI-----SDYWGQ 108
QY      121 GTTIVTPSGGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRVVISCSGSSSDIGSN 180
DB      109 GTLVTVSSGGGGSGGGSGGGSGGS---ALSYVLTPPSASGTPGQRVVISCSAGSSSNIGN 165
QY      181 TVNMWYQQLPPTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCAAW 240
DB      166 TVNMWYQQLPATAPKLLIYSNNQRPSPGVDRFSGSKSGTSASLVISGLQSEDEADYYCATW 225
QY      241 DESLNGVVFEGGPR 254
DB      226 DDSRGWVFGGGTK 239

```

```

RESULT 11
US-09-880-748-1642
; Sequence 1642, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15

```

```

; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1642
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1642

```

```

Query Match          71.7%; Score 975; DB 10; Length 255;
Best Local Similarity 74.5%; Pred. No. 6.8e-60;
Matches 190; Conservative 23; Mismatches 36; Indels 6; Gaps 2;

```

```

QY      1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIQHDYMSWIRQPPGEGLEWIGIFFDGSTNYN 60
DB      1 QVQLQWAGALLKPSSETLSLTCAVYGSFSGYMSWIRQSPGKLEWIGIEINHGSTNYN 60
QY      61 PSLNGRVTISLDTSKNQSLRLTSVTADTAVYFCARLKGAWLSEPPYFSSDGMVWG 119
DB      61 PSLKSRVTISVDASKNQFSLKSSVTADTAVYCARERSYVDILTGYSPRSKYGMVWG 120
QY      120 QGTTIVTPSGGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRVVISCSGSSSDIGS 179
DB      121 RGLLVTV-----SSGGGGSGGGSGGGSGSVLTQPPSASGTPGQRVVISCSGSSSNIGS 175
QY      180 NTVMWYQQLPPTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCAA 239
DB      176 NTVMWYQRLPGAAPQLLIYNNQRPSPGIPDRFSGSKSGTSGLVVISGLQSEDEADYYCAS 235
QY      240 WDESLNGVVFEGGPR 254
DB      236 WDDSLNGRVFEGGGTK 250

```

```

RESULT 12
US-10-293-418-1642
; Sequence 1642, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1642
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1642

```

## Query Match

Best Local Similarity 71.7%; Score 975; DB 12; Length 255;  
Matches 190; Conservative 23; Mismatches 36; Indels 6; Gaps 2;

```
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRPPGEGLEWIGFIFPDGSTN 60
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRPPGEGLEWIGFIFPDGSTN 60
QY 61 PSLNGRVTISLDTSKNQSLRLTSVTAADTAVYFCARLKGAW-LLSEPPYFSSDGMVWG 119
DB 61 PSLKSRVTISVDASKNQFSLKLSVTAADTAVYFCARERSYDILTGYSPPRSKYGMVWG 120
QY 120 QGTITVTPSGGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRVISICSGSSSDIGS 179
DB 121 RGLTVT-----SSGGSGSGGGSGGGSGGGSVLTQPPSASGTPGQRVITISCGSSSNIGS 175
QY 180 NTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCA 239
DB 176 NTVMWYQRLPGAAPQLLIYNNDQRPSPGIPDRFSGSKSGTSGLVISGLQSEDEADYYCA 235
QY 240 WDESINGVVFSGGPR 254
DB 236 WDSLNGRVFVGGTK 250
```

## RESULT 13

```
US-09-880-748-1994
; Sequence 1994, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1994
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1994
```

## Query Match

Best Local Similarity 70.9%; Score 963.5; DB 10; Length 252;  
Matches 187; Conservative 22; Mismatches 36; Indels 11; Gaps 3;

```
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSI--GHYMSWIRPPGEGLEWIGFIFPDGSTN 58
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSI--GHYMSWIRPPGEGLEWIGFIFPDGSTN 58
QY 59 YNPISLNGRVTISLDTSKNQSLRLTSVTAADTAVYFCARLKGAWLLSEPPYFSSDGMVWG 118
DB 61 YNPISLKRVSMSVDTSKNQYSLKLSVTAADTAVYFCARLR-----PDADYGDYGFDMW 114
QY 119 GGGTITVTPSGGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRVISICSGSSSDIG 178
DB 115 GGGTMTVTVSSGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRVISICSGSSSDIG 178
QY 179 SNTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCA 238
DB 172 SNTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCA 231
```

QY 239 AMDESINGVVFSGGPR 254

DB 232 TWDDRRLGLVFGGTK 247

## RESULT 14

```
US-10-293-418-1994
; Sequence 1994, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1994
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1994
```

## Query Match

Best Local Similarity 70.9%; Score 963.5; DB 12; Length 252;  
Matches 187; Conservative 22; Mismatches 36; Indels 11; Gaps 3;

```
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSI--GHYMSWIRPPGEGLEWIGFIFPDGSTN 58
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSI--GHYMSWIRPPGEGLEWIGFIFPDGSTN 58
QY 59 YNPISLNGRVTISLDTSKNQSLRLTSVTAADTAVYFCARLKGAWLLSEPPYFSSDGMVWG 118
DB 61 YNPISLKRVSMSVDTSKNQYSLKLSVTAADTAVYFCARLR-----PDADYGDYGFDMW 114
QY 119 GGGTITVTPSGGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRVISICSGSSSDIG 178
DB 115 GGGTMTVTVSSGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRVISICSGSSSDIG 178
QY 179 SNTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCA 238
DB 172 SNTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCA 231
QY 239 AMDESINGVVFSGGPR 254
DB 232 TWDDRRLGLVFGGTK 247
```

## RESULT 15

```
US-10-039-785-50
; Sequence 50, Application US/10039785
; Publication No. US20020067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
```

; CURRENT APPLICATION NUMBER: US/10/039,785  
; CURRENT FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: 60/369,860  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 60/341,237  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 60/331,310  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/331,044  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/327,364  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/323,807  
; PRIOR FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 60/309,176  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: 60/294,981  
; PRIOR FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: 60/293,473  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 50  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: T1015A02 scfv  
; NAME/KEY: SITE  
; LOCATION: (250)  
; OTHER INFORMATION: Xaa equals either Gly or Ser  
US-10-039-785-50

Query Match 70.7%; Score 960.5; DB 13; Length 250;  
Best Local Similarity 74.0%; Pred. No. 6.7e-59;  
Matches 188; Conservative 22; Mismatches 31; Indels 13; Gaps 5;

QY 1 QVQLQESGPGLVKPSETLSLTCTVSGSGSI GHD--YMSWIRQPPGEGLEWIGFIFFDGS TN 58  
DB 1 QVQLQESGPGLVKPSETLSLTCTVSGSGSI GHD--YMSWIRQPPGEGLEWIGFIFFDGS TN 60  
QY 59 YNPSTLNGRVTISLDTSKNQLSLRLTSVTADTAVYFCARLKGAWLSEPPYFSSDGM DVW 118  
DB 61 YKPSLRSLRSLTSMDSRNQFSLKLTSTADTALYYCVR--EW--ANGDHWSA--FDLW 113  
QY 119 GQGTTVTVPSGGGGSGGGSGGGSGGSGNFM LTOPPSASGTPGQRVVISCSGSSSDIG 178  
DB 114 GQGTLVTVSSGGGGSGGGSGGGSGGSG-- --AQA VLTQPSASGTPGQRVTI PCSGSSSNIG 169  
QY 179 SNTVNMVYQQLPGTAPKLLIYSNNQRP SGVDFRSGFKSGTSASLVISGLQSEDEADYYCA 238  
DB 170 GNTVNMVYQQLPGTAPKLLIYGNDRP SGVDFRSGFKSGTSASLVITGLQSEDEADYYCA 229  
QY 239 AWDESLNGVVFEGG 252  
DB 230 AWDSLIGYVFGTG 243

Search completed: May 13, 2004, 15:43:31  
Job time : 38.6068 secs

THIS PAGE OF THE REPORT  
IS NOT TO BE REPRODUCED



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:50:27 ; Search time 11.467 Seconds  
(without alignments)  
2130.694 Million cell updates/sec

Title: US-10-072-301-19

Perfect score: 1359

Sequence: 1 QVQLQESGPGLVKPSSETLSL.....YYCAWDESLNGVVFGGGPR 254

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	559.5	41.2	268	2	A56446	Ig heavy chain V r
2	534	39.3	249	2	S41374	single chain Fv an
3	509	37.5	233	2	S25752	Ig lambda chain -
4	490	36.1	112	2	D44151	Ig lambda chain V
5	487.5	35.9	135	2	S78051	Ig heavy chain pre
6	486.5	35.8	155	2	S31511	Ig heavy chain - h
7	485.5	35.7	149	2	S23626	Ig lambda chain V
8	483.5	35.6	155	2	S31512	Ig heavy chain - h
9	483	35.5	234	2	S25757	Ig lambda chain -
10	481	35.4	117	2	S23627	Ig lambda chain pr
11	479	35.2	112	2	A44151	Ig lambda chain V
12	479	35.2	112	2	B44151	Ig lambda chain V
13	478.5	35.2	140	2	I37782	Ig variable region
14	478.5	35.2	233	2	JC5322	p53 specific singl
15	478	35.2	98	2	S36047	Ig lambda chain -
16	478	35.2	129	2	S78058	Ig lambda chain pr
17	476	35.0	137	2	S31676	Ig heavy chain V r
18	475	35.0	110	2	S57408	Ig lambda chain V-
19	475	35.0	112	2	C44151	Ig lambda chain V
20	475	35.0	216	2	A42193	Ig lambda chain (B
21	474.5	34.9	130	2	S31690	Ig heavy chain V r
22	474.5	34.9	146	2	S09711	Ig heavy chain V r
23	474	34.9	130	2	S78057	Ig lambda chain pr
24	472.5	34.8	235	2	S25754	Ig lambda chain -
25	471	34.7	233	2	S25744	Ig lambda chain -
26	467	34.4	130	2	S30534	Ig heavy chain V r
27	466	34.3	235	2	S25750	Ig lambda chain -
28	464	34.1	118	2	S20780	Ig heavy chain V r
29	460	33.8	139	2	S31586	Ig heavy chain V r

30	456	33.6	110	2	S57428	Ig light chain V-J
31	453.5	33.4	147	2	S13519	Ig heavy chain V r
32	449	33.0	98	2	S36048	Ig lambda chain -
33	447	32.9	146	1	G1H0H2	Ig heavy chain pre
34	446.5	32.9	129	1	D2H0WA	Ig heavy chain V-I
35	444.5	32.7	105	2	S44125	Ig lambda chain V
36	444.5	32.7	121	2	S44113	Ig heavy chain V r
37	444	32.7	220	2	A49444	Ig gamma-1 heavy c
38	444	32.7	231	2	B23746	Ig Fab region IV-J
39	443.5	32.6	143	2	B49028	Ig heavy chain V-I
40	443	32.6	97	2	S26906	Ig heavy chain V r
41	442.5	32.6	146	2	S09710	Ig heavy chain V r
42	442	32.5	116	2	B26340	Ig heavy chain pre
43	440	32.4	97	2	S12416	Ig heavy chain V r
44	440	32.4	145	2	S78055	Ig heavy chain pre
45	439	32.3	118	2	S24443	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996  
C;Accession: A56446  
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.  
J. Biol. Chem. 270, 7829-7835, 1995  
A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident  
A;Reference number: A56446; MUID:95229583; PMID:7713873  
A;Accession: A56446  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-268 <TRAN>  
A;Cross-references: GB:U20617  
A;Keywords: heterotetramer; immunoglobulin

Query Match 41.2%; Score 559.5; DB 2; Length 268;  
Best Local Similarity 47.3%; Pred. No. 2.2e-29;  
Matches 121; Conservative 35; Mismatches 77; Indels 23; Gaps 6;

QY	1	QVQLQESGPGLVKPSSETLSLTCTVSGSGIGHDYMSWIRQPPGEGLEWIGFIF-FDGSTNY 59
DB	3	QVQLQESGABLVKPGASVKLSCTTSGFNIKDTYMAWVKQRPQGLEWIGRIAPANGITKY 62
QY	60	NPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWG 119
DB	63	DPKFGKATIAADTSNTAYLQJSSLTSEDYAVYCA-----SYLTRENYWG 111
QY	120	QGTIVTPSGGGSGGGSGGGSGGSGNFMLTQPPS-ASGTPGQRVISICSGSSSDIG 178
DB	112	QGTIVTV-----SSGGSGGGSGGGSGGSDIELTQSPAIMSASLGEKVTWSCRASSS--- 163
QY	179	SNTVNWYQQLPGTAPKLLIYSNQRPSGVPDRFSGFKSGTSASLVISGLQSEDEADYYCA 238
DB	164	VNFIYVYQKSDASPKLWVYVYTSHLPGVPARFSGSGSGNSYSLTSSMEGEDATYYCQ 223
QY	239	AWDESLNGVVFGGGPR 254
DB	224	QFTSS--PFTFGSGTK 237

RESULT 2

S41374  
single chain Fv antibody - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C;Accession: S41374  
R;Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.  
submitted to the EMBL Data Library, January 1994  
A;Description: Construction and functional characterization of a single chain Fv antibod  
A;Reference number: S41374

A/Accession: S41374  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-249 <ART>  
A/Cross-references: EMBL:Z29480

Query Match  
Best Local Similarity 39.3%; Score 534; DB 2; Length 249;  
Matches 122; Conservative 34; Mismatches 81; Indels 22; Gaps 7;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIQHDYMSWIRQPPGEGLEWIGFIF-FDGSTNY 59  
Db 1 QVQLQESGAEIVRPGASVKLSCTASGFNPKDYLHWVKQRPKEGLEWIAIAPASGNTKY 60  
QY 60 NPSLNGRVTISLDTSKNQLSLRLTSVTADTAIVYFCARLKGAWLSEPPYFSSDGMVWG 119  
Db 61 VPRFQDKATITADTSNTAYLLSLTSEDTAVYYCAR-----RDTLYTS---LGWVG 110  
QY 120 QGTTVTVPSSGGSGSGGGSGGGSGGNFMLTQ-PPSASGTPGQRVISICSGSSSDI- 177  
Db 111 QGSTVTV-----SSRGGSGGGSGGGSGGSDIELTQSPPSVVVIPGESVISICRSSKSLLY 165  
QY 178 --GSNTVWVYQQLPGTAPKLLIYSNNQRPSGVPPDRFSGFKSGTSASLVISGLQSEDEADY 235  
Db 166 SDGDSYLFWFLQRPQGSPQLLIYRMSNLASGVPPDRFSGSGSGTSFTLRISRVEADVGIVY 225  
QY 236 YCAAWDESLNGVVFSGGPR 254  
Db 226 YCMQHRE--YPLTFGAGTK 242

RESULT 3  
S25752  
Ig lambda chain - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_\_revision 26-May-1995 #text\_change 21-Jan-2000  
C/Accession: S25752  
R/Combrlato, G.; Klobeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin 1ar  
A/Reference number: S16439; MUID:91257162; PMID:19043362  
A/Accession: S25752  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-233 <COM>  
A/Cross-references: EMBL:X57817; NID:G33733; PIDN:CAA40954.1; PID:G33734  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/148-216/Domain: immunoglobulin homology <IMM>

Query Match  
Best Local Similarity 37.5%; Score 509; DB 2; Length 233;  
Matches 96; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
QY 145 GGGSNFMLTOPPSASGTPGQRVISICSGSSSDIGSNTVWVYQQLPGTAPKLLIYSNNQRP 204  
Db 14 GSWAQSVLTQPPSASGTPGQRVITISCGSSSNIGSNTVWVYQQLPGTAPKLLIYRNNQRP 73  
QY 205 SGVPDRFSGFKSGTSASLVISGLQSEDEADYYCAAWDESLNGVVFSGGPR 254  
Db 74 SGVPDRFSGFKSGTSASLVISGLQSEDEADYYCAAWDESLNGVVFSGGPR 123

RESULT 4  
D44151  
Ig lambda chain V region (BO-12) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 27-Jun-1994 #sequence\_\_revision 27-Jun-1994 #text\_change 21-Jan-2000  
C/Accession: D44151  
R/Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.; Graff, R.; Degraw, J.; Pye  
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992  
A/Title: Human combinatorial antibody libraries to hepatitis B surface antigen.  
A/Reference number: A44151; MUID:92228746; PMID:1373487

A/Accession: D44151  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-112 <ZEB>  
A/Note: nucleotide translation is not given  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/14-90/Domain: immunoglobulin homology <IMM>

Query Match  
Best Local Similarity 36.1%; Score 490; DB 2; Length 112;  
Matches 92; Conservative 6; Mismatches 5; Indels 0; Gaps 0;  
QY 152 LTQPPSASGTPGQRVISICSGSSSDIGSNTVWVYQQLPGTAPKLLIYSNNQRPSPGPR 211  
Db 3 LTQPPSASGTPGQRVITISCGSSSNIGSNTVWVYQQLPGTAPKLLIYSNNRPSGVPPDRF 62  
QY 212 SGFKSGTSASLVISGLQSEDEADYYCAAWDESLNGVVFSGGPR 254  
Db 63 SASKSGTSASLVISGLQSEDEADYYCAAWDESLHGPVFGGTR 105

RESULT 5  
S78051  
Ig heavy chain precursor V-D-J region (clone mAb 61VH) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-Nov-1997 #sequence\_\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C/Accession: S78051; S23716  
R/Harindranath, N.  
submitted to the EMBL Data Library, August 1990  
A/Reference number: S78051  
A/Accession: S78051  
A/Molecule type: mRNA  
A/Residues: 1-135 <HAR>  
A/Cross-references: EMBL:X54437; NID:G37814; PIDN:CAA38306.1; PID:G930117  
R/Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Nockins  
Int. Immunol. 3, 865-875, 1991  
A/Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h  
patient.  
A/Reference number: S23716; MUID:92031262; PMID:1718404  
A/Accession: S23716  
A/Molecule type: mRNA  
A/Residues: 13-111 <HAW>  
A/Cross-references: EMBL:X54437  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F/1-13/Domain: signal sequence (fragment) #status predicted <SIG>  
F/14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>  
F/27-111/Domain: immunoglobulin homology <IMM>

Query Match  
Best Local Similarity 35.9%; Score 487.5; DB 2; Length 135;  
Matches 95; Conservative 12; Mismatches 14; Indels 9; Gaps 2;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSI--GHDYMSWIRQPPGEGLEWIGFIFFDGSTN 58  
Db 13 QVQLQESGPGLVKPSSETLSLTCTVSGGSI--GHDYMSWIRQPPGEGLEWIGFIFFDGSTN 58  
QY 59 YNPSLNGRVTISLDTSKNQLSLRLTSVTADTAIVYFCARLKGAWLSEPPYFSSDGMVW 118  
Db 73 YNPSLNGRVTISLDTSKNQLSLRLTSVTADTAIVYFCARLKGAWLSEPPYFSSDGMVW 118  
QY 119 GGGTTVTVPSS 128  
Db 126 GGGTTVTVPSS 135

RESULT 6  
S31511  
Ig heavy chain - human  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C/Accession: S31511





A; Introns: 16/1  
C; Superfamily: immunoglobulin V region; immunoglobulin homology  
C; Keywords: heterotetramer; immunoglobulin  
F; 34-110/Domain: immunoglobulin homology <IMM>

Query Match	35.4%	Score 481;	DB 2;	Length 117;
Best Local Similarity	89.2%	Pred. No. 1.1e-24;		
Matches 91; Conservative				

[illegible]

RESULT 11  
A44151  
Ig lambda chain V region (BO-08) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 21-Jan-2000  
C/Accession: A44151  
R/Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caethien, R.H.; Graff, R.; Degraw, J.; Pya  
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992  
A/Title: Human combinatorial antibody libraries to hepatitis B surface antigen.  
A/Reference number: A44151; MUID:92228746; PMID:1373487  
A/Accession: A44151  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-112 <ZEB>  
A/Note: nucleotide translation not given  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/14-90/Domain: immunoglobulin homology <IMM>

```

Query Match          35.2%; Score 479; DB 2; Length 112;
Best Local Similarity 86.4%; Pred. No. 1.4e-24;
Matches      89; Conservative      8; Mismatches    6; Indels     0; Gaps     0;

QY      152 LTOPPSASGTPGQRVSISSGSSSDIGSNTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRF   211
        ||| | | | | | | | | | : | | | | | : | | | | | | | | | | | | | | | |
Db       3    LTQPFSASGTGGQRVTISCSGSSSNIGTNTVMWYQQLPGRAPKLLIYSNNERPSPGVDRF   62
        ||| | | | | | | | | | : | | | | | : | | | | | | | | | | | | | | | |

QY      212 SGFKSGTSASLVISGLSEDEADYYCAAMDESILNGVFGGPR   254
        ||| | | | | | | | | | : | | | | | : | | | | | | | | | | | | | | | |
Db       63 SSKAGTSASLAIISGLSEDEADYYCEAMDNDNLHGEVFGGTR   105

```

RESULT 12  
B44151  
Ig lambda chain V region (BO-09) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 21-Jan-2000  
C/Accession: B44151  
R/Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caochien, R.H.; Graff, R.; Degraw, J.; Pyra  
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992  
A/Title: Human combinatorial antibody libraries to hepatitis B surface antigen.  
A/Reference number: A44151; MUID:9228746; PMID:1373487  
A/Accession: B44151  
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A/Molecule type: mRNA  
A/Residues: 1-112 <ZEB>  
A/Cross-references: GB:M88310; NID:g183954; PIDN:AAA35968.1; PID:g183955  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/14-90/Domain: immunoglobulin homology <IMM>

Query Match	35.2%;	Score 479;	DB 2;	Length 112;
Best Local Similarity	86.4%;	Pred. No. 1.4e-24;		
Matches 89;	Conservative 7;	Mismatches 7;	Indels 0;	Gaps 0;

**QY**      152 LTPPSASGTPGORVSISSCGSSSDIGSNTVMWYOQLPGTAPKLLIYSNNQRPSGVDRF    211  
||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :  
**Dd**         3 LTQPSPASGTPEGRTVISCSGSSSNIGNTVNMWOQLPGAARKLLIYSNNERPISGVDRF    62  
||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :  
**QY**      212 SGFKSGTSASLYISGLQSEDEADYYCAAMDESINGVPFGGPR    254  
||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :  
**Dd**         63 SGGSKGSTASIATISGLQSEDEADYYCEAMDSDLQGPIFGGTR    105  
||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 13  
137782  
Ig variable region (VDJ) (clone T23-9) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Feb-1996 #sequence\_reviseion 13-Mar-1997 #text\_change 23-Jul-1999  
C/Accession: I37782; S25476  
R/Dematson, C.; Chastagner, P.; Theze, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A/Title: Somatic diversification in the heavy chain variable region genes expressed by  
A/Reference number: A36876; MUID:94119917; PMID:8290556  
A/Accession: I37782  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-140 <RES>  
A/Cross-references: EMBL:X67906; NID:g33582; PIDN:CA448104.1; PID:g33583  
C/Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>  
F/46-128/Domain: immunoglobulin homology <IMM>

Query Match	35.2%;	Score 478.5;	DB 2;	Length 140;
Best local Similarity	73.6%;	Pred. No. 1.9e-24;		
Matches	95; Conservative	9; Mismatches	16; Indels	9; Gaps
QY	1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRPPQEGLEWIGFIFDGSNTYN	60		
Db	20 QVQLQESGPGLVKPSSETLSLTCTVSGSGSISSYMSWIRQPPQGLEWIGIYISGSNTYN	79		
QY	61 PSINGRVTISLDTSKNQLSLRLTSVTAADTAVFYFCAR-LKGAWLLSEPPYFSSDGMVWG	119		
Db	80 PSLKSRVTISVDTSKNGPSLKLSSVTAADTAAYVYCARHNSSSWY---GRYF-----DYWG	131		
QY	120 QGTTVTVP	128		
Db	132 QGTLVTSS	140		

RESULT 14  
JC5322  
p53 specific single-chain antibody Pab421 - human  
C:Species: Homo sapiens (man)  
C:Date: 15-May-1997 #sequence  
C/Accession: JC5322  
R:Jannot, C.B.; Hynes, N.E.  
Biochem. Biophys. Res. Commun. 230, 242-246, 1997  
A:/Title: Characterization of scFv-421, a single-chain antibody targeted to p53.  
A:/Reference number: JC5322; MUID:97168950; PMID:9016757  
A:/Accession: JC5322  
A:/Molecule type: mRNA  
A:/Residues: 1-233 <JAN>  
A:/Experimental source: hybridoma cell  
C:/Comment: This protein sequence is identical to the one in the database.



Db 105 VTV-----SSGGGGSGGRASGGGSDIELTQSPASLAVSLGQRATISCRASVSSTSGYS 159

QY 181 TVNMWYQQLPGTAPKLLIYSNNQRPSCVPDRFSGFKSGTSASLVISGLQSEDEADYYC 237

Db 160 YMHWNQOKPGQPPRLLIYLVSNLESGVPARFSGSGSGDTFTLNHHVVEEEDAAITYYC 216

## RESULT 15

S36047  
Ig lambda chain - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 01-Dec-1995 #text\_change 21-Jan-2000  
C/Accession: S36047  
R,Williams, S.C.  
submitted to the EMBL Data Library, April 1993  
A/Reference number: S36046  
A/Accession: S36047  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-98 <WIL>  
A/Cross-references: EMBL:Z22188; NID:G312291; PIDN:CAA80198.1; PID:G312292  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;15-91/Domain: immunoglobulin homology <IMM>

Query Match	35.2%	Score 478;	DB 2;	Length 98;
Best Local Similarity	93.8%	Pred. No. 1.4e-24;		
Matches	90;	Conservative	4;	Mismatches 2;
			Indels	0;
			Gaps	0;

```
QY 151 MLTQPPSASGTPGQRVISICSSGSSSDIGSNTVNWYQQLPGTAPKLLIYSNNORPSGVDPDR 210
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 VLTQPPSASGTPGQRVITISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPSGVDPDR 62

QY 211 FSGFKSGTSASLVIISGLQSEDEADYYCAAWDESLNG 246
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 FSGSKSGTSASLAIISGLQSEDEADYYCAAWDDSLNG 98
```

```
Search completed: May 13, 2004, 15:08:42
Job time : 13.467 secs
```

... PAGE 04/11 (08/09)

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:01 ; Search time 7.15146 Seconds  
(Without alignments)  
1849.388 Million cell updates/sec

Title: US-10-072-301-19  
Perfect score: 1359  
Sequence: 1 QVQLQESGPGLVKPSSETLSL.....YYCAWDESLNGVFGGPR 254

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	447	32.9	146	1 HV2I_HUMAN	P06331 homo sapien
2	446.5	32.9	129	1 HV2F_HUMAN	P01824 homo sapien
3	436.5	32.1	112	1 LV1H_HUMAN	P06887 homo sapien
4	435	32.0	111	1 LV1A_HUMAN	P01699 homo sapien
5	429	31.6	109	1 LV1F_HUMAN	P04208 homo sapien
6	418	30.8	130	1 LV1G_HUMAN	P06316 homo sapien
7	416	30.6	111	1 LV1D_HUMAN	P01702 homo sapien
8	413.5	30.4	112	1 LV1B_HUMAN	P01700 homo sapien
9	403.5	29.7	117	1 HV2G_HUMAN	P01825 homo sapien
10	400	29.4	111	1 LV1C_HUMAN	P01701 homo sapien
11	394	29.0	109	1 LV1I_HUMAN	P06888 homo sapien
12	365.5	26.9	137	1 HV46_MOUSE	P01822 mus musculu
13	362.5	26.7	113	1 HV47_MOUSE	P01823 mus musculu
14	359	26.4	111	1 LV2G_HUMAN	P01710 homo sapien
15	346.5	25.5	111	1 LV6D_HUMAN	P06318 homo sapien
16	346	25.5	111	1 LV2F_HUMAN	P01709 homo sapien
17	344.5	25.3	116	1 HV60_MOUSE	P18531 mus musculu
18	341.5	25.1	112	1 LV2K_HUMAN	P04209 homo sapien
19	341.5	25.1	144	1 HV43_MOUSE	P01819 mus musculu
20	340	25.0	111	1 LV2B_HUMAN	P01705 homo sapien
21	337	24.8	103	1 LV1E_HUMAN	P01703 homo sapien
22	335	24.7	111	1 LV2D_HUMAN	P01707 homo sapien
23	333	24.5	111	1 LV2C_HUMAN	P01706 homo sapien
24	333	24.5	111	1 LV2H_HUMAN	P01711 homo sapien
25	329.5	24.2	116	1 HV61_MOUSE	P18532 mus musculu
26	324.5	23.9	110	1 LV2J_HUMAN	P01713 homo sapien
27	324.5	23.9	131	1 LV6E_HUMAN	P06319 homo sapien
28	324	23.8	109	1 LV2E_HUMAN	P01708 homo sapien
29	324	23.8	111	1 LV2I_HUMAN	P01712 homo sapien
30	324	23.8	117	1 HV62_MOUSE	P18533 mus musculu
31	320.5	23.6	112	1 LV6A_HUMAN	P01721 homo sapien
32	319	23.5	111	1 LV3B_HUMAN	P80748 homo sapien
33	319	23.5	135	1 HV02_XENLA	P20957 xenopus lae

34	318	23.4	106	1 LV4B_HUMAN	P01716 homo sapien
35	316	23.3	111	1 LV2A_HUMAN	P01704 homo sapien
36	313	23.0	106	1 LV4A_HUMAN	P01715 homo sapien
37	309	22.7	106	1 LV4E_HUMAN	P06889 homo sapien
38	305	22.4	108	1 LV5A_HUMAN	P01719 homo sapien
39	305	22.4	120	1 HV2B_HUMAN	P01815 homo sapien
40	302.5	22.3	125	1 HV2D_HUMAN	P01817 homo sapien
41	301	22.1	107	1 LV4C_HUMAN	P01717 homo sapien
42	301	22.1	111	1 LV6C_HUMAN	P06317 homo sapien
43	300	22.1	115	1 HV44_MOUSE	P01820 mus musculu
44	299	22.0	147	1 HV2H_HUMAN	P04438 homo sapien
45	292.5	21.5	119	1 HV2C_HUMAN	P01816 homo sapien

ALIGNMENTS

RESULT 1

ID	HV2I_HUMAN	STANDARD;	PRT;	146 AA.
AC	P06331;			
DT	01-JAN-1988 (Rel. 06, Created)			
DT	01-JAN-1988 (Rel. 06, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig heavy chain V-II region ARH-77 precursor.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85205332; PubMed=3922855;			
RA	Kudo A., Ishihara T., Nishimura Y., Watanabe T.;			
RT	"A cloned human immunoglobulin heavy chain gene with a novel direct-			
RT	repeat sequence in 5' flanking region.";			
RL	Gene 33:181-189(1985).			
DR	PIR; A02101; GIH0H2.			
DR	HSSP; P01825; 7FAB.			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	GO; GO:0003823; F:antigen binding; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PSS0835; IG LIKE; 1.			
KW	Immunoglobulin V region; Signal.			
FT	SIGNAL 1 19			
FT	CHAIN 20 146			
FT	DOMAIN 20 117			
FT	DOMAIN 118 127			
FT	DOMAIN 128 146			
FT	DISULFID 42 115			
FT	NON_TER 146 146			
SQ	SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;			

Query Match 32.9%; Score 447; DB 1; Length 146;  
Best Local Similarity 70.8%; Pred. No. 8.8e-25;  
Matches 92; Conservative 8; Mismatches 24; Indels 6; Gaps 3;

Qy	1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRPPGEGLEWIGFIFPDGSTNN 60
Db	21 QVQLQGWAGLVKPSSETLSLTCAVFGGSGYWSWIRQPPRGLEWIGELNHSGSTNYK 80
Qy	61 PSINGRVTISLDTSKNQLSLRLTSVTAADTAVYFCAR--LKGAWLSEPPYFSSDGMVW 118
Db	81 TSLKSRVTISLDTSKNLSFKLSSSVTAADTAVYCARGLRGW--NDVDYTY--GMDVW 136
Qy	119 GGGTVTVPS 128
Db	137 GGGTVTVSS 146

## RESULT 2

```

ID HV2F_HUMAN STANDARD; PRT; 129 AA.
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region WAF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=8222235; PubMed=6806818;
RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
RL immunoglobulin D.";
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02099; D2HUMA.
DR HSSP; P01825; 7FAB.
DR GLYCOSULEDB; P01824; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region.
KW DOMAIN
FT NON_TER 1 113 IG-LIKE.
FT SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;
SQ
Query Match
Best Local Similarity 32.9%; Score 446.5; DB 1; Length 129;
Matches 88; Conservative 15; Mismatches 19; Indels 13; Gaps 3;
QY 1 QVQLQESGGPGLVKPSETLSLTCTVSGSGISGHD--YMSWIRQPPGEGLEWIGFIFPDGSTN 58
DB 1 RLQLQESGPGLVKPSSETLSLTCTVSGGPIRRTGYTWGIRQPPGKLEWIGVYTGSTY 60
QY 59 YNPSLNGRVTISLDTSKNQISLRITSVTAADFAVYFCARLKGAMLISEPPYF-----SSD 113
DB 61 YNPSLRGRVTISVDTSRNQFSLNLRMSAADTAMYYCAR-----GNPPPYDIDIGTGSDD 114
QY 114 GMDVWGQGTITVTPS 128
DB 115 GIDVWGQGTIVHVS 129
```

## RESULT 3

```

ID LV1H_HUMAN STANDARD; PRT; 112 AA.
AC P06887;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-I region MEM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=85257662; PubMed=2410269;
RA Mihaesco E., Roy J.P., Congy N., Peran-Rivat L., Mihaesco C.;
RT "The amino acid sequence of a lambda light chain presenting abnormal
RT physicochemical and antigenic features.";
```

```

RL Eur. J. Biochem. 150:349-357(1985).
CC -1- MISCELLANEOUS: RESIDUES 33-36 AND SOME OF THE SEQUENCED PEPTIDES
CC WERE POSITIONED BY HOMOLOGY.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+
CC MARKERS.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A25479; LIHUM.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody;
KW Pyroliidone carboxylic acid.
FT MOD_RES 1 106 IG-LIKE.
FT DISULFID 22 90 PYROLIDONE CARBOXYLIC ACID.
FT NON_TER 112 112 BY SIMILARITY.
SQ SEQUENCE 112 AA; 11789 MW; 748124F079CFB84 CRC64;
```

Query Match

Best Local Similarity 32.1%; Score 436.5; DB 1; Length 112;  
Matches 84; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

```

QY 151 MLTPPSASGTPGQRVISCSGSSSDIGSN-TVMWYQQLPGTAPKLLIYSNNQRPSCVDP 209
DB 3 VLTQPSASGTPGQRVITISCSGSSSNWGSNZPAYWYQQLPGTAPKLLIYNQRPSCVDP 62
QY 210 RFSGFKSGTSASLVISGLQSEDEADYYCAAMDESLNGVFGGPR 254
DB 63 RFSASRSGTSASLAISGLQSEDEADYYCAAMWDSLDGYVFGTGTK 107
```

## RESULT 4

```

ID LV1A_HUMAN STANDARD; PRT; 111 AA.
AC P01699;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-I region VOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023790; PubMed=809332;
RA Engelhard M., Hillechmann N.;
RT "Pattern of antibody structure. The amino acid sequence of a
RT monoclonal immunoglobulin L-chain of lambda-type, subgroup I
RT (Bence-Jones-protein Vor.). A contribution to the elucidation of the
RT origin of antibody specificity.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:1413-1444(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE OZ+ MARKER.
CC -1- SIMILARITY: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01962; LIHUV.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein;
KW Pyroliidone carboxylic acid.
```



```

FT DOMAIN 1 105 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 89 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11514 MW; 21D9F64250DFC8E0 CRC64;

Query Match
Best Local Similarity 32.0%; Score 435; DB 1; Length 111;
Matches 81; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 151 MLTOPPSASGTPGQRVSTISCGSSSDIGSNTVMWYQQLPGTAPKLLIYSNNORPSGVPPDR 210
DB 3 VLTQPPSASGTPGQRVTITSCSGNFDIGRNSVMWYQVHPGTAPRLILLIYSSDQRSSGVPPDR 62

QY 211 FSGFKSGTSASLVIISGLQSEDEADYYCAAMDESINGVFEGGGPR 254
DB 63 FSGSKSGTSASLAISGLRSEDEADYYCATWDSLDGPVFGGGTK 106

RESULT 5
LVIF_HUMAN
ID LVIF_HUMAN STANDARD; PRT; 109 AA.
AC P04208;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
OS Ig lambda chain V-I region WAH.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83221661; PubMed=6407018;
RA Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
RT "Complete covalent structure of a human immunoglobulin D: sequence of
RL the lambda light chain.";
Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
DR PIR; A01967; LIHUWA.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 97 V SEGMENT.
FT DOMAIN 98 109 J SEGMENT.
FT DISULFID 22 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;

Query Match
Best Local Similarity 31.6%; Score 429; DB 1; Length 109;
Matches 84; Conservative 6; Mismatches 10; Indels 2; Gaps 1;

QY 151 MLTOPPSASGTPGQRVSISCGSSSDIGSNTVMWYQQLPGTAPKLLIYSNNORPSGVPPDR 210
DB 3 VLTQPPSASGTPGQRVTITSCGSSSNIGRYVYWYQQLPGTTPKLLIKDNQRPSPGVPPDR 62

QY 211 FSGFKSGTSASLVIISGLQSEDEADYYCAAMDESINGVFEGGG 252
DB 63 FSGSKSGTSASLAISGLRSEDEADYYCAAMDLSL--WVFGGG 102

RESULT 6
LVIG_HUMAN
ID LVIG_HUMAN STANDARD; PRT; 130 AA.
AC P06316;
DT 01-JAN-1988 (Rel. 06, Created)

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DT 01-JAN-1988 (Rel. 06, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE Ig lambda chain V-I region BL2 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=85062823; PubMed=6095199;
RA Tsujimoto Y., Croce C.M.;
RT "Molecular cloning of a human immunoglobulin lambda chain variable
RT sequence.";
RL Nucleic Acids Res. 12:8407-8414(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; X01147; CAA25598.1; -.
DR PIR; A01966; L1HUBL.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT 1 19
FT CHAIN IG LAMBDA CHAIN V-I REGION BL2.
FT DOMAIN 20 115 V SEGMENT.
FT DOMAIN 116 130 J SEGMENT.
FT DISULFID 41 108 BY SIMILARITY.
FT NON TER 130 130
FT SEQUENCE 130 AA; 13564 MW; FA44BB17D3A55EBF CRC64;
SQ
Query Match 30.8%; Score 418; DB 1; Length 130;
Best Local Similarity 69.1%; Pred. No. 8.1e-23;
Matches 76; Conservative 17; Mismatches 17; Indels 0; Gaps 0;
QY 145 GGSNFMLTQPPSASGTPGQRVISICSGSSDIGNTVNMWYQQLPGTAPKLLIYSNNQRP 204
| : : ||||| : ||| : ||||| : ||| : ||||| : ||| : ||||| : ||| : ||
Db 16 GSWAQSVLTQPPSVSAAPGQKVTISCSGSSSINIGNDVYSWYQVPGTAPKLLIYDNNKRP 75
QY 205 SGVPDRFSGFKSGTSASLVISGLQSEDEADYYCAAWDESLNGVFFGGPR 254
||:|||||:|||||:|:|:|:|||||:|:|:|:|||||:|:|:|:|||||:|:|:|:
Db 76 SGIPDRFSGSKSGTSATLTGTLQTGDEADYYCGTWNNSLSGWVFGGGTK 125
RESULT 7
LVID HUMAN
ID LVID_HUMAN STANDARD; PRT; 111 AA.
AC P01702;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE Ig lambda chain V-I region NIG-64.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE.
RX MEDLINE=83186114; PubMed=6404900;
RA Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA Shimitzu A.;

```

RT "Comparative studies on the structure of the light chains of human  
immunoglobulins. IV. Assignment of a subgroup.",  
J. Biochem. 93:421-429(1963).  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01965; L1HUNG.  
DR HSSP; P01703; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.  
FT DOMAIN 1 105  
FT MOD RES 1 105  
FT DISULFID 22 89  
FT NON TER 111  
SQ SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;

Query Match 30.6%; Score 416; DB 1; Length 111;  
Best Local Similarity 74.0%; Pred. No. 9.4e-23;  
Matches 77; Conservative 11; Mismatches 16; Indels 0; Gaps 0;  
QY 151 MLTPPPSASGTPGQRVISCSGSSSDIGSNTVNMWYQQLPGTAPKLLIYSNORPSGVDPDR 210  
DB 3 VLTQPPSVSAPGQEVTVISCSGSSSNIGDNFVSWYQQLPGTAPKLLIYDNNKRPSPGIPDR 62  
QY 211 FSGFKSGTSASLVISGLQSEDEADYYCAAMDESLNGVFGGPR 254  
DB 63 FSGSKSGTSATLGITGLQGTDEADYYCGTWDSLSVGMFGGTR 106

RESULT 8  
LV1B HUMAN  
ID LV1B\_HUMAN STANDARD; PRT; 112 AA.  
AC P01700;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-I region HA.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71103824; PubMed=5532227;  
RA Shinoda T., Tltani K., Putnam F.W.;  
RT "Amino acid sequence of human lambda chains. II. Chymotryptic  
peptides and sequence of protein Ha.";  
RL J. Biol. Chem. 245:4475-4487(1970).  
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01963; L1HUNH.  
DR HSSP; P01703; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein;  
KW Pyrrolidone carboxylic acid.  
FT DOMAIN 1 106  
FT MOD RES 1 106  
FT DISULFID 22 90  
FT NON TER 112  
SQ SEQUENCE 112 AA; 11896 MW; 8D73378F3F5CD039 CRC64;

Query Match 30.4%; Score 413.5; DB 1; Length 112;  
Best Local Similarity 77.7%; Pred. No. 1.4e-22;  
Matches 80; Conservative 10; Mismatches 12; Indels 1; Gaps 1;  
QY 151 MLTPPPSASGTPGQRVISCSGSSSDIGSNTVNMWYQQLPGTAPKLLIYSNORPSGVDPDR 209  
DB 3 VLTQPPSVSAPGQEVTVISCSGSSSNIGDNFVSWYQQLPGTAPKLLIYRDDKRPSPGIPDR 62  
QY 210 FSGFKSGTSASLVISGLQSEDEADYYCAAMDESLNGVFGG 252  
DB 63 FSGSKSGTSASLVISGLRSEDEADHYCAAMDYRLSAVFGG 105

RESULT 9  
HV2G HUMAN  
ID HV2G\_HUMAN STANDARD; PRT; 117 AA.  
AC P01825;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-II region NEMW.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=77242302; PubMed=407927;  
RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;  
RT "Amino acid sequence of the VH region of a human myeloma  
immunoglobulin (IgG New).";  
RL Biochemistry 16:3412-3420(1977).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.  
RX MEDLINE=78066916; PubMed=618887;  
RA Saul F.A., Amzel L.M., Poljak R.J.;  
RT "Preliminary refinement and structural analysis of the Fab fragment  
from human immunoglobulin new at 2.0-A resolution.";  
RL J. Biol. Chem. 253:585-597(1978).  
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA  
PROTEIN.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A90404; G1HUNM.  
DR PDB; 7FAB; 31-JAN-94.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.  
FT DOMAIN 1 111  
FT MOD RES 1 111  
FT STRAND 3 7  
FT STRAND 11 12  
FT TURN 14 15  
FT STRAND 18 25  
FT TURN 30 31  
FT STRAND 33 39  
FT TURN 41 42  
FT STRAND 46 51  
FT TURN 53 54  
FT STRAND 57 59  
FT HELIX 61 63  
FT TURN 64 66  
FT STRAND 67 72  
FT TURN 73 76  
FT STRAND 77 82  
FT HELIX 87 89  
FT STRAND 91 98  
FT STRAND 104 107

FT STRAND 111 115  
FT NON TER 117 117  
SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;  
  
Query Match  
Best Local Similarity 29.7%; Score 403.5; DB 1; Length 117;  
Matches 76; Conservative 22; Mismatches 17; Indels 15; Gaps 2;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
Db 1 QVQLQESGPGLVKPSQTSLSLTCTVSGSFTSNDYTWVRQPPGRLGEMIGVVFYHGTSDDT 60  
QY 61 PSLNGRVTISLDTSKNQLSLRFTSVTAADTAVYFCAR--LKGAWLISEPPYFSSDGMVW 118  
Db 61 TPLRSRYTMLVDTSKNQFSLRLSSVTAAADTAVYVCARNLIAGC-----IDVM 107  
QY 119 GGGTVTVPS 128  
Db 108 GGGSLTVSS 117

RESULT 10  
LV1C\_HUMAN STANDARD; PRT; 111 AA.  
AC P01701;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-I region NEW.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=69060892; PubMed=4177823;  
RA langer B., Steimetz-Kayne M., Hilschmann N.;  
RT "The complete amino acid sequence of Bence Jones protein New (lambda-type). Subgroups in the variable part of immunoglobulin L-chains of the lambda-type.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 349:945-951(1968).  
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01964; LIHUNW.  
DR HSSP; P01703; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein;  
KW Pyroglutamate carboxylic acid.  
FT DOMAIN 1 105 IG-LIKE.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 89 BY SIMILARITY.  
FT NON\_TER 111  
SQ SEQUENCE 111 AA; 11453 MW; AAECBCA3C49F2AD3 CRC64;

Query Match  
Best Local Similarity 29.4%; Score 400; DB 1; Length 111;  
Matches 72; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 151 MLTPPSASGTPGQRVVISCSGSSSDIGSNTVNMWYQQLPGTAPKLLIYSNNORPSGVPR 210  
Db 3 VLTQPPSVSAAPGQKVTISCSGSGSTINIGNNYVSMQHLPGTAPKLLIYEDNKRPSGIPDR 62  
QY 211 FSGFKSGTSASLVISGLQSEDEADYYCAAMDESLNGVFGGPR 254  
Db 63 ISAKSGTSATLTGTLRTGDEADYYCATWDSLSNAVVFGGGTR 106

RESULT 11  
LV1I\_HUMAN STANDARD; PRT; 109 AA.  
AC P06888;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-I region EPS.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=86000126; PubMed=3929803;  
RA Toft K.G., Sletten K., Husby G.;  
RT "The amino-acid sequence of the variable region of a carbohydrate-containing amyloid fibril protein EPS (immunoglobulin light chain, type lambda).";  
RL Biol. Chem. Hoppe-Seyler 366:617-625(1985).  
CC -I- MISCELLANEOUS: RESIDUES 1-2, 56-62, AND 74-78 AND THE SEQUENCED PEPTIDES WERE POSITIONED BY HOMOLOGY.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A24656; LIHUEP.  
DR HSSP; P01703; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Amyloid; Glycoprotein.  
FT DOMAIN 1 105 IG-LIKE.  
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .).  
FT DISULFID 22 89 BY SIMILARITY.  
FT NON\_TER 109 109  
SQ SEQUENCE 109 AA; 11414 MW; 556A313E24D5AC73 CRC64;  
  
Query Match  
Best Local Similarity 29.0%; Score 394; DB 1; Length 109;  
Matches 75; Conservative 11; Mismatches 14; Indels 2; Gaps 1;  
  
QY 151 MLTPPSASGTPGQRVVISCSGSSSDIGSNTVNMWYQQLPGTAPKLLIYSNNORPSGVPR 210  
Db 3 VLTQPPSVSAAPGQRVVISCSGSSSNIGKNYVDWYQQLPGTAPKLLIFNNKRPSGIPDR 62  
QY 211 FSGFKSGTSASLVISGLQSEDEADYYCAAMDESLNGVFGG 252  
Db 63 FSGSKSGTSATLTGTLGTGDEADYYCGTWDNRRS--VFGGG 102

RESULT 12  
HV46\_MOUSE STANDARD; PRT; 137 AA.  
AC P01822;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ig heavy chain V region MOPC 315 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89238351; PubMed=2497341;  
RA Rinfret A., Horne C., Dorrington K.J., Klein M.;  
RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH gene segment.";  
RL Mol. Immunol. 26:431-434(1989).



[2]  
RN SEQUENCE OF 1-31.  
RP MEDLINE=78094475; PubMed=414225;  
RX Jilka R.L., Peetka S.;  
RA "Amino acid sequence of the precursor region of MOPC-315 mouse  
RT immunoglobulin heavy chain.";  
RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).  
RN [3]  
RP SEQUENCE OF 1-21.  
RX MEDLINE=79148758; PubMed=428562;  
RA Schechter I., Wolf O., Zemell R., Burstein Y.;  
RT "Structure and function of immunoglobulin genes and precursors.";  
RL Fed. Proc. 38:1839-1845(1979).  
RN [4]  
RP SEQUENCE OF 19-136.  
RX MEDLINE=74170779; PubMed=4524622;  
RA Francis S.H., Leslie R.G.O., Hood L., Eisen H.N.;  
RT "Amino-acid sequence of the variable region of the heavy (alpha)  
RL chain of a mouse myeloma protein with anti-hapten activity.";  
RN Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).  
RP REVISION TO 53.  
RX MEDLINE=77244979; PubMed=268248;  
RA Hood L., Margolies M.N., Givol D., Zakut R.;  
RL Unpublished results, cited by:  
RL Padlan E.A., Davies D.R., Peetka S., Givol D., Wright C.;  
RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).  
CC -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA  
CC PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL; M27638; AAA61337.1; -  
DR EMBL; X07880; CAA30727.1; -  
DR PIR; P10102; AVMS35.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 18  
FT CHAIN 19 137  
FT DOMAIN 19 48  
FT DOMAIN 49 54  
FT DOMAIN 55 68  
FT DOMAIN 69 84  
FT DOMAIN 85 116  
FT DOMAIN 117 126  
FT DOMAIN 127 137  
FT DISULFID 40 114  
FT CONFLICT 15 15  
FT CONFLICT 15 15  
FT CONFLICT 77 78  
FT CONFLICT 102 102  
FT CONFLICT 123 123  
FT NON\_TER 137 137  
SQ SEQUENCE 137 AA; 15399 MW; PB3828304C2B81DC CRC64;

Query Match 26.9%; Score 365.5; DB 1; Length 137;  
Best Local Similarity 58.6%; Pred. No. 3.9e-19;  
Matches 75; Conservative 16; Mismatches 26; Indels 11; Gaps 3;

QY 2 VQLQESGPGLVKPSSETLSLTCTVSGSIGHDY-MSWIRQPPGEGLEWIGFIFPDGSTN 60  
DB 20 VQLQESGPGLVKPSQSLTCSVTGYSLISGFWNWRQPPGKLEWLGFIKXDGSGNGYN 79

QY 61 PSINGRVTISLDTSKNQLSLRTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ 120  
DB 80 PSINGRVSTIRDTSENQFLKLSVTTEDTATYYCAG-----DNDHLYY----FDYWGQ 129  
QY 121 GTTVTVPS 128  
DB 130 GTTLTVSS 137

RESULT 13  
HV47\_MOUSE  
ID HV47\_MOUSE STANDARD; PRT; 113 AA.  
AC P01823;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region 36-60.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=A/J;  
RX MEDLINE=84024551; PubMed=6414509;  
RA Juszczak E.C., Margolies M.N.;  
RT "Amino acid sequence of the heavy chain variable region from the A/J  
RT mouse anti-arsenate monoclonal antibody 36-60 bearing a minor  
RT idiotype.";  
RL Biochemistry 22:4291-4296(1983).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE  
CC MONOCLONAL ANTIBODY OF THE IG2A SUBCLASS. IT REPRESENTS A SECOND  
CC IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF  
CC STRAIN A/J MICE.  
DR PIR; A02098; G2MS60.  
DR PDB; 1J10; 18-FEB-03.  
DR PDB; 1J1P; 18-FEB-03.  
DR PDB; 1J1X; 18-FEB-03.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; 3D-structure.  
FT NON\_TER 113 113  
SQ SEQUENCE 113 AA; 12734 MW; 38DC0E0E3F5075B7 CRC64;

Query Match 26.7%; Score 362.5; DB 1; Length 113;  
Best Local Similarity 56.3%; Pred. No. 5.1e-19;  
Matches 71; Conservative 17; Mismatches 23; Indels 15; Gaps 1;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIGHDYMSWIRQPPGEGLEWIGFIFPDGSTN 60  
DB 1 EVQLQESGPGLVKPSQSLTCSVTGDSITSDYMWIRKFPGNKLEHMGYISYSTYNN 60  
QY 61 PSINGRVTISLDTSKNQLSLRTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ 120  
DB 61 PSINGRVSTIRDTSENQFLKLSVTTEDTATYYCAG-----DNDHLYY----FDYWGQ 129  
QY 121 GTTVTV 126  
DB 106 GTTLTV 111

RESULT 14  
LV2G\_HUMAN  
ID LV2G\_HUMAN STANDARD; PRT; 111 AA.  
AC P01710;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-II region BO.



OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71103825; PubMed=5532228;  
RA Wikler M., Putnam F.W.;  
RT "Amino acid sequence of human lambda chains. 3. Tryptic peptides,  
chymotryptic peptides, and sequence of protein Bo.";  
RL J. Biol. Chem. 245:4488-4507(1970).  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01976; L2HUBO.  
DR HSSP; P01709; 2MCG.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IgV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein;  
KW Pyridolone carboxylic acid.  
FT DOMAIN 1 106 IG-LIKE.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 90 BY SIMILARITY.  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 11785 MW; 92F5A1BF72421BAC CRC64;

Query Match 26.4%; Score 359; DB 1; Length 111;  
Best Local Similarity 65.4%; Pred. No. 8.7e-19;  
Matches 68; Conservative 19; Mismatches 15; Indels 2; Gaps 2;

OY 152 LTQPPSASGTPGQRVISICSGSSSDIGSNT-VNMYQQLPGTAPKLLIYSNNQRPSPGVPDR 210  
DB 4 LTQPPSASGSPGQSVTISCTGTSSDVGNKVVSWYQHPGRAPKLVIIEVVSQRPSPGVPDR 63  
OY 211 FSGFKSGTSASLVISGLQSEDEADYYCAWDESLNGVFGGPR 254  
DB 64 FSGSKSDNTASLVTVSGLRAEDEADYYCQSYVDN-NMFVFGGGTK 106

RESULT 15  
LV6D\_HUMAN  
ID LV6D\_HUMAN STANDARD; PRT; 111 AA.  
AC P06318;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig lambda chain V-VI region WLT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=86122667; PubMed=4089539;  
RA Dwulet F.E., Strako K., Benson M.D.;  
RT "Amino acid sequence of a lambda VI primary (AL) amyloid protein  
(WLT).";  
RL Scand. J. Immunol. 22:653-660(1985).  
DR PIR; A01989; L6HULT.  
DR HSSP; P01709; 2MCG.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IgV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.

KW Immunoglobulin V region.  
FT DOMAIN 1 22 FRAMEWORK-1.  
FT DOMAIN 23 35 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 36 50 FRAMEWORK-2.  
FT DOMAIN 51 57 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 58 91 FRAMEWORK-3.  
FT DOMAIN 92 101 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 102 111 FRAMEWORK-4.  
FT DISULFID 22 91 BY SIMILARITY.  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 11966 MW; 0C88B2FE378CE24F CRC64;

Query Match 25.5%; Score 346.5; DB 1; Length 111;  
Best Local Similarity 66.7%; Pred. No. 6.5e-18;  
Matches 70; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

OY 149 NFMLTQPPSASGTPGQRVISICSGSSSDIGSNTVNMYQQLPGTAPKLLIYSNNQRPSPGVP 208  
DB 1 NFMLTQPLSVSGSPEKTVTISCTGTSSSGISNYYQWYQRPSPAPTNTVYENNQRPSEVP 60  
OY 209 DRFSGF--KSGTSASLVISGLQSEDEADYYCAWDESLNGVFGG 251  
DB 61 DRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDNN-NHVFVFGG 104

Search completed: May 13, 2004, 15:02:04  
Job time : 8.15146 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:31 ; Search time 34.1544 Seconds  
(without alignments)  
2346.453 Million cell updates/sec

Title: US-10-072-301-19

Perfect score: 1359  
Sequence: 1 QVQLQESGPGLVKPSSETLSL.....YYCAAWDESLNGVVFGGGPR 254

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	559	41.1	298	11	Q9QYF0	Q9qyf0 mus musculu
2	515.5	37.9	243	11	Q7TQM2	Q7tqm2 mus musculu
3	494.5	36.4	241	11	Q921A6	Q921a6 mus musculu
4	491	36.1	613	4	Q96EY0	Q96ey0 homo sapien
5	480.5	35.4	119	4	Q9UL73	Q9ul73 homo sapien
6	469.5	34.5	588	4	Q8WUX4	Q8wux4 homo sapien
7	469.5	34.5	597	4	Q9BU10	Q9bu10 homo sapien
8	469.5	34.5	618	4	Q96AA6	Q96aa6 homo sapien
9	463.5	34.1	597	4	Q9BQB8	Q9bqb8 homo sapien
10	456	33.6	218	11	Q925S1	Q925s1 mus musculu
11	454	33.4	478	4	Q7Z379	Q7z379 homo sapien
12	449.5	33.1	236	4	Q8NEJ1	Q8nej1 homo sapien
13	445	32.7	108	4	Q96SB0	Q96sb0 homo sapien
14	443	32.6	139	4	Q86SX2	Q86sx2 homo sapien
15	429	31.6	150	4	Q95973	Q95973 homo sapien
16	427.5	31.5	492	4	Q7Z374	Q7z374 homo sapien

17	425	31.3	496	4	Q96KX8	Q96kx8 homo sapien
18	417	30.7	237	4	Q8WUK4	Q8wuk4 homo sapien
19	408	30.0	110	4	Q8TE63	Q8te63 homo sapien
20	407	29.9	130	4	Q8IZD7	Q8izd7 homo sapien
21	403	29.7	237	4	Q8WTU6	Q8wtu6 homo sapien
22	392	28.8	116	4	Q7Z3Y6	Q7z3y6 homo sapien
23	390	28.7	479	11	Q99M22	Q99m22 mus musculu
24	385.5	28.4	236	4	Q96E61	Q96e61 homo sapien
25	376	27.7	112	4	Q96UD2	Q96jd2 homo sapien
26	367	27.0	101	4	Q8IZD8	Q8izd8 homo sapien
27	356.5	26.2	473	4	Q8TC63	Q8tc63 homo sapien
28	354	26.0	116	4	Q96JD0	Q96jd0 homo sapien
29	347	25.5	482	11	Q91X92	Q91x92 mus musculu
30	346	25.5	121	11	Q99NG4	Q99ng4 mus musculu
31	338	24.9	122	4	Q9UL75	Q9ul75 homo sapien
32	338	24.9	170	11	Q925S2	Q925s2 mus musculu
33	335.5	24.7	112	4	Q96JD1	Q96jd1 homo sapien
34	325	23.9	118	11	Q81IU5	Q81iu5 mus musculu
35	325	23.9	613	4	Q8WUK1	Q8wuk1 homo sapien
36	323.5	23.8	121	4	Q9UL96	Q9ul96 homo sapien
37	314.5	23.1	234	4	Q8N355	Q8n355 homo sapien
38	312.5	23.0	597	4	Q96BB9	Q96bb9 homo sapien
39	309	22.7	233	4	Q8TBC9	Q8tbc9 homo sapien
40	308.5	22.7	147	4	Q9Y509	Q9y509 homo sapien
41	302.5	22.3	499	4	Q8N5K4	Q8n5k4 homo sapien
42	302	22.2	482	4	Q7Z351	Q7z351 homo sapien
43	300.5	22.1	613	11	Q8VCX7	Q8vcx7 mus musculu
44	298	21.9	124	6	Q9N0W6	Q9n0w6 oryctolagus
45	298	21.9	573	4	Q8WU38	Q8wu38 homo sapien

ALIGNMENTS

RESULT 1

ID	Q9QYF0	PRELIMINARY;	PRT;	298 AA.
AC	Q9QYF0;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	CN 8 scfv.			
GN	CN 8.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Balb/c; TISSUE=Spleen;			
RX	MEDLINE=20183931; PubMed=10706631;			
RA	Shinohara N., Demura T., Fukuda H.;			
RT	"Isolation of a vascular cell wall-specific monoclonal antibody			
RT	recognizing a cell polarity by using a phage display subtraction			
RT	method."			
RL	Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).			
DR	EMBL; AB036341; BAA8633.1; ..			
DR	PIR; A33933; A33933.			
DR	PIR; S19112; S19112.			
DR	HSSP; P01607; IREI.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig; 2.			
DR	SMART; SM00406; IGv; 2.			
DR	PROSITE; PSS0835; IG_LIKE; 2.			
SQ	SEQUENCE 298 AA; 31867 MW; E0P96B8A17004317 CRC64;			

QY	1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRQPPGGLGIEWIGFIFPDST-NY 59
	Query Match 41.1%; Score 559; DB 11; Length 298;
	Best Local Similarity 48.2%; Pred. No. 8.5e-37;
	Matches 124; Conservative 29; Mismatches 80; Indels 24; Gaps 8;





DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match 36.1%; Score 491; DB 4; Length 613;  
Best Local Similarity 47.5%; Pred. No. 5.5e-31;  
Matches 114; Conservative 20; Mismatches 62; Indels 44; Gaps 5;

QY 1 QVQLQESGPGILVKPSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYYN 60  
DB 20 QVQLQESGPGILVKPSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGRITYSGSTNYYN 79  
QY 61 PSLNGRVTISLDTSKNQLSLRLTSVTAADTAAYVFCARLKGAWLSEPPYFSSDGMVWGQ 120  
DB 80 PSLKSRVTISVDTSKNQFLKSLSSVTAADTAAYVYCA-----SQPMELPTVGLFYWGQ 131  
QY 121 GTTVTVPSGGGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRVISCSGSSSDIGSN 180  
DB 132 GTLVTVSSG-----SASAPTLFPLVSCENSPSDTSSV 163  
QY 181 TVNMYQQ--LPGTAPKLLIYSNNQRP--GVPDRFSGFKSGTSASLVI--LQSEDE 232  
DB 164 AVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGKXAATSQVLLPSKDVMOGTDE 223

## RESULT 5

Q9UL73 PRELIMINARY; PRT; 119 AA.

AC Q9UL73;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035041; AAD56277.1; --.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 119  
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;

Query Match 35.4%; Score 480.5; DB 4; Length 119;  
Best Local Similarity 74.2%; Pred. No. 5.3e-31;  
Matches 95; Conservative 8; Mismatches 16; Indels 9; Gaps 3;

QY 1 QVQLQESGPGILVKPSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYYN 60  
DB 1 QVQLQESGPGILVKPSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGRITYSGSTNYYT 60  
QY 61 PSLNGRVTISLDTSKNQLSLRLTSVTAADTAAYVFCARLKGAWLSEPPYFSSDGMVWGQ 120  
DB 61 PSLKSRVTISVDTSKNQFLKSLTSLTAADTAAYVFCARLSN-W---GPYY---FDYWGQ 111  
QY 121 GTTVTVPS 128

DB 112 GTLVTVSS 119

## RESULT 6

Q8WUX4 PRELIMINARY; PRT; 588 AA.

AC Q8WUX4;  
DT 01-MAR-2002 (Tremblrel. 20, Created)  
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BC019235; AAH19235.1; --.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;

Query Match 34.5%; Score 469.5; DB 4; Length 588;  
Best Local Similarity 46.7%; Pred. No. 2.7e-29;  
Matches 112; Conservative 19; Mismatches 70; Indels 39; Gaps 5;

QY 1 QVQLQESGPGILVKPSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYYN 60  
DB 20 QVQLQESGPGILVKPSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGRITYSGSTNYYN 79  
QY 61 PSLNGRVTISLDTSKNQLSLRLTSVTAADTAAYVFCARLKGAWLSEPPYFSSDGMVWGQ 120  
DB 80 PSLKSRVTISVDTSKNQFLKSLSSVTAADTAAYVYCARV---ITRASPTDGRYGMVWGQ 136  
QY 121 GTTVTVPSGGGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRVISCSGSSSDIGSN 180  
DB 137 GTTVTVSSG-----SASAPTLFPLVSCENSPSDTSSV 168  
QY 181 TVNMYQQ--LPGTAPKLLIYSNNQRP--GVPDRFSGFKSGTSASLVI--LQSEDE 232  
DB 169 AVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGKXAATSQVLLPSKDVMOGTDE 228

## RESULT 7

Q9BU10 PRELIMINARY; PRT; 597 AA.

AC Q9BU10;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BC002963; AAH02963.1; --.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PS50835; Ig LIKE; 5.  
DR PROSITE; PS00290; Ig\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8F37E055851 CRC64;

Query Match  
Best Local Similarity 34.5%; Score 469.5; DB 4; Length 597;  
Matches 112; Conservative 19; Mismatches 70; Indels 39; Gaps 5;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSI~~GH~~DYMSWIRQPPGEGLEWIGFI~~FD~~SGSTNN 60  
DB 20 QVQLQGWGAGLLKPSSETLSLTCTGVYGGSFSGYMSWIRQPPGKLEWIGELINHS~~GT~~NN 79  
QY 61 PSINGRVTISLDTSKNQLSLRTSVTAADTAVYFCARLKGAWLSEPPYFSSDGM~~DV~~WGQ 120  
DB 80 PSLSRVTVISVDTSKQSLSLKSSVNAADTAVYCARV---ITRASPGTDGRYGM~~DV~~WGQ 136  
QY 121 GTTVTPSGGGSGGGSGGGSGGGSNFMLTQPPSASGTPGQRVISISCGSSSDIGSN 180  
DB 137 GTTVTVSSG-----SASAPTLPLVSCENSPSDTSSV 168  
QY 181 TVNMVYQQ--LPGTAPKLLIYSNNQRP~~S~~---GVPDRFSGFKSGT~~S~~ASLVISG---LQSEDE 232  
DB 169 AVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGKYAATSOVLPLSKDV~~MG~~QTDE 228

RESULT 8

Q96AA6 PRELIMINARY; PRT; 618 AA.  
AC Q96AA6;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC017356; AAH17356.1; --  
DR PIR; S15590; S15590.  
DR InterPro; IPR007110; Ig-1like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PS50835; Ig LIKE; 5.  
DR PROSITE; PS00290; Ig\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 618 AA; 67758 MW; 96BBD4C7C696E0A6 CRC64;

Query Match  
Best Local Similarity 34.5%; Score 469.5; DB 4; Length 618;  
Matches 112; Conservative 19; Mismatches 70; Indels 39; Gaps 5;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSI~~GH~~DYMSWIRQPPGEGLEWIGFI~~FD~~SGSTNN 60  
DB 20 QVQLQGWGAGLLKPSSETLSLTCTGVYGGSFSGYMSWIRQPPGKLEWIGELINHS~~GT~~NN 79  
QY 61 PSINGRVTISLDTSKNQLSLRTSVTAADTAVYFCARLKGAWLSEPPYFSSDGM~~DV~~WGQ 120  
DB 80 PSLSRVTVISVDTSKQSLSLKSSVNAADTAVYCARV---ITRASPGTDGRYGM~~DV~~WGQ 136  
QY 121 GTTVTPSGGGSGGGSGGGSGGGSNFMLTQPPSASGTPGQRVISISCGSSSDIGSN 180  
DB 137 GTTVTVSSG-----SASAPTLPLVSCENSPSDTSSV 168

DB 137 GTTVTVSSG-----SASAPTLPLVSCENSPSDTSSV 168  
QY 181 TVNMVYQQ--LPGTAPKLLIYSNNQRP~~S~~---GVPDRFSGFKSGT~~S~~ASLVISG---LQSEDE 232  
DB 169 AVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGKYAATSOVLPLSKDV~~MG~~QTDE 228

RESULT 9

Q9BQB8 PRELIMINARY; PRT; 597 AA.  
AC Q9BQB8;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Muscle, and Lymph;  
RA Strausberg R.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC006180; AAH06180.1; --  
DR EMBL; BC001872; AAH01872.1; --  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-1like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PS50835; Ig LIKE; 5.  
DR PROSITE; PS00290; Ig\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match  
Best Local Similarity 34.1%; Score 463.5; DB 4; Length 597;  
Matches 111; Conservative 19; Mismatches 71; Indels 39; Gaps 5;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSI~~GH~~DYMSWIRQPPGEGLEWIGFI~~FD~~SGSTNN 60  
DB 20 QVQLQGWGAGLLKPSSETLSLTCTGVYGGSFSGYMSWIRQPPGKLEWIGELINHS~~GT~~NN 79  
QY 61 PSINGRVTISLDTSKNQLSLRTSVTAADTAVYFCARLKGAWLSEPPYFSSDGM~~DV~~WGQ 120  
DB 80 PSLSRVTVISVDTSKQSLSLKSSVNAADTAVYCARV---ITRASPGTDGRYGM~~DV~~WGQ 136  
QY 121 GTTVTPSGGGSGGGSGGGSGGGSNFMLTQPPSASGTPGQRVISISCGSSSDIGSN 180  
DB 137 GTTVTVSSG-----SASAPTLPLVSCENSPSDTSSV 168  
QY 181 TVNMVYQQ--LPGTAPKLLIYSNNQRP~~S~~---GVPDRFSGFKSGT~~S~~ASLVISG---LQSEDE 232  
DB 169 AVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGKYAATSOVLPLSKDV~~MG~~QTDE 228

RESULT 10

Q925S1 PRELIMINARY; PRT; 218 AA.  
AC Q925S1;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE MRP5 (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;





```
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96394; AAB68783.1; -.
DR PDB; 1KU4; 29-MAY-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;

Query Match
Best Local Similarity 32.7%; Score 445; DB 4; Length 108;
Matches 84; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 151 MLTOPSASGTPGQRVISICSGSSSDIGSNVWYQQLPGTAPKLLIYSNNQPSGVPR 210
Db 3 VLTQPSASGTPGQRVITISCGSSSNIGSNVWYQQLPGTAPKLLIYSNNQPSGVPR 62

QY 211 FSGFKSGTSASLVISGLQSEDEADYCAAMDESINGVF 249
Db 63 FSGSKSGTSASLAISGLRSEDEADYCAAMDRLSGFMW 101

RESULT 14
Q86SX2 PRELIMINARY; PRT; 139 AA.
AC Q86SX2;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Human full-length cDNA clone CSODL004YM19 of B cells (Ramos cell line)
DE of Homo sapiens (Human) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Li W.B., Gruber C., Jesse J., Polayes D.;
RT "Full-length cDNA libraries and normalization."
RT Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DE EMBL; BX248300; CAD62627.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Plasmid.
FT NON_TER 1
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;
```

```
Query Match
Best Local Similarity 32.6%; Score 443; DB 4; Length 139;
Matches 82; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGISGHDYMSWIRQPPGEGLEWIGFIFPDGSTNN 60
Db 33 QVQLQESGPGLVKPSSETLSLTCTVSGSGISSTYMSWIRQPPGEGLEWIGIYISGSTNN 92

QY 61 PSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCAR 97
Db 93 PSLKSRVTISVDTSKNQLSLRLTSVTAADTAVYFCAR 129

RESULT 15
Q95973 PRELIMINARY; PRT; 150 AA.
AC Q95973;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE VH4 heavy chain variable region precursor (Fragment).
GN IGM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RT "Clonal proliferation of Igm secreting B cell in the synovium of
RT Behcet's patient with arthritis."
RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF103795; AAC79084.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1
FT CHAIN 20 >150 POTENTIAL.
FT NON_TER 150 VH4 HEAVY CHAIN VARIABLE REGION.
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match
Best Local Similarity 31.6%; Score 429; DB 4; Length 150;
Matches 89; Conservative 10; Mismatches 21; Indels 16; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGIG--HDYMSWIRQPPGEGLEWIGFIFPDGSTN 58
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGSGISSTYMGWIRQPPGEGLEWIGLHNSGSDY 79

QY 59 YNPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARL-KGAWLLSEPPYFSSDGMV 117
Db 80 YNPSLKSRTVISVDTSKNQLSLRLTSVTAADTAVYFCARLGMGAF-----DF 126

QY 118 WQGQTTVTPSGGGGS 133
Db 127 WGHGTMVTVSSGSASA 142
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Search completed: May 13, 2004, 15:06:56  
Job time : 35.1544 secs



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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:48:56 ; Search time 51.4563 Seconds  
(without alignments)  
1372.754 Million cell updates/sec

Title: US-10-072-301-21  
Perfect score: 1336  
Sequence: 1 QVQLQGWGAGLLKSWGTLSTL.....CLQHDNFPPLTFGGGTKEIK 250

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp19808:\*  
2: geneseqp19908:\*  
3: geneseqp20008:\*  
4: geneseqp20018:\*  
5: geneseqp20028:\*  
6: geneseqp20038:\*  
7: geneseqp20038:\*  
8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	835	62.5	249	5	ABP45310	Abp45310 Human Bly
2	816.5	61.1	249	5	AAU75150	Aau75150 Amino aci
3	771.5	57.7	256	3	AAAY5072	Aay55072 Interleuk
4	771.5	57.7	260	3	AAAY5075	Aay55075 Single ch
5	771.5	57.7	367	3	AAAY5078	Aay55078 Single ch
6	771.5	57.7	381	3	AAAY5079	Aay55079 Single ch
7	771.5	57.7	519	3	AAAY5080	Aay55080 Single ch
8	771.5	57.7	546	3	AAAY5074	Aay55074 Single ch
9	771.5	57.7	626	3	AAAY5081	Aay55081 Single ch
10	771.5	57.7	640	3	AAAY5082	Aay55082 Single ch
11	756	56.6	251	5	ABP45038	Abp45038 Human Bly
12	740.5	55.4	252	5	ABP45315	Abp45315 Human Bly
13	738.5	55.3	248	5	ABP45349	Abp45349 Human Bly
14	738.5	55.3	255	5	ABP45402	Abp45402 Human Bly
15	735	55.0	255	5	ABP45631	Abp45631 Human Bly
16	733.5	54.9	250	5	ABP45634	Abp45634 Human Bly
17	730.5	54.7	253	5	AAU72867	Aau72867 PS-9 sing
18	730	54.6	253	5	ABP45322	Abp45322 Human Bly
19	729.5	54.6	254	5	ABP45648	Abp45648 Human Bly
20	728.5	54.5	244	2	AAAY21883	Aay21883 Amino aci
21	718	53.7	241	4	AAB46061	Aab46061 Human TF
22	716	53.6	909	2	AAR50092	Aar50092 Humanised
23	715	53.5	253	5	ABP44943	Abp44943 Human Bly
24	714.5	53.5	240	4	AAB46020	Aab46020 Human MUC
25	713	53.4	249	5	ABP44946	Abp44946 Human Bly

26	712.5	53.3	241	7	ADC64791	Adc64791 Hu-B-A5 c
27	711.5	53.3	241	7	ADC64785	Adc64785 Hu-E4-1 c
28	709	53.1	255	5	ABP45586	Abp45586 Human Bly
29	708.5	53.0	240	4	AAB45592	Aab45592 Human MUC
30	705.5	52.8	242	3	AAAY58236	Aay58236 Internal i
31	704	52.7	253	5	ABP45591	Abp45591 Human Bly
32	700.5	52.4	240	4	AAB46039	Aab46039 Human TF
33	699.5	52.4	240	4	AAB46021	Aab46021 Human MUC
34	699	52.3	239	5	ABP45871	Abp45871 Human Bly
35	699	52.3	245	2	AAAY06714	Aay06714 Antibody
36	698	52.2	237	5	ABP45895	Abp45895 Human Bly
37	697	52.2	255	5	ABP45615	Abp45615 Human Bly
38	696.5	52.1	240	4	AAB46018	Aab46018 Human MUC
39	696	52.1	239	5	ABP45911	Abp45911 Human Bly
40	695.5	52.1	241	7	ADC64788	Adc64788 Hu-A-E5 c
41	695.5	52.1	251	5	AAU72868	Aau72868 PS-10 gin
42	694.5	52.0	240	4	AAB45993	Aab45993 Human MUC
43	694.5	52.0	240	4	AAB45991	Aab45991 Human MUC
44	694	51.9	253	5	ABP45328	Abp45328 Human Bly
45	693.5	51.9	241	7	ADC64787	Adc64787 Hu-A-D2 c

ALIGNMENTS

RESULT 1	
ABP45310	ABP45310 standard; protein; 249 AA.
XX	AC ABP45310;
XX	AC
XX	DT 19-AUG-2002 (first entry)
XX	DE Human Blys binding scFv SEQ ID 1321.
XX	KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW	tumour necrosis factor; B cell proliferation; B cell differentiation;
KW	immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX	common variable immunodeficiency; acquired immunodeficiency syndrome.
OS	Homo sapiens.
XX	XX
PN	WO200202641-A1.
XX	XX
PD	10-JAN-2002.
XX	XX
PF	15-JUN-2001; 2001WO-US019110.
XX	XX
PR	16-JUN-2000; 2000US-0212210P.
PR	17-OCT-2000; 2000US-0240816P.
PR	16-MAR-2001; 2001US-0276248P.
PR	21-MAR-2001; 2001US-0277379P.
PR	25-MAY-2001; 2001US-0293499P.
XX	XX
PA	(HUMA-) HUMAN GENOME SCI INC.
PA	(CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX	WPI; 2002-114799/15.
DR	Antibodies against B lymphocyte Stimulating polypeptides, useful for the
XX	diagnosis and treatment of cancers and immune disorders.
PT	Claim 1; Page 1979-1980; 3148pp; English.
XX	XX
CC	This invention describes novel antibodies that immunospecifically bind to
CC	B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC	tumour necrosis factor (TNF) super family and induces B cell
CC	proliferation and differentiation. The antibodies of the invention have
CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 249 AA;

Query Match 62.5%; Score 835; DB 5; Length 249;  
Best Local Similarity 63.8%; Pred. No. 1.2e-44;  
Matches 166; Conservative 26; Mismatches 46; Indels 22; Gaps 3;

QY 1 QVQLQOMGAGLLKSWGTLSTLCAVSGASFSGYVSWIRQPPGKGLEWIGIINRGSTTYN 60  
DB 1 QVQLQOMGAGLLKPSSETLSLCAVYGSFSGYVSWIRQPPGKLEWIGIINHGSTTYN 60  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTAADTAVYVCAR-----TVAQTS---DYWGQGT 110  
DB 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARGPRYDILLGTRYNMFDPWGRGT 120  
QY 111 LTVSSGSASAPITGGSGSGGSGGSGGSKTTLTQSPAFMSATPDKVISICKASR 170  
DB 121 LTVSS-----SGGGSGSGGSGGSGGSDIVMTQSPSTLSASVGDRTITCRASQ 168  
QY 171 DVDDVNMVYQRPGEAPIFIIEATTLVPGISPRFSGSGYVNDFTLTINNIDSEDAAYF 230  
DB 169 GISSWLAWYQOKRGRAPKVLTKASTLESQVPSRFSGSGSGTDFTLTISLQPEDPATYY 228  
QY 231 CLQHDNFPLTPGGGTKEIK 250  
DB 229 CQGSYSTPWTFGQGTKEIK 248

RESULT 2  
AAU75150  
ID AAU75150 standard; protein; 249 AA.  
XX  
AC AAU75150;

DT 23-APR-2002 (first entry)

DE Amino acid sequence of human anti-IL8 scFv clone 123-57.

KW Human antibody; immunoglobulin; Ig; variable heavy-chain; VH;  
XX variable light-chain; VL; anti-IL8; interleukin-8; scFv clone.

OS Homo sapiens.  
XX Synthetic.

PN WO200200729-A2.

PD 03-JAN-2002.

PF 25-JUN-2001; 2001WO-US020542.

PR 23-JUN-2000; 2000US-00602373.  
PR 23-JUN-2000; 2000US-00602972.  
PR 23-JUN-2000; 2000US-00603658.  
PR 23-JUN-2000; 2000US-00603663.

PA (GENE-) GENETASTIX CORP.

PI Zhu L, Hua SB;

DR WPI; 2002-090521/12.  
DR N-PSDB; ABK32984.

XX Screening libraries of tester proteins against protein, peptide or  
PT nucleic acid target(s) using a two-hybrid method in yeast, useful for  
PT generating recombinant human antibodies and screening for their affinity  
PT binding with target antigens.  
XX  
PS Example 8; Fig 16; 251pp; English.

CC The present invention relates to compositions and methods for high  
CC throughput generation and screening of a human antibody or immunoglobulin  
CC (Ig) library in yeast. The method comprises expressing a library of  
CC tester fusion proteins in yeast cells, each tester fusion protein of  
CC comprising either an activation domain or a DNA binding domain of a  
CC transcription activator and a tester protein having a large diverse  
CC subunit (e.g. human variable heavy-chain, VH) whose sequence varies  
CC within the library, a second polypeptide subunit (e.g. human variable  
CC light-chain, VL) whose sequence varies within the library independently  
CC of the first polypeptide, and a linker peptide which links the first and  
CC second polypeptide subunits. The method is useful for generating  
CC recombinant human antibodies and screening for their affinity binding  
CC with target antigens. The present sequence represents the amino acid  
CC sequence for an anti-IL8 scFv clone as described in the methods of the  
CC present invention  
XX  
SQ Sequence 249 AA;

Query Match 61.1%; Score 816.5; DB 5; Length 249;  
Best Local Similarity 62.4%; Pred. No. 1.6e-43;  
Matches 156; Conservative 33; Mismatches 60; Indels 1; Gaps 1;

QY 1 QVQLQOMGAGLLKSWGTLSTLCAVSGASFSGYVSWIRQPPGKGLEWIGIINRGSTTYN 60  
DB 1 QVQLQESGPGIVTPSETLSLFCNVSGASISSYCSWLRQPAKRLIEWIGRVCTSGKTYYN 60  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTAADTAVYVCARTVAGTSDYWGQGTLVVSSGSAS 120  
DB 61 PSLSRITVSLDASKNFFSLKLSITAADTAVYVCARE-AGWFGPMGPGTLVAVSSASTK 119  
QY 121 APTGGSGSGGSGGSGGSGGSKTTLTQSPAFMSATPDKVISICKASRDVDDVNMVYQ 180  
DB 120 GPSGGSGSGGSGGSGGSGGSETTLTQSPSSLSASVGDRTITTCQASEDIDQYLMWYQ 179  
QY 181 QRPGEAPIFIIEATTLVPGISPRFSGSGYVNDFTLTINNIDSEDAAYFCLQHDNFPLT 240  
DB 180 QKPGKAPTLILYDASNLCGTGVPSPRSFGTGSVTDFTTITSLQPEDIATYYCQOYNNLPIT 239  
QY 241 FGGGTKEIK 250  
DB 240 FGGGTKEIK 249

RESULT 3  
AAY55072  
ID AAY55072 standard; protein; 256 AA.  
XX  
AC AAY55072;

DT 25-FEB-2000 (first entry)

DE Interleukin-6 specific ScFv protein sequence.

KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
XX antigen-binding cell; secretable functional protein; antigenic protein;  
XX protein isolation; diagnosis; interleukin-6; ScFv.

OS Synthetic.  
XX Homo sapiens.

PN WO9960113-A1.

PD 25-NOV-1999.

PF 30-APR-1999; 99WO-JP002341.  
XX  
PR 20-MAY-1998; 98JP-00138652.  
PR 01-OCT-1998; 98JP-00279876.  
XX  
PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Tauchiya M, Saito M, Ohtomo T;  
XX  
DR WPI; 2000-039382/03.  
DR N-PSDB; AAZ40291.  
XX  
PT Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
PT production of drugs treating abnormal functions of the protein.  
XX  
PS Example 1; Page 54-56; 120pp; Japanese.  
XX  
CC This sequence represents a ScFv specific for human interleukin-6. The  
CC invention relates to a method for isolating a gene encoding a membrane-  
CC bound protein, comprising introducing a vector into a cell, contacting an  
CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the cDNA.  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for  
CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein  
XX  
SQ Sequence 256 AA;

Query Match 57.7%; Score 771.5; DB 3; Length 256;  
Best Local Similarity 59.7%; Pred. No. 1.1e-40;  
Matches 151; Conservative 37; Mismatches 50; Indels 15; Gaps 3;

QY 1 QVQLQOWGAGILKSWGTLSLTCAVSGASF-SGYWWSWIRPPGKLEWIGEINHRGSTTY 59  
Db 1 QVQLQESGPGILVRPSQTLSTCTVSGYSITSDHAWSWVRQPPGRGLEWIGYISYGITTY 60  
QY 60 NPSLDGRVTISLDTSTNQISLKTSMTADTAIVYYCARTVAGTS--DYWGQGLVTVSSG 117  
Db 61 NPSLKSRYTMLRDTSKNQFSLRLSSVTADTAIVYYCARSLARTTAMDYWGQGLVTVS-- 118  
QY 118 SASAPTGGGGSGGGSGGGSGGGSKTTLTQSPAFMSATPGDKVSIACKASRDVDDVN 177  
Db 119 -----SGGGSGGGSGGGSGGGSDIQMTQSPSSLASVGDRTVITCRASQDISSYLN 168  
QY 178 WYQORPGEAPIFIIEDATTLVPGISPRFSGSGYGTFTLTINNIDSEDAAYYFCLQHDNF 237  
Db 169 WYQOKPKAKPKLLIYYTSRLHSGVPSRFSGSGSGTDFTFTISSLQPEDIATVYYCQGGNTL 228  
QY 238 PLTFGGGTKEVEIK 250  
Db 229 PYTFGGGTKEVEIK 241

RESULT 4  
AAV55075  
ID AAV55075 standard; protein; 260 AA.  
XX  
AC AAV55075;  
XX  
DT 25-FEB-2000 (first entry)  
XX  
DE Single chain Fv protein sequence shpM1(deltaEL).  
XX  
KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretable functional protein; antigenic protein;  
KW protein isolation; diagnosis; ScFv.  
XX

OS Synthetic.  
XX  
PN WO9960113-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 30-APR-1999; 99WO-JP002341.  
XX  
PR 20-MAY-1998; 98JP-00138652.  
PR 01-OCT-1998; 98JP-00279876.  
XX  
PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Tauchiya M, Saito M, Ohtomo T;  
XX  
DR WPI; 2000-039382/03.  
DR N-PSDB; AAZ40305.  
XX  
PT Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
PT production of drugs treating abnormal functions of the protein.  
XX  
PS Example 7; Page 80-82; 120pp; Japanese.  
XX  
CC This sequence represents a single chain Fv (ScFv) sequence. The invention  
CC relates to a method for isolating a gene encoding a membrane-bound  
CC protein, comprising introducing a vector into a cell, contacting an  
CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the cDNA.  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for  
CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein  
XX  
SQ Sequence 260 AA;

Query Match 57.7%; Score 771.5; DB 3; Length 260;  
Best Local Similarity 59.7%; Pred. No. 1.1e-40;  
Matches 151; Conservative 37; Mismatches 50; Indels 15; Gaps 3;

QY 1 QVQLQOWGAGILKSWGTLSLTCAVSGASF-SGYWWSWIRPPGKLEWIGEINHRGSTTY 59  
Db 20 QVQLQESGPGILVRPSQTLSTCTVSGYSITSDHAWSWVRQPPGRGLEWIGYISYGITTY 79  
QY 60 NPSLDGRVTISLDTSTNQISLKTSMTADTAIVYYCARTVAGTS--DYWGQGLVTVSSG 117  
Db 80 NPSLKSRYTMLRDTSKNQFSLRLSSVTADTAIVYYCARSLARTTAMDYWGQGLVTVS-- 137  
QY 118 SASAPTGGGGSGGGSGGGSGGGSKTTLTQSPAFMSATPGDKVSIACKASRDVDDVN 177  
Db 138 -----SGGGSGGGSGGGSGGGSDIQMTQSPSSLASVGDRTVITCRASQDISSYLN 187  
QY 178 WYQORPGEAPIFIIEDATTLVPGISPRFSGSGYGTFTLTINNIDSEDAAYYFCLQHDNF 237  
Db 188 WYQOKPKAKPKLLIYYTSRLHSGVPSRFSGSGSGTDFTFTISSLQPEDIATVYYCQGGNTL 247  
QY 238 PLTFGGGTKEVEIK 250  
Db 248 PYTFGGGTKEVEIK 260

RESULT 5  
AAV55078  
ID AAV55078 standard; protein; 367 AA.  
XX  
AC AAV55078;  
XX  
DT 25-FEB-2000 (first entry)  
XX







```

Db          248 PYTFGGGTKEIK 260
          |||||
RESULT 7
AAV55080
ID  AAV55080 standard; protein; 519 AA.
XX
AC  AAV55080;
XX
DT  25-FEB-2000 (first entry)
XX
DE  Single chain Fv protein sequence shPM1(deltaEL)-BvGS3.
XX
KW  Gene isolation; membrane-bound protein; fusion protein; drug production;
KM  antigen-binding cell; secretable functional protein; antigenic protein;
XX  protein isolation; diagnosis; ScFv.
OS  Synthetic.
XX
PN  WO9960113-A1.
XX
PD  25-NOV-1999.
XX
PF  30-APR-1999; 99WO-JP002341.
XX
PR  20-MAY-1998; 98JP-00138652.
PR  01-OCT-1998; 98JP-00279876.
XX
PA  (CHUS ) CHUGAI SEIYAKU KK.
XX
PI  Tsuchiya M, Saito M, Ohtomo T;
XX
DR  WPI; 2000-039382/03.
DR  N-PSDB; AAZ40312.
XX
XX  Efficient and selective isolation of a gene encoding membrane protein
PT  with low or no antigenic binding activity, for diagnosis, study of, and
PT  production of drugs treating abnormal functions of the protein.
XX
PS  Example 7; Page 95-100; 120pp; Japanese.
XX
CC  This sequence represents a single chain Fv (ScFv) sequence. The invention
CC  relates to a method for isolating a gene encoding a membrane-bound
CC  protein, comprising introducing a vector into a cell, contacting an
CC  antigen with the cell expressing the fused protein encoded by the vector
CC  on its surface to select an antigen-binding cell, and isolating the vector.
CC  The vector contains DNA encoding a secretable functional protein with
CC  antigenicity and binding affinity, and a cDNA ligated to DNA downstream
CC  of the 3' end of the coding sequence. The method can be used to isolate a
CC  membrane-bound protein for diagnosis and study. It can also be used for
CC  producing drugs treating abnormal functions of the protein. Such a
CC  technique is efficient and selective, which is different from the prior-
CC  art transmembrane trap (TMT) method wherein an epitope recognised by an
CC  antibody is carried in a fused protein
XX
SQ  Sequence 519 AA;

Query Match          57.7%; Score 771.5; DB 3; Length 519;
Best Local Similarity 59.7%; Pred. No. 2.1e-40;
Matches 151; Conservative 37; Mismatches 50; Indels 15; Gaps 3;

OY  1 QVQLQWAGALLKSWGTLSTLTCAVSGASF-SGYYSWIRPPGKGLEWIGEINHRGSTTY 59
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB  20 QVQLQESGPGLVPRPSQTLSTLCTVSGYSITSDHAWSWVRQPPGRLRWIGYISYGITTY 79
OY  60 NPSLDGRVTISLDTSTNQISLKLTSMTAADTAIVYVCARTVAGTS--DYWGQGLVTVSSG 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB  80 NPSLKSRTVLRDTSKQFSLRLSSVTADTAIVYCARSLARTAMDYWGQGLVTVS-- 137
OY  118 SASAPRTGGGSGGSGGSGGSGGSKTTLTQSPAFMSATPGDKVSIACKASRDVDDVN 177
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB  138 -----SGGGGSGGSGGSGGSGGSDICMTQSPSSLSASVGDRTITCRASQDISSYLN 187
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OY  178 WYQORPGEAPIFIIEDATTLVPGISPRFSGSGYGTDTFTLTINNIDSEDAAYVFCLQHDNF 237
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB  188 WYQOKPGKAPKLLIYYTSRLHSGVPRFSGSGSDTFTFTISSLOPEDIAITYYCCQGNLT 247
OY  238 PLTFGGGTKEIK 250
    |||||
DB  248 PYTFGGGTKEIK 260

RESULT 8
AAV55074
ID  AAV55074 standard; protein; 546 AA.
XX
AC  AAV55074;
XX
DT  25-FEB-2000 (first entry)
XX
DE  Single chain Fv protein sequence hPM1-BvGS3.
XX
KW  Gene isolation; membrane-bound protein; fusion protein; drug production;
KM  antigen-binding cell; secretable functional protein; antigenic protein;
XX  protein isolation; diagnosis; ScFv.
OS  Synthetic.
XX
PN  WO9960113-A1.
XX
PD  25-NOV-1999.
XX
PF  30-APR-1999; 99WO-JP002341.
XX
PR  20-MAY-1998; 98JP-00138652.
PR  01-OCT-1998; 98JP-00279876.
XX
PA  (CHUS ) CHUGAI SEIYAKU KK.
XX
PI  Tsuchiya M, Saito M, Ohtomo T;
XX
DR  WPI; 2000-039382/03.
DR  N-PSDB; AAZ40303.
XX
XX  Efficient and selective isolation of a gene encoding membrane protein
PT  with low or no antigenic binding activity, for diagnosis, study of, and
PT  production of drugs treating abnormal functions of the protein.
XX
PS  Example 5; Page 73-78; 120pp; Japanese.
XX
CC  This sequence represents a single chain Fv (ScFv) sequence. The invention
CC  relates to a method for isolating a gene encoding a membrane-bound
CC  protein, comprising introducing a vector into a cell, contacting an
CC  antigen with the cell expressing the fused protein encoded by the vector
CC  on its surface to select an antigen-binding cell, and isolating the cDNA.
CC  The vector contains DNA encoding a secretable functional protein with
CC  antigenicity and binding affinity, and a cDNA ligated to DNA downstream
CC  of the 3' end of the coding sequence. The method can be used to isolate a
CC  membrane-bound protein for diagnosis and study. It can also be used for
CC  producing drugs treating abnormal functions of the protein. Such a
CC  technique is efficient and selective, which is different from the prior-
CC  art transmembrane trap (TMT) method wherein an epitope recognised by an
CC  antibody is carried in a fused protein
XX
SQ  Sequence 546 AA;

Query Match          57.7%; Score 771.5; DB 3; Length 546;
Best Local Similarity 59.7%; Pred. No. 2.2e-40;
Matches 151; Conservative 37; Mismatches 50; Indels 15; Gaps 3;

OY  1 QVQLQWAGALLKSWGTLSTLTCAVSGASF-SGYYSWIRPPGKGLEWIGEINHRGSTTY 59
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB  20 QVQLQESGPGLVPRPSQTLSTLCTVSGYSITSDHAWSWVRQPPGRLRWIGYISYGITTY 79
OY  60 NPSLDGRVTISLDTSTNQISLKLTSMTAADTAIVYVCARTVAGTS--DYWGQGLVTVSSG 117
```

Db 80 NPSLKSRTVMTLRDTSKNQFSLRLSSVTAADTA VYCARSLARTTAMDYWGQSLVTVS-- 137  
QY 118 SASAPGTGGGSGGGSGGGGSKTTLTQSPAFMSATPGDKVISICKASRDVDDVN 177  
Db 138 -----SGGGSGGGSGGGSGGSDIQMTQSPSSLASVGDRTTICRASQDISSYLN 187  
QY 178 WYQORPGEAPFIIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAAYFCLQHDNF 237  
Db 188 WYQOKPGKAPKLLIYTSRLHSGVPSRFSGSGGTDFTFTISSLPEDIATYYCQCGNTL 247  
QY 238 PLTFGGGTKEIK 250  
Db 248 PYTFGGGTKEIK 260

RESULT 9  
AAV55081  
ID AAV55081 standard; protein, 626 AA.  
XX  
AC AAV55081;  
XX  
DT 25-FEB-2000 (first entry)  
XX  
DE Single chain Fv protein sequence shPM1-kappa-BVGS3.  
XX  
KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretable functional protein; antigenic protein;  
XX protein isolation; diagnosis; ScFv.  
OS Synthetic.  
XX  
PN WO9960113-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 30-APR-1999; 99WO-JP002341.  
XX  
PR 20-MAY-1998; 98JP-00138652.  
PR 01-OCT-1998; 98JP-00279876.  
XX  
PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Tsuchiya M, Saito M, Ohtomo T;  
XX  
DR WPI; 2000-039382/03.  
DR N-PSDB; AAZ40316.  
XX

PT Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
XX production of drugs treating abnormal functions of the protein.  
PS Example 7; Page 103-109; 120pp; Japanese.  
XX

CC This sequence represents a single chain Fv (ScFv) sequence. The invention  
CC relates to a method for isolating a gene encoding a membrane-bound  
CC protein, comprising introducing a vector into a cell, contacting an  
CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the vector  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for  
CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
XX antibody is carried in a fused protein  
SQ Sequence 626 AA;

Query Match 57.7%; Score 771.5; DB 3; Length 626;  
Best Local Similarity 59.7%; Pred. No. 2.5e-40;  
Matches 151; Conservative 37; Mismatches 50; Indels 15; Gaps 3;

QY 1 QVOIQOWGAGLLKSMGTLTLTCAVSGASF-SGIYWSWIRPPGKGLEWIGELNHRGTTY 59  
Db 20 QVOIQESGPGVLVRPSQTLSTLCTVSGYSLTSDHAWSMWRQPPGRGLEWIGYISYGITTY 79  
QY 60 NPSLDGRVTISLPTSTNQISLKLTSMTADTA VYCCARTVAGTS--DYWGQTLVTVSSG 117  
Db 80 NPSLKSRTVMTLRDTSKNQFSLRLSSVTAADTA VYCARSLARTTAMDYWGQSLVTVS-- 137  
QY 118 SASAPGTGGGSGGGSGGGGSKTTLTQSPAFMSATPGDKVISICKASRDVDDVN 177  
Db 138 -----SGGGSGGGSGGGSGGSDIQMTQSPSSLASVGDRTTICRASQDISSYLN 187  
QY 178 WYQORPGEAPFIIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAAYFCLQHDNF 237  
Db 188 WYQOKPGKAPKLLIYTSRLHSGVPSRFSGSGGTDFTFTISSLPEDIATYYCQCGNTL 247  
QY 238 PLTFGGGTKEIK 250  
Db 248 PYTFGGGTKEIK 260

RESULT 10  
AAV55082  
ID AAV55082 standard; protein, 640 AA.  
XX  
AC AAV55082;  
XX  
DT 25-FEB-2000 (first entry)  
XX  
DE Single chain Fv protein sequence shPM1-MCH4-BVGS3.  
XX  
KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretable functional protein; antigenic protein;  
XX protein isolation; diagnosis; ScFv.  
OS Synthetic.  
XX  
PN WO9960113-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 30-APR-1999; 99WO-JP002341.  
XX  
PR 20-MAY-1998; 98JP-00138652.  
PR 01-OCT-1998; 98JP-00279876.  
XX  
PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Tsuchiya M, Saito M, Ohtomo T;  
XX  
DR WPI; 2000-039382/03.  
DR N-PSDB; AAZ40321.  
XX

PT Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
XX production of drugs treating abnormal functions of the protein.  
PS Example 7; Page 111-117; 120pp; Japanese.  
XX

CC This sequence represents a single chain Fv (ScFv) sequence. The invention  
CC relates to a method for isolating a gene encoding a membrane-bound  
CC protein, comprising introducing a vector into a cell, contacting an  
CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the vector  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for  
CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
XX antibody is carried in a fused protein

XX Sequence 640 AA;  
SQ  
Query Match 57.7%; Score 771.5; DB 3; Length 640;  
Best Local Similarity 59.7%; Pred. No. 2.6e-40;  
Matches 151; Conservative 37; Mismatches 50; Indels 15; Gaps 3;  
QY 1 QVQLQOWGAGLKSMTLSLTCAVSGASF-SGYWWSWIRPPGKLEWIGEINHRGSTTY 59  
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGYSITSDHAWSWVRQPPGRLRWIGYISYGITTY 79  
QY 60 NPSLDGRVTISLDTSTNQISLKLTSMTAADTAVYYCARTVAGTS--DYWGQGLVTVSSG 117  
Db 80 NPSLKSRTVMTLSDTSKNQFSLRLSSVTADTAVYYCARSLARTAMDYWGQGLVTVS-- 137  
QY 118 SASAPTGGSGGGSGGGSGGGGSKTTLTQSPAFMSATPGDKVSIACKASRDVDDVN 177  
Db 138 -----SGGGSGGGSGGGSGGGSDIQMTQSPSSLASVGDRTVITCRASQDISSYLN 187  
QY 178 WYQQRPEAPIFIIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAAYYFCLQHDNF 237  
Db 188 WYQQRPEKAPKLLIYTSRLHSGVPSRFSGSGSTDTFTTISLQPEDIAITYCCQGNLT 247  
QY 238 PLTFGGGTKEIK 250  
Db 248 PYTFGGGTKEIK 260

RESULT 11  
ABP45038  
ID ABP45038 standard; protein; 251 AA.  
XX AC ABP45038;  
XX DT 19-AUG-2002 (first entry)  
XX DE Human Blys binding scFv SEQ ID 1049.  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX OS Homo sapiens.  
XX PN WO200202641-A1.  
XX PD 10-JAN-2002.  
XX PF 15-JUN-2001; 2001WO-US019110.  
XX PR 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
XX diagnosis and treatment of cancers and immune disorders.  
XX PS Claim 1; Page 1654-1655; 3148pp; English.  
XX CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the

CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 251 AA;

Query Match 56.6%; Score 756; DB 5; Length 251;  
Best Local Similarity 59.5%; Pred. No. 9.8e-40;  
Matches 156; Conservative 29; Mismatches 53; Indels 24; Gaps 6;  
QY 1 QVQLQOWGAGLKSMTLSLTCAVSGASFSG--YWWSWIRPPGKLEWIGEINHRGSTT 58  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGFRISRTSYWGWIRPPGKPEWIGNIYTGKTY 60  
QY 59 YNPSLDGRVTISLDTSTNQISLKLTSMTAADTAVYYCARTVAGTS-----DYWGQ 109  
Db 61 YSPSLKSRTVITSDTSKNQSLKLSNVTAAADTAVYYCAR--AGYDLLTGYPFYFDSWGKG 118  
QY 110 TLVTVSSGSASAPITGGGGSGGGSGGGGSKTTLTQSPAFMSATPGDKVSIACKAS 169  
Db 119 TLVTVSS-----GGGGSGGGSGGGGS--ALEIVLTQSPATISLSPGERATLSCKAS 168  
QY 170 RDVDDPVNMYQQRPEAPIFIIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAAY 229  
Db 169 QSVSSYLAWYQQRPGQAPRLIYDASNRATGIPARFSGSGSTDTFTTISLSEPEFAVY 228  
QY 230 FCLQHDNFP-LTFGGGTKEIK 250  
Db 229 YCQQRNWPFLTFGGGTKEIK 250

RESULT 12  
ABP45315  
ID ABP45315 standard; protein; 252 AA.  
XX AC ABP45315;  
XX DT 19-AUG-2002 (first entry)  
XX DE Human Blys binding scFv SEQ ID 1326.  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX OS Homo sapiens.  
XX PN WO200202641-A1.  
XX PD 10-JAN-2002.  
XX PF 15-JUN-2001; 2001WO-US019110.  
XX PR 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.



XX (HUMA-) HUMAN GENOME SCI INC.  
PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.  
XX  
PS Claim 1; Page 1985-1986; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, and  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
XX the invention  
SQ Sequence 252 AA;  
  
Query Match 55.4%; Score 740.5; DB 5; Length 252;  
Best Local Similarity 58.6%; Pred. No. 9.1e-39;  
Matches 154; Conservative 26; Mismatches 56; Indels 27; Gaps 6;  
  
QY 1 QVQLQQMGAGLLKSWGTLSLTCAVSGASFSGYWMSWIRQPPGKLEWIGRIHNRGSTTN 60  
Db 1 QVQLQQMGAGLLKRPSETLSLTCAVYGGSFSGYWSWIRQPPGKPEWIKITHSGSTTN 60  
QY 61 PSLDGRVTISLDTSTNOISLKLTSMTADTAIVYVCARAVAGTS-----DYWGQGT 110  
Db 61 PSLKSRVTMSVDTSTNQFSLKLSVTAADTAIVYCARERADYDILTGYYFYGMVWGQGT 120  
QY 111 LVTWSSGSASAPFTGGSGGGSGGGSGGSKTTLTQSPAFMSATPGDKVISICK-AS 169  
Db 121 MVTVS-----GGGGSGGGSGGGSGGSSQSVLTQ-PASVSGSPGQSITISCTGTS 167  
QY 170 RDVD--DDVNMVYQRPGEAFIIFEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDA 227  
Db 168 SDVGYNVSWYQHPGKAPKLMIEGSKRPSGVSNRFGSGSGNTASLTISGLQAEDEA 227  
QY 228 YFFCLQH-DNFPITFGGCTKVEI 249  
Db 228 DYYCSSYTRSTRYFGGTKLTV 250  
  
RESULT 13  
ABP45349  
ID ABP45349 standard; protein; 248 AA.  
XX  
AC ABP45349;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scFv SEQ ID 1360.  
XX  
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX Homo sapiens.  
XX OS  
XX WO200202641-A1.  
XX  
PN 10-JAN-2002.  
XX  
PD 15-JUN-2001; 2001WO-US019110.  
PF  
XX  
XX 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
DR Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
DR diagnosis and treatment of cancers and immune disorders.  
XX  
PT Claim 1; Page 2025-2026; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, and  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
XX the invention  
SQ Sequence 248 AA;  
  
Query Match 55.3%; Score 738.5; DB 5; Length 248;  
Best Local Similarity 58.9%; Pred. No. 1.2e-38;  
Matches 152; Conservative 30; Mismatches 57; Indels 19; Gaps 5;  
  
QY 1 QVQLQQMGAGLLKSWGTLSLTCAVSGASFSGYWMSWIRQPPGKLEWIGRIHNRGSTTN 60  
Db 1 QVQLQESGPGLVKPSSETLSLCTVSGSIRSYWSWIRQPPGKLEWIGHIYHSGSTDN 60  
QY 61 PSLDGRVTISLDTSTNOISLKLTSMTADTAIVYCAR---TVAGT---SDYWGQGTIV 112  
Db 61 PSLKSRVTMSIDTSKQPSLNLTSVTAADTAIVYCARHDYDLTGSYLAQFVWGQGTIV 120  
QY 113 TVSSGSASAPFTGGSGGGSGGGSGGSKTTLTQSPAFMSATPGDKVISICKASRDV 172  
Db 121 TVSS-----GGGGSGGGSGGGSGG---ALDIQLTQSPSSLSASVGDRTVITCRASQSI 170  
QY 173 DDDVNMVYQRPGEAFIIFEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAAYYFCL 232  
Db 171 GRYLNMVYQRPGEAPRLIFVTSSLSHSDVPSRFGSGSGGTDFSLTISNLOPEDFATYYCQ 230  
QY 233 QHDNFPITFGGCTKVEIK 250  
Db 231 QSYTDP-TFGGTRLEIK 247



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RESULT 14
ABP45402
ID ABP45402 standard; protein; 250 AA.
XX
XX ABP45402;
AC
XX 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv SEQ ID 1413.
DE
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
OS Homo sapiens.
XX
XX WO200202641-A1.
PN
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX 17-OCT-2000; 2000US-0240816P.
XX 16-MAR-2001; 2001US-0276248P.
XX 21-MAR-2001; 2001US-0277379P.
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
XX WPI; 2002-114799/15.
XX
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
XX Claim 1; Page 2088-2089; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method of
XX the invention
XX
XX Sequence 250 AA;
XX
XX Query Match 55.3%; Score 738.5; DB 5; Length 250;
XX Best Local Similarity 59.0%; Pred. No. 1.2e-38;
XX Matches 154; Conservative 26; Mismatches 56; Indels 25; Gaps 7
XX
XX 1 QVQLQWAGALLKSWGTLSTLCAVSGASFSGYYSWIRQPPGKGLWIGINHRGSTTNN 60
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 1 QAQLQWAGALLKPSFTLSTCLVDGDPFSGYYSWIRQPPGKGLWIGINHSGSTNN 60
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX
XX 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAVYYCAR----TVAG----TSDYWGQGLTV 112
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 61 PSLSKRVITISVDTSKNQFSLKLSSVTAADTAVYYCARGERDILTGYYLDGMDVWGRGTWV 120

Qy 113 TVSSGSASAPRTGGGSGGGSGGGGSKTTLTQSPAFMSATPGDKVSI5CK-ASRD 1711

Db 121 TVS-----SGGGSGGGSGGGSGSVLTQPPS-VSAAFGKVTISCTGTSSD 167

Qy 172 VD--DDVNWYQQRPGEAPIFIIEBATLVLPGISPRFSGSGYGTDFTLTINNIDSEDAAYY 229

Db 168 VGGTNYVSWYQOHPGKAPKLMIEGSKRPSGVSNRFSGSKSGNTASLTISGLQADEADY 227

Qy 230 FCLQH-DNFPDLTGGGTKEI 249

Db 228 YCSSYTTTRSTRVFGGKTLTV 248

RESULT 15

ABP45631

ID ABP45631 standard; protein; 255 AA.

XX ABP45631;

AC

XX 19-AUG-2002 (first entry)

XX DT

XX DE Human Blys binding scFv SEQ ID 1642.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;

KW tumour necrosis factor; B cell proliferation; B cell differentiation;

KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

KM common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

OS

XX WO200202641-A1.

PN

XX 10-JAN-2002.

PD

XX 15-JUN-2001; 2001WO-US019110.

XX PF

XX 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX

PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the

PT diagnosis and treatment of cancers and immune disorders.

XX

XX Claim 1; Page 2362-2363; 3148pp; English.

XX

CC This invention describes novel antibodies that immunospecifically bind to

CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the

CC tumour necrosis factor (TNF) super family and induces B cell

CC proliferation and differentiation. The antibodies of the invention have

CC cytosolic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to

CC inhibit the expression and activity of Blys. The antibodies bind to Blys

CC and so may be used to detect and quantitate the presence of Blys in

CC biological samples and may be used in this way to diagnose disease

CC associated with aberrant expression of Blys. They may also be

CC administered to treat diseases associated with aberrant Blys expression

CC and activity such as cancer, immune, and autoimmune disorders and

CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,

CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and

CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent

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**Page 10**

CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 255 AA;

Query Match	55.0%;	Score 735;	DB 5;	Length 255;
Best Local Similarity	58.6%;	Pred. No. 2e-38;		
Matches 156;	Conservative 21;	Matched 21;		

QY	1	QVQLQQMGAGLIKSGWTLISLTCAVSGASFSGYYMSWIRQPPGKLEWIGEINHRGSTYN	60
Db	1	QVQLQQMGAGLIKPSSETLSLTCAVSGSFSGYMSWIRQPPGKLEWIGEINHGSTNYN	60
QY	61	PSLDGRVTISLDTSTNQISLKLSTMTAADTAVYYCAR-----TVAGTS-----DYWG	107
Db	61	PSLKSRTVISVDASKNQFSLKLISVTADTAVYYCARERSYYDILTGYSRASKYGMDDWG	120
QY	108	QGLTIVTSSGSASAPFTGGSGSGSGSGSGSKTLLTQSPAFMSATPDQVYSISCK	167
Db	121	RGTLVTVS-----SGGGSGSGSGSGSGSQSVLTQPPS-ASGTPQGRVTISCS	167
QY	168	ASRD--VDDDVNMWYQQRPEGAFFIIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSED	225
Db	168	GSSSNIGSNTVMWYQRLPGAAPQLLYNNDRPSGIPDRFSGSKSGTISGLVTSGLQSED	227
QY	226	AAYYFCLQHDNF--PLTFGGGTKEI	249
Db	228	EADYYCASWDDSLNGRAVFGGGTKLTIV	253

Search completed: May 13, 2004, 15:00:57  
Job time : 52.4563 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 14:53:42 ; Search time 13.7136 Seconds  
(without alignments)  
941.146 Million cell updates/sec

Title: US-10-072-301-21

Perfect score: 1336  
Sequence: 1 QVQLQQWAGLLKSWGTLTL.....CLQHDNFPITFGGKVEIK 250

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	699	52.3	245	4 US-08-918-148-75	Sequence 75, Appl
2	688.5	51.5	248	2 US-08-887-352B-22	Sequence 22, Appl
3	688.5	51.5	248	3 US-09-109-207C-22	Sequence 22, Appl
4	688.5	51.5	248	3 US-09-296-005-22	Sequence 22, Appl
5	688.5	51.5	248	4 US-09-920-171-22	Sequence 22, Appl
6	684.5	51.2	248	2 US-08-887-352B-23	Sequence 23, Appl
7	684.5	51.2	248	3 US-09-109-207C-23	Sequence 23, Appl
8	684.5	51.2	248	3 US-09-296-005-23	Sequence 23, Appl
9	684.5	51.2	248	4 US-09-920-171-23	Sequence 23, Appl
10	681.5	51.0	244	4 US-08-918-148-79	Sequence 79, Appl
11	679	50.8	245	4 US-08-918-148-78	Sequence 78, Appl
12	677.5	50.7	244	4 US-08-918-148-77	Sequence 77, Appl
13	675	50.5	482	4 US-09-509-031-16	Sequence 16, Appl
14	674.5	50.5	240	4 US-10-092-246-36	Sequence 36, Appl
15	674.5	50.5	240	4 US-10-092-246-37	Sequence 37, Appl
16	671.5	50.3	244	4 US-10-039-785-44	Sequence 44, Appl
17	669	50.1	240	1 US-08-488-113B-148	Sequence 148, Appl
18	669	50.1	240	1 US-08-477-484B-148	Sequence 148, Appl
19	669	50.1	240	2 US-08-646-360-148	Sequence 148, Appl
20	669	50.1	240	3 US-08-839-765-148	Sequence 148, Appl
21	669	50.1	240	3 US-09-136-389-148	Sequence 148, Appl
22	669	50.1	240	3 US-09-610-838-148	Sequence 148, Appl
23	669	50.1	240	4 US-09-711-485-148	Sequence 148, Appl
24	669	50.1	281	4 US-09-025-769B-178	Sequence 178, Appl
25	668.5	50.0	240	4 US-10-092-246-35	Sequence 35, Appl
26	665.5	49.8	359	4 US-09-646-028-16	Sequence 16, Appl
27	665.5	49.8	361	4 US-09-646-028-13	Sequence 13, Appl

28	664	49.7	249	2 US-08-797-689-18	Sequence 18, Appl
29	664	49.7	249	4 US-09-984-186-18	Sequence 18, Appl
30	661	49.5	245	4 US-08-918-148-76	Sequence 76, Appl
31	657	49.2	235	2 US-08-190-199A-61	Sequence 61, Appl
32	656.5	49.1	243	1 US-07-958-140-2	Sequence 2, Appl
33	656.5	49.1	243	5 PCT-US93-09166-2	Sequence 2, Appl
34	650.5	48.7	269	3 US-08-646-265A-109	Sequence 109, Appl
35	649	48.6	239	4 US-10-092-246-33	Sequence 33, Appl
36	648.5	48.5	270	2 US-08-652-507-2	Sequence 2, Appl
37	646.5	48.4	239	3 US-08-279-772A-8	Sequence 8, Appl
38	646.5	48.4	239	3 US-08-902-486-11	Sequence 11, Appl
39	646.5	48.4	599	1 US-08-463-163-3	Sequence 3, Appl
40	642.5	48.1	240	4 US-10-092-246-34	Sequence 34, Appl
41	642.5	48.1	553	2 US-08-661-052-16	Sequence 16, Appl
42	642.5	48.1	553	3 US-09-188-082-16	Sequence 16, Appl
43	642.5	48.1	553	4 US-09-364-088-16	Sequence 16, Appl
44	642.5	48.1	553	4 US-09-102-716-16	Sequence 16, Appl
45	640.5	47.9	256	4 US-09-526-738A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1					
US-08-918-148-75					
; Sequence 75, Application US/08918148A					
; Patent No. 6342220					
; GENERAL INFORMATION:					
; APPLICANT: Adams, Camellia					
; APPLICANT: W.					
; APPLICANT: Carter, Paul J.					
; APPLICANT: Fendly, Brian M.					
; APPLICANT: Gurney, Austin L.					
; TITLE OF INVENTION: Agonist Antibodies					
; FILE REFERENCE: P0979					
; CURRENT APPLICATION NUMBER: US/08/918,148A					
; CURRENT FILING DATE: 1997-08-25					
; NUMBER OF SEQ ID NOS: 79					
; SEQ ID NO 75					
; LENGTH: 245					
; TYPE: PRT					
; ORGANISM: artificial					
US-08-918-148-75					
Query Match					
Best Local Similarity 52.3%; Score 699; DB 4; Length 245;					
Matches 138; Conservative 38; Mismatches 62; Indels 14; Gaps 3;					
QY	1	QVQLQQWAGLLKSWGTL	SLTCAVSGASFGYYWSWIRQPPGKLEWIG	INHRGTT-y	59
DB	3	EVQLVQSGGGLVKKPG	SLRLSCASGFTFS	DYMSWIRQAPGKLEWVSISSG	STIYY 62
QY	60	NPSLDGRVTISLDT	STNQISLKLSTMTA	ADTAVYYCAR-TVAGTSDYWGQGL	LVTVSSGS 118
DB	63	ADSVKGRFTISR	DNSKNTLVYLNMSLRAEDTAVYYCAR	WGSGBDAFDIWGQTMVTS---	119
QY	119	ASAPITGGGSGGGSG	GGGSKTTLTQSPAFMSATP	GDVKVISCKASRDVDDVNV	178
DB	120	-----SGGGSGGGSG	GGGSDIVMTQSPSTLSASVGRVAITCRASEGI	YHWLAW	170
QY	179	YQQRPGEA	PIFIIEDATTLVPGISPRFSGSGYGTDFLT	TINNIDSEDAVYFCLQHDNFP	238
DB	171	YQQRPGKAPKLLIT	KASLSASGAPSRFSGSGGADFTLT	ISLQPD	FATYYCQQYSNYP 230
QY	239	LTPGGGKVEIK	250		
DB	231	LTPGGGKLEVK	242		
RESULT 2					
US-08-887-352B-22					
; Sequence 22, Application US/08887352B					
; Patent No. 5994511					

## GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
NUMBER OF INVENTION: Improving Polypeptides  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,352B  
FILING DATE: 03-Jul-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P1123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 248 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-887-352B-22

Query Match 51.5%; Score 688.5; DB 2; Length 248;  
Best Local Similarity 54.4%; Pred. No. 4e-46;  
Matches 143; Conservative 33; Mismatches 58; Indels 29; Gaps 5;

QY 1 QVQLQWAGLLIKSWGTLSTLCVSGASF-SGYVSWIRQPPGKLEWIGEHNRGTTY 59  
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWMWIRQAPGKLEWVASITYDGSTNY 60  
QY 60 NPSLDGRVTISLDTSTNQISLKLSTMTADTAAYVCARTVAGTSDY-----WGQGT 111  
DB 61 NPSVKGRIITISRDTSKNTFYLMNSLRADTAAYVCAR-----GSHYFGHWHFAVWGQGT 116  
QY 112 VTVSSGSASAPLTGGGSGGSGGSGGSKTTLTQSPAFMSATPGDKVISICKASRD 171  
DB 117 VTVS-----SEGGSEGGSEGGSDIQLTQSPSSLSASVGDRTVITCRASKP 164  
QY 172 VDDD-----VNWYQQRPEGEAPIFIIEDATTLVPGISPRFSGSGYGTDTLTINNIDSEDA 227  
DB 165 VDGEGLSYLWYQKPKAPKLLIYAASYLESGVPSRFSGSGSDTFTLTISSLPEDFA 224  
QY 228 YVFCLOHDFLITFGGQTKVEIK 250  
DB 225 TYVCCQSHEDPYTFGGQTKVEIK 247

## RESULT 3

US-09-109-207C-22  
Sequence 22, Application US/09109207C  
Patent No. 6172213  
GENERAL INFORMATION:  
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
FILE REFERENCE: P1123R1  
CURRENT APPLICATION NUMBER: US/09/109,207C  
CURRENT FILING DATE: 1998-06-30  
PRIOR APPLICATION NUMBER: US 60/051,554  
PRIOR FILING DATE: 1997-07-03  
NUMBER OF SEQ ID NOS: 44

SEQ ID NO 22  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
NAME/KEY: Artificial  
LOCATION: 1-248  
OTHER INFORMATION: sfv sequence derived from MAE11  
US-09-109-207C-22

Query Match 51.5%; Score 688.5; DB 3; Length 248;  
Best Local Similarity 54.4%; Pred. No. 4e-46;  
Matches 143; Conservative 33; Mismatches 58; Indels 29; Gaps 5;

QY 1 QVQLQWAGLLIKSWGTLSTLCVSGASF-SGYVSWIRQPPGKLEWIGEHNRGTTY 59  
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWMWIRQAPGKLEWVASITYDGSTNY 60  
QY 60 NPSLDGRVTISLDTSTNQISLKLSTMTADTAAYVCARTVAGTSDY-----WGQGT 111  
DB 61 NPSVKGRIITISRDTSKNTFYLMNSLRADTAAYVCAR-----GSHYFGHWHFAVWGQGT 116  
QY 112 VTVSSGSASAPLTGGGSGGSGGSGGSKTTLTQSPAFMSATPGDKVISICKASRD 171  
DB 117 VTVS-----SEGGSEGGSEGGSDIQLTQSPSSLSASVGDRTVITCRASKP 164  
QY 172 VDDD-----VNWYQQRPEGEAPIFIIEDATTLVPGISPRFSGSGYGTDTLTINNIDSEDA 227  
DB 165 VDGEGLSYLWYQKPKAPKLLIYAASYLESGVPSRFSGSGSDTFTLTISSLPEDFA 224  
QY 228 YVFCLOHDFLITFGGQTKVEIK 250  
DB 225 TYVCCQSHEDPYTFGGQTKVEIK 247

## RESULT 4

US-09-296-005-22  
Sequence 22, Application US/09296005  
Patent No. 6290957  
GENERAL INFORMATION:  
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides  
FILE REFERENCE: P1123C1F  
CURRENT APPLICATION NUMBER: US/09/296,005  
CURRENT FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 08/887,352  
EARLIER FILING DATE: 1997-07-02  
NUMBER OF SEQ ID NOS: 26  
SEQ ID NO 22  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
NAME/KEY: Artificial  
LOCATION: 1-248  
OTHER INFORMATION: sfv sequence derived from MAE11  
US-09-296-005-22

Query Match 51.5%; Score 688.5; DB 3; Length 248;  
Best Local Similarity 54.4%; Pred. No. 4e-46;  
Matches 143; Conservative 33; Mismatches 58; Indels 29; Gaps 5;

QY 1 QVQLQWAGLLIKSWGTLSTLCVSGASF-SGYVSWIRQPPGKLEWIGEHNRGTTY 59  
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWMWIRQAPGKLEWVASITYDGSTNY 60  
QY 60 NPSLDGRVTISLDTSTNQISLKLSTMTADTAAYVCARTVAGTSDY-----WGQGT 111  
DB 61 NPSVKGRIITISRDTSKNTFYLMNSLRADTAAYVCAR-----GSHYFGHWHFAVWGQGT 116  
QY 112 VTVSSGSASAPLTGGGSGGSGGSGGSKTTLTQSPAFMSATPGDKVISICKASRD 171  
DB 117 VTVS-----SEGGSEGGSEGGSDIQLTQSPSSLSASVGDRTVITCRASKP 164





US-09-109-207C-23

Query Match 51.2%; Score 684.5; DB 3; Length 248;  
Best Local Similarity 54.0%; Pred. No. 8.1e-46;  
Matches 142; Conservative 33; Mismatches 59; Indels 29; Gaps 5;

QY 1 QVQLQOMGAGLLKSWGTLISLTCAVSGASF-SGYYSWIRQPPGKLEWIGELNHRGTTY 59  
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWMIRQAPGKLEWVASIKYSGETKY 60  
QY 60 NPSLDGRVTISLDTSTNQISLKTSMTADTAIVYYCARTVAGTSDY-----WGQGTL 111  
DB 61 NPSVKGRITISRDSKNTFYLMNSLRAEDTAIVYYCAR-----GSHYFGHWHFAVMGQGTL 116  
QY 112 VTVSSGSASAPTTGGSGGGSGGGSGGSKTTLTQSPAFMSATPGDKVISCKASRD 171  
DB 117 VTVS-----SEGGSSEGGSEGGSGSDIQLTQSPSSLSASVGDRTVITCRASKP 164  
QY 172 VDDD-----VNMYYQORPGEAPFIIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDA 227  
DB 165 VDGEEDSYLNMYYQOKPKAPKLLIYAASYLESGVPSRFSGSGGTDFTLTISLQPEDFA 224  
QY 228 YFCLQHDNFPPLTFGGGTKEIK 250  
DB 225 TYCCQSHEDPYTFGGGTKEIK 247

RESULT 8

US-09-296-005-23  
Sequence 23, Application US/09296005  
Patent No. 6290957

GENERAL INFORMATION:  
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides  
FILE REFERENCE: P1123C11  
CURRENT APPLICATION NUMBER: US/09/296, 005  
EARLIER FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 08/887,352  
NUMBER OF SEQ ID NOS: 26  
SEQ ID NO 23  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
NAME/KEY: Artificial  
LOCATION: 1-248  
OTHER INFORMATION: sfv sequence derived from MAE11  
US-09-296-005-23

Query Match 51.2%; Score 684.5; DB 3; Length 248;  
Best Local Similarity 54.0%; Pred. No. 8.1e-46;  
Matches 142; Conservative 33; Mismatches 59; Indels 29; Gaps 5;

QY 1 QVQLQOMGAGLLKSWGTLISLTCAVSGASF-SGYYSWIRQPPGKLEWIGELNHRGTTY 59  
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWMIRQAPGKLEWVASIKYSGETKY 60  
QY 60 NPSLDGRVTISLDTSTNQISLKTSMTADTAIVYYCARTVAGTSDY-----WGQGTL 111  
DB 61 NPSVKGRITISRDSKNTFYLMNSLRAEDTAIVYYCAR-----GSHYFGHWHFAVMGQGTL 116  
QY 112 VTVSSGSASAPTTGGSGGGSGGGSGGSKTTLTQSPAFMSATPGDKVISCKASRD 171  
DB 117 VTVS-----SEGGSSEGGSEGGSGSDIQLTQSPSSLSASVGDRTVITCRASKP 164  
QY 172 VDDD-----VNMYYQORPGEAPFIIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDA 227  
DB 165 VDGEEDSYLNMYYQOKPKAPKLLIYAASYLESGVPSRFSGSGGTDFTLTISLQPEDFA 224  
QY 228 YFCLQHDNFPPLTFGGGTKEIK 250  
DB 225 TYCCQSHEDPYTFGGGTKEIK 247

RESULT 9

US-09-920-171-23  
Sequence 23, Application US/09920171  
Patent No. 6682735

GENERAL INFORMATION:  
APPLICANT: Lowman, Henry B.  
APPLICANT: Presta, Leonard G.  
APPLICANT: Jardieu, Paula M.  
APPLICANT: Lowe, John  
TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)  
FILE REFERENCE: P1123C2US  
CURRENT APPLICATION NUMBER: US/09/920,171  
CURRENT FILING DATE: 2001-08-01  
PRIOR APPLICATION NUMBER: US 08/887,352  
PRIOR FILING DATE: 1997-07-02  
PRIOR APPLICATION NUMBER: US 09/296,005  
PRIOR FILING DATE: 1999-04-21  
NUMBER OF SEQ ID NOS: 44  
SEQ ID NO 23  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: sfv sequence derived from MAE11  
US-09-920-171-23

Query Match 51.2%; Score 684.5; DB 4; Length 248;  
Best Local Similarity 54.0%; Pred. No. 8.1e-46;  
Matches 142; Conservative 33; Mismatches 59; Indels 29; Gaps 5;

QY 1 QVQLQOMGAGLLKSWGTLISLTCAVSGASF-SGYYSWIRQPPGKLEWIGELNHRGTTY 59  
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWMIRQAPGKLEWVASIKYSGETKY 60  
QY 60 NPSLDGRVTISLDTSTNQISLKTSMTADTAIVYYCARTVAGTSDY-----WGQGTL 111  
DB 61 NPSVKGRITISRDSKNTFYLMNSLRAEDTAIVYYCAR-----GSHYFGHWHFAVMGQGTL 116  
QY 112 VTVSSGSASAPTTGGSGGGSGGGSGGSKTTLTQSPAFMSATPGDKVISCKASRD 171  
DB 117 VTVS-----SEGGSSEGGSEGGSGSDIQLTQSPSSLSASVGDRTVITCRASKP 164  
QY 172 VDDD-----VNMYYQORPGEAPFIIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDA 227  
DB 165 VDGEEDSYLNMYYQOKPKAPKLLIYAASYLESGVPSRFSGSGGTDFTLTISLQPEDFA 224  
QY 228 YFCLQHDNFPPLTFGGGTKEIK 250  
DB 225 TYCCQSHEDPYTFGGGTKEIK 247

RESULT 10

US-08-918-148-79  
Sequence 79, Application US/08918148A  
Patent No. 6342220

GENERAL INFORMATION:  
APPLICANT: Adams, Camellia  
APPLICANT: W.  
APPLICANT: Carter, Paul J.  
APPLICANT: Fendly, Brian M.  
APPLICANT: Gurney, Austin L.  
TITLE OF INVENTION: Agonist Antibodies  
FILE REFERENCE: P0979  
CURRENT APPLICATION NUMBER: US/08/918,148A  
CURRENT FILING DATE: 1997-08-25  
NUMBER OF SEQ ID NOS: 79  
SEQ ID NO 79  
LENGTH: 244  
TYPE: PRT  
ORGANISM: artificial  
US-08-918-148-79

Query Match 51.0%; Score 681.5; DB 4; Length 244;  
Best Local Similarity 56.9%; Pred. No. 1.4e-45;  
Matches 144; Conservative 28; Mismatches 62; Indels 19; Gaps 6;

```
QY 1 QVQLQOWGAGLKSNGTHLSLTCAVSGASFSGYWMSWIRQPPGKGLWIGETINHRGSTTYN 60
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 3 QVQLQOSGPGLVKPSSETLSLTCTVSGDSISSYWSWIRQPPGKGLWIGETIYSGSTNYN 62
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAIVYVCARTVAGTSDYWGQGLTVTVSSGSAS 120
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 63 PSLKSRVTISVDTSKSQFSLKLSVTADTAIVYCAR--GRYPDVWGRGTWTVS----- 115
QY 121 APTGGSGSGSGSGSGSGSKTTLTQSPAFMSATPGDKVISCK-ASRDVD--DDVN 177
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 116 -----SGGGSGSGSGSGSGSSYVLTQPPS-VSGSPQISITISCTGTSDVGYNVYS 167
QY 178 WYQORPGEAPIFIEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAYFCLQHDN 236
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 168 WYQHPGKAPKLMYEGSKRPSGVSNRFGSGKSGNTASLTISGLQAEDEADYCCSYTTR 227
QY 237 PPLTFGGGTKEIK 249
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 228 STRVFGGKTLTV 240
```

## RESULT 11

US-08-918-148-78

```
; Sequence 78, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 78
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; NAME/KEY: unknown
; LOCATION: 208
; OTHER INFORMATION: unknown amino acid
US-08-918-148-78
```

Query Match 50.8%; Score 679; DB 4; Length 245;  
Best Local Similarity 53.2%; Pred. No. 2.1e-45;  
Matches 134; Conservative 40; Mismatches 64; Indels 14; Gaps 3;

```
QY 1 QVQLQOWGAGLKSNGTHLSLTCAVSGASFSGYWMSWIRQPPGKGLWIGETINHRGS-TTY 59
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 3 QVQLVESGGGLVPRGSLRLSCAASGFTFSHMMWVRQAPGKLEWVSSISSSSYIYY 62
QY 60 NPSLDGRVTISLDTSTNQISLKLTSMTADTAIVYVCARTVAGTS-DYWGQGLTVTVSSGS 118
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 63 ADSVKGRFTISRDNKNSLYLQMSLRADTAIVYVCARDGSTGMDVWGRGTLTVS--- 119
QY 119 ASAPTGGSGSGSGSGSGSKTTLTQSPAFMSATPGDKVISCKASRDVDDVNM 178
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 120 -----SGGGSGSGSGSGSGSKIQMTQSPSTLSASIGDRVITTCRASEGITYHWLAW 170
QY 179 YQORPGEAPIFIEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAYFCLQHDNFP 238
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 171 YQKPGKAPKLLIYKASSLASGAPSRFSGSGSTDTFTXTISSLQPDFAITYYCCQYSNYP 230
QY 239 LTFGGGTKEIK 250
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
```

Db 231 LTFGGGTKEIK 242

## RESULT 12

US-08-918-148-77

```
; Sequence 77, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 77
; LENGTH: 244
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-77
```

Query Match 50.7%; Score 677.5; DB 4; Length 244;  
Best Local Similarity 53.4%; Pred. No. 2.8e-45;  
Matches 134; Conservative 40; Mismatches 64; Indels 13; Gaps 2;

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QY 1 QVQLQOWGAGLKSNGTHLSLTCAVSGASFSGYWMSWIRQPPGKGLWIGETINHRG-STTY 59
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Db 3 QVQLVSGGGLVPRGSLSLSCAVSGITLRTYGMHWVRQAPGKLEWVAGISFDGRSEYY 62
QY 60 NPSLDGRVTISLDTSTNQISLKLTSMTADTAIVYVCARTVAGTSDYWGQGLTVTVSSGSA 119
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Db 63 ADSVQGRFTISRDSKNTLYLQMSLRADTAIVYVCARGAHYGFDIWQGTWTVS---- 118
QY 120 SAPTGGSGSGSGSGSGSKTTLTQSPAFMSATPGDKVISCKASRDVDDVNMWY 179
   |||||:|:~|:|:~|:|:~|:|:~|:|:~|:|:~|:|:~|:|:~|:|:~|:|:~|:|:~|:|:~
Db 119 -----SGGGGTGGSGSGSGSGSDIQMTQSPSTLSASIGDRVITTCRASEGITYHWLAWY 170
QY 180 QORPGEAPIFIEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAYFCLQHDNFP 239
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Db 171 QQKPGKAPKLLIYKASSLASGAPSRFSGSGSTDTFTLTSSLQPDFAITYYCCQYSNYP 230
QY 240 TFGGGTKEIK 250
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Db 231 TFGGGTKEIK 241
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## RESULT 13

US-09-509-031-16

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; Sequence 16, Application US/09509031
; Patent No. 6590080
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Sues, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/09/509,031
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cmTlgL protein
US-09-509-031-16
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Query Match 50.5%; Score 675; DB 4; Length 482;  
Best Local Similarity 49.2%; Pred. No. 9.4e-45;  
Matches 129; Conservative 52; Mismatches 63; Indels 18; Gaps 4;

QY 1 QVQLQOWGAGLTKSWGTLSTLTCAVSGASFSGYTWSWIRQPPGKLEWIGELINHRG--ST 57  
Db 31 EVKLVESGGGLVQPGGSLRLSCATSGFTFSDYMEWVRQPPGKLEWIAASRNKGNKTT 90  
QY 58 TYNPSLDGRVTISLDTSTNQISLKTSMTAADTAIVYICARTVAGTS---DYWGQGLTVTV 114  
Db 91 EYSASAVKGRFIVSRDTSQSIYLQMNALRAEDTAIYCARNYGSTWCDFDWGAGTTVTV 150  
QY 115 SSGSASAPTTGGGGSGGGSGGGSGGGSKTTLTQSPAFMSATPGDKVISCKASRDVDD 174  
Db 151 SSG-----GGGGSGGGSGGGSGGGSDIVMTQSPSSISVAGERVTMSCKSSQSLTN 204  
QY 175 DVN-----WYQRPGEAPIFIIEDATTLVPGISPRFSGSGYGTFTLTINNIDSEDAAY 228  
Db 205 SGNQKNFLAMYQOKPGQPKLLICGASTRESGVPRFTGSGSGTDTLTLTSSVQAEADLAV 264  
QY 229 YFCLQHDNFPPLTFGGGTVKEIK 250  
Db 265 YCCQNDHSYPLTFGAGTKLEIK 286

RESULT 14  
US-10-092-246-36  
; Sequence 36, Application US/100922246  
; Patent No. 6501314  
; GENERAL INFORMATION:  
; APPLICANT: The Minister of National Defence, Government of Canada  
; APPLICANT: Fulton, R E  
; APPLICANT: Alvi, Azhar E  
; APPLICANT: Nagata, Leslie  
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo  
; FILE REFERENCE: scfv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)  
; CURRENT APPLICATION NUMBER: US/10/092,246  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 36  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Mouse hybridoma cell line 1A4A1  
US-10-092-246-36

Query Match 50.5%; Score 674.5; DB 4; Length 240;  
Best Local Similarity 51.6%; Pred. No. 4.7e-45;  
Matches 130; Conservative 48; Mismatches 57; Indels 17; Gaps 4;  
QY 1 QVQLQOWGAGLTKSWGTLSTLTCAVSGASFSGYTWSWIRQPPGKLEWIGELINHRG--STT 58  
Db 3 QVQLQESGPELVKPGASVKISCKASGYFTFDYHVMWVKGPQGLEWIG-MTYPGFDNTN 61  
QY 59 YNPSLDGRVTISLDTSTNQISLKTSMTAADTAIVYICARTVAGTSDYWGQGLTVTVSSGS 118  
Db 62 YSETFKGKATLTVDTSNTVMQLSLTSEDYAVYFCARGVG--LDYWGQGLTVTVS--- 116  
QY 119 ASAPTGGGGSGGGSGGGSGGGSKTTLTQSPAFMSATPGDKVISCKASRDVDDVNM 178  
Db 117 -----SGGGSGGGSGGGSGGGSDIELTQSPNSLSTSIGDRIRITCKASQDVDTAVGW 167  
QY 179 YQORPGEAPIFIIEDATTLVPGISPRFSGSGYGTFTLTINNIDSEDAAYYFCLQHDNFP 238  
Db 168 YQORPQSPKLLIFWSTRTHTGVPDRFTGSGSGTDTLTISNVQSEDLADYFCHQYSYP 227  
QY 239 LTFGGGTVKEIK 250  
Db 228 FTFGSGTKLEIK 239

RESULT 15

US-10-092-246-37  
; Sequence 37, Application US/100922246  
; Patent No. 6501314  
; GENERAL INFORMATION:  
; APPLICANT: The Minister of National Defence, Government of Canada  
; APPLICANT: Fulton, R E  
; APPLICANT: Alvi, Azhar E  
; APPLICANT: Nagata, Leslie  
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo  
; FILE REFERENCE: scfv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)  
; CURRENT APPLICATION NUMBER: US/10/092,246  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Mouse hybridoma cell line 1A4A1  
US-10-092-246-37

Query Match 50.5%; Score 674.5; DB 4; Length 240;  
Best Local Similarity 51.6%; Pred. No. 4.7e-45;  
Matches 130; Conservative 48; Mismatches 57; Indels 17; Gaps 4;  
QY 1 QVQLQOWGAGLTKSWGTLSTLTCAVSGASFSGYTWSWIRQPPGKLEWIGELINHRG--STT 58  
Db 3 QVQLQESGPELVKPGASVKISCKASGYFTFDYHVMWVKGPQGLEWIG-MTYPGFDNTN 61  
QY 59 YNPSLDGRVTISLDTSTNQISLKTSMTAADTAIVYICARTVAGTSDYWGQGLTVTVSSGS 118  
Db 62 YSETFKGKATLTVDTSNTVMQLSLTSEDYAVYFCARGVG--LDYWGQGLTVTVS--- 116  
QY 119 ASAPTGGGGSGGGSGGGSGGGSKTTLTQSPAFMSATPGDKVISCKASRDVDDVNM 178  
Db 117 -----SGGGSGGGSGGGSGGGSDIELTQSPNSLSTSIGDRIRITCKASQDVDTAVGW 167  
QY 179 YQORPGEAPIFIIEDATTLVPGISPRFSGSGYGTFTLTINNIDSEDAAYYFCLQHDNFP 238  
Db 168 YQORPQSPKLLIFWSTRTHTGVPDRFTGSGSGTDTLTISNVQSEDLADYFCHQYSYP 227  
QY 239 LTFGGGTVKEIK 250  
Db 228 FTFGSGTKLEIK 239

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Job time : 14.7136 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:07:07 ; Search time 37.0146 Seconds  
(without alignments)  
1879.405 Million cell updates/sec

Title: US-10-072-301-21  
Perfect score: 1336  
Sequence: 1 QVQLQQMGAGLLKSWGTLSTL.....CLQHDFNPLTFGGGTVEIK 250

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
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9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
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14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1336	100.0	250	14 US-10-072-301-21	Sequence 21, Appl
2	1336	100.0	250	14 US-10-071-866-21	Sequence 21, Appl
3	1336	100.0	250	15 US-10-360-828-21	Sequence 21, Appl
4	1332	99.7	250	14 US-10-072-301-29	Sequence 29, Appl
5	1332	99.7	250	14 US-10-071-866-29	Sequence 29, Appl
6	1332	99.7	250	15 US-10-360-828-29	Sequence 29, Appl
7	835	62.5	249	10 US-09-880-748-1321	Sequence 1321, Ap
8	835	62.5	249	12 US-10-293-418-1321	Sequence 1321, Ap
9	805	60.3	286	12 US-10-406-830-8	Sequence 8, Appl1
10	756	56.6	251	10 US-09-880-748-1049	Sequence 1049, Ap
11	756	56.6	251	12 US-10-293-418-1049	Sequence 1049, Ap
12	740.5	55.4	252	10 US-09-880-748-1326	Sequence 1326, Ap
13	740.5	55.4	252	12 US-10-293-418-1326	Sequence 1326, Ap
14	738.5	55.3	248	10 US-09-880-748-1360	Sequence 1360, Ap
15	738.5	55.3	248	12 US-10-293-418-1360	Sequence 1360, Ap

16	738.5	55.3	250	10 US-09-880-748-1413	Sequence 1413, Ap
17	738.5	55.3	250	12 US-10-293-418-1413	Sequence 1413, Ap
18	735	55.0	255	10 US-09-880-748-1642	Sequence 1642, Ap
19	735	55.0	255	12 US-10-293-418-1642	Sequence 1642, Ap
20	733.5	54.9	250	10 US-09-880-748-1645	Sequence 1645, Ap
21	733.5	54.9	250	12 US-10-293-418-1645	Sequence 1645, Ap
22	730.5	54.7	253	12 US-10-239-656-63	Sequence 63, Appl
23	730	54.6	253	10 US-09-880-748-1333	Sequence 1333, Ap
24	730	54.6	253	12 US-10-293-418-1333	Sequence 1333, Ap
25	729.5	54.6	254	10 US-09-880-748-1659	Sequence 1659, Ap
26	729.5	54.6	254	12 US-10-293-418-1659	Sequence 1659, Ap
27	715	53.5	253	10 US-09-880-748-954	Sequence 954, App
28	715	53.5	253	12 US-10-293-418-954	Sequence 954, App
29	713	53.4	249	10 US-09-880-748-957	Sequence 957, App
30	713	53.4	249	12 US-10-293-418-957	Sequence 957, App
31	709	53.1	255	10 US-09-880-748-1597	Sequence 1597, Ap
32	709	53.1	255	12 US-10-293-418-1597	Sequence 1597, Ap
33	706	52.8	258	14 US-10-072-301-27	Sequence 27, Appl
34	706	52.8	258	14 US-10-071-866-27	Sequence 27, Appl
35	706	52.8	258	15 US-10-360-828-27	Sequence 27, Appl
36	704	52.7	253	10 US-09-880-748-1602	Sequence 1602, Ap
37	704	52.7	253	12 US-10-293-418-1602	Sequence 1602, Ap
38	699	52.3	239	10 US-10-293-418-1882	Sequence 1882, Ap
39	699	52.3	239	12 US-10-293-418-1882	Sequence 1882, Ap
40	698	52.2	237	10 US-09-880-748-1906	Sequence 1906, Ap
41	698	52.2	237	12 US-10-293-418-1906	Sequence 1906, Ap
42	697	52.2	255	10 US-09-880-748-1626	Sequence 1626, Ap
43	697	52.2	255	12 US-10-293-418-1626	Sequence 1626, Ap
44	696	52.1	239	10 US-09-880-748-1922	Sequence 1922, Ap
45	696	52.1	239	12 US-10-293-418-1922	Sequence 1922, Ap

ALIGNMENTS

RESULT 1  
US-10-072-301-21  
; Sequence 21, Application US/10072301  
; Publication No. US20030152913A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEFICIENCY VIRUS  
; FILE REFERENCE: 25636-718  
; CURRENT APPLICATION NUMBER: US/10/072,301  
; CURRENT FILING DATE: 2002-02-08  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.12  
US-10-072-301-21

Query Match	100.0%;	Score 1336;	DB 14;	Length 250;
Best Local Similarity	100.0%;	Pred. No. 8e-85;		
Matches	250;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	QVQLQQMGAGLLKSWGTLSTLTCAVSGASFSGYWISWIRQPPKGLWIGELNHRGSTTYN	60	
DB	1	QVQLQQMGAGLLKSWGTLSTLTCAVSGASFSGYWISWIRQPPKGLWIGELNHRGSTTYN	60	
QY	61	PSLDGRVTISLDTSTNQISLKLTSMTAADVYVCARTVAGTSDYWGQGLVTVSSGSAS	120	
DB	61	PSLDGRVTISLDTSTNQISLKLTSMTAADVYVCARTVAGTSDYWGQGLVTVSSGSAS	120	
QY	121	APTGGGSGGGSGGGSGGGSKTTLTQSPAFMSATPGDKVSISSCKASRDVDDVNNWYQ	180	
DB	121	APTGGGSGGGSGGGSGGGSKTTLTQSPAFMSATPGDKVSISSCKASRDVDDVNNWYQ	180	

QY 181 QRPGEAPIFIIEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAYYFCLQHDNFPPLT 240  
Db 181 QRPGEAPIFIIEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAYYFCLQHDNFPPLT 240  
QY 241 FGGGTKEIK 250  
Db 241 FGGGTKEIK 250

RESULT 2

US-10-071-866-21  
; Sequence 21, Application US/10071866  
; Publication No. US20030165988A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST  
; FILE REFERENCE: 25636-717  
; CURRENT APPLICATION NUMBER: US/10/071,866  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 21  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.12  
US-10-071-866-21

Query Match 100.0%; Score 1336; DB 14; Length 250;  
Best Local Similarity 100.0%; Pred. No. 8e-85;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQQWAGLLKSWGTLSTLTCVAVSGASFSGYWSWIRQPPGKLEWIGELNHRGSTTYN 60  
Db 1 QVQLQQWAGLLKSWGTLSTLTCVAVSGASFSGYWSWIRQPPGKLEWIGELNHRGSTTYN 60  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAAYVCARTVAGTSDYWGQGLTVTVSSGSAS 120  
Db 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAAYVCARTVAGTSDYWGQGLTVTVSSGSAS 120  
QY 121 APTGGGSGGGSGGGSGGSKTTLTQSPAFMSATPGDKVISCKASRDVDDVWYQ 180  
Db 121 APTGGGSGGGSGGGSGGSKTTLTQSPAFMSATPGDKVISCKASRDVDDVWYQ 180  
QY 181 QRPGEAPIFIIEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAYYFCLQHDNFPPLT 240  
Db 181 QRPGEAPIFIIEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAYYFCLQHDNFPPLT 240  
QY 241 FGGGTKEIK 250  
Db 241 FGGGTKEIK 250

RESULT 3

US-10-360-828-21  
; Sequence 21, Application US/10360828  
; Publication No. US20030206909A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS  
; FILE REFERENCE: 25636-727  
; CURRENT APPLICATION NUMBER: US/10/360,828  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: US 10/071,866  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/072,301

; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/133,978  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 21  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.12  
US-10-360-828-21

Query Match 100.0%; Score 1336; DB 15; Length 250;  
Best Local Similarity 100.0%; Pred. No. 8e-85;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQQWAGLLKSWGTLSTLTCVAVSGASFSGYWSWIRQPPGKLEWIGELNHRGSTTYN 60  
Db 1 QVQLQQWAGLLKSWGTLSTLTCVAVSGASFSGYWSWIRQPPGKLEWIGELNHRGSTTYN 60  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAAYVCARTVAGTSDYWGQGLTVTVSSGSAS 120  
Db 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAAYVCARTVAGTSDYWGQGLTVTVSSGSAS 120  
QY 121 APTGGGSGGGSGGGSGGSKTTLTQSPAFMSATPGDKVISCKASRDVDDVWYQ 180  
Db 121 APTGGGSGGGSGGGSGGSKTTLTQSPAFMSATPGDKVISCKASRDVDDVWYQ 180  
QY 181 QRPGEAPIFIIEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAYYFCLQHDNFPPLT 240  
Db 181 QRPGEAPIFIIEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAYYFCLQHDNFPPLT 240  
QY 241 FGGGTKEIK 250  
Db 241 FGGGTKEIK 250

RESULT 4

US-10-072-301-29  
; Sequence 29, Application US/10072301  
; Publication No. US20030152913A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF  
; FILE REFERENCE: 25636-718  
; CURRENT APPLICATION NUMBER: US/10/072,301  
; CURRENT FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 29  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.12 Variant  
US-10-072-301-29

Query Match 99.7%; Score 1332; DB 14; Length 250;  
Best Local Similarity 99.6%; Pred. No. 1.5e-84;  
Matches 249; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQQWAGLLKSWGTLSTLTCVAVSGASFSGYWSWIRQPPGKLEWIGELNHRGSTTYN 60  
Db 1 QVQLQQWAGLLKSWGTLSTLTCVAVSGASFSGYWSWIRQPPGKLEWIGELNHRGSTTYN 60  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAAYVCARTVAGTSDYWGQGLTVTVSSGSAS 120  
Db 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAAYVCARTVAGTSDYWGQGLTVTVSSGSAS 120

[illegible]

RESULT 5  
US-10-071-866-29

```

; Sequence 29, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST E
; TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.12 Variant
US-10-071-866-29

```

Query Match	99.7%	Score 1332;	DB 14;	Length 250;
Best Local Similarity	99.6%	Pred. No. 1.5e-84;		
Matches 249;	Conservative	1;	Mismatches 0;	Indels 0;
				Gaps 0;

QY	1	QVQLQQWAGALLKSWGTLSTLCAVSGASFSGYYWSWIRQPPGKGLEWIGETINHRGSTTYN	60
Db	1	QVQLQQWAGALLKSWGTLSTLCAVSGASFSGYYWSWIRQPPGKGLEWIGETINHRGSTTYN	60
QY	61	PSLDGRVTISLDTSTNQISLKLSTMTAADTAVYYCARTVAGTSDYWGQGLTVTSSGSAS	120
Db	61	PSLDGRVTISLDTSTNQISLKLSTMTAADTAVYYCARTVAGTSDYWGQGLTVTSSGSAS	120
QY	121	APTGGGSGGGSGGGSGGGSKTTLTQSPAFMSATPGDKVISISCKASRDVDDVNWYQ	180
Db	121	APTGGGSGGGSGGGSGGGSETTLTQSPAFMSATPGDKVISISCKASRDVDDVNWYQ	180
QY	181	QRPGEAFIFIIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAVYFCLQHDNFPLT	240
Db	181	QRPGEAFIFIIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAVYFCLQHDNFPLT	240
QY	241	FGGGTKVEIK 250	
Db	241	FGGGTKVEIK 250	

RESULT 6  
US-10-36

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; Sequence 29, Application US/10360828
; Publication No. US20030206909A1
;
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
;
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07

```

```

; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.12 Variant
US-10-360-828-29

```

Query Match	99.7%	Score 1332;	DB 15;	Length 250;
Best Local Similarity	99.6%	Pred. No. 1.5e-84;		
Matches 249; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	QVQLQQWAGLGLKSWGTLISLTCAVSGASFSGYYWSMIRQPPGKGLEWIGELNHRGSTTYYN	60
Db	1	QVQLQQWAGLGLKSWGTLISLTCAVSGASFSGYYWSMIRQPPGKGLEWIGELNHRGSTTYYN	60
QY	61	PSLDGRVTISLDTSTNQISLKLSTMTAADTAVYYCARTVAGTSDYWGQGLTVTVSSGSAS	120
Db	61	PSLDGRVTISLDTSTNQISLKLSTMTAADTAVYYCARTVAGTSDYWGQGLTVTVSSGSAS	120
QY	121	APTGSGSGSGSGSGSGSGSKTLLTQSPAFMSATPGDKVISISCKASRDYDDDVNWYQ	180
Db	121	APTGSGSGSGSGSGSGSGSKTLLTQSPAFMSATPGDKVISISCKASRDYDDDVNWYQ	180
QY	181	QRPGEAPIFIIEDATTLVPGISPRFSGSGYDTFTLTINNIDSEDAAYYFCLQHDNFPLT	240
Db	181	QRPGEAPIFIIEDATTLVPGISPRFSGSGYDTFTLTINNIDSEDAAYYFCLQHDNFPLT	240
QY	241	EGGGTKVEIK 250	
Db	241	EGGGTKVEIK 250	

RESULT 7  
US-09-880-748-1321

```

; Sequence 1321, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1321
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1321

```

Query Match	62.5%;	Score 835;	DB 10;	Length 249;
Best Local Similarity	63.8%;	Pred. No. 3.3e-50;		
Matches 166;	Conservative 26;	Mismatches 46;	Indels 22;	Gaps 3;



QY 1 QVQLQWAGALLKSWGTLSTLCAVSGASFSGYYSWIRQPPGKGLEWIGELINHRGSTTYN 60  
Db 1 QVQLQWAGALLKPSSETLSLTCAVYGSFSGYYSWIRQPPGKGLEWIGELINHRGSTTYN 60  
QY 61 PSLDGRVTISLDTSTNQISLKLSTMTADTAIVYCAR-----TVAGTS---DYMGGGT 110  
Db 61 PSLKSRVTISVDTSKNQFSLKLSVTADTAIVYCARGPYYDILTGYYRNMFPDPMGRGT 120  
QY 111 LTVVSSGSASAPITGGGSGGGSGGGGSKTTLTQSPAFMSATPGDKVISICKASR 170  
Db 121 LTVVS-----SGGGSGGGSGGGSGGSDIVMTQSPSTLSASVGDRTVITCRASQ 168  
QY 171 DVDDVNMYYQORPGEAFIIFIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAAYYF 230  
Db 169 GISSWLAWYQOKPGRAPKVLITYKASTLESVPSRFSGSGSGTDFTLTISLQPEDFATYY 228  
QY 231 CLQHDNFPITFGGKTVEIK 250  
Db 229 CQGSYSTPWTFGGKTLEIK 248

RESULT 8  
US-10-293-418-1321  
; Sequence 1321, Application US/10293418  
; Publication No. US20030223996A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523P2  
; CURRENT APPLICATION NUMBER: US/10/293,418  
; PRIOR FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/212,210  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1321  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-1321

Query Match 62.5%; Score 835; DB 12; Length 249;  
Best Local Similarity 63.8%; Pred. No. 3.3e-50;  
Matches 166; Conservative 26; Mismatches 46; Indels 22; Gaps 3;

QY 1 QVQLQWAGALLKSWGTLSTLCAVSGASFSGYYSWIRQPPGKGLEWIGELINHRGSTTYN 60  
Db 1 QVQLQWAGALLKPSSETLSLTCAVYGSFSGYYSWIRQPPGKGLEWIGELINHRGSTTYN 60  
QY 61 PSLDGRVTISLDTSTNQISLKLSTMTADTAIVYCAR-----TVAGTS---DYMGGGT 110  
Db 61 PSLKSRVTISVDTSKNQFSLKLSVTADTAIVYCARGPYYDILTGYYRNMFPDPMGRGT 120  
QY 111 LTVVSSGSASAPITGGGSGGGSGGGGSKTTLTQSPAFMSATPGDKVISICKASR 170  
Db 121 LTVVS-----SGGGSGGGSGGGSGGSDIVMTQSPSTLSASVGDRTVITCRASQ 168  
QY 171 DVDDVNMYYQORPGEAFIIFIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAAYYF 230  
Db 169 GISSWLAWYQOKPGRAPKVLITYKASTLESVPSRFSGSGSGTDFTLTISLQPEDFATYY 228

QY 231 CLQHDNFPITFGGKTVEIK 250  
Db 229 CQGSYSTPWTFGGKTLEIK 248

RESULT 9  
US-10-406-830-8  
; Sequence 8, Application US/10406830  
; Publication No. US20040071696A1  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, GREGORY P.  
; APPLICANT: HORAK, EVA M.  
; APPLICANT: WEINER, LOUIS M.  
; APPLICANT: JAMES, MARKS D.  
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE  
; FILE REFERENCE: THEREOF  
; CURRENT APPLICATION NUMBER: US/10/406,830  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US 60/370,276  
; PRIOR FILING DATE: 2002-04-05  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 286  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic antibody.  
US-10-406-830-8

Query Match 60.3%; Score 805; DB 12; Length 286;  
Best Local Similarity 62.8%; Pred. No. 4.4e-48;  
Matches 159; Conservative 31; Mismatches 47; Indels 16; Gaps 3;  
QY 1 QVQLQWAGALLKSWGTLSTLCAVSGASFSGYYSWIRQPPGKGLEWIGELINHRGSTTYN 60  
Db 23 QVQLQWAGALLKPSSETLSLTCTVSGSFRSYYSWIR-PPGKGLEWIGELINHRGSTTYN 81  
QY 61 PSLDGRVTISLDTSTNQISLKLSTMTADTAIVYCAR---TVAGTS---DYMGGGT 117  
Db 82 PSLKSRVTISVDTSKNQFSLKLSLTADTAIVYCARGLHGLGWFDPWGQGLTVVS-- 139  
QY 118 SASAPITGGGSGGGSGGGGSKTTLTQSPAFMSATPGDKVISICKASRDVDDVN 177  
Db 140 -----SSGGSGGGSGGGSGGSDIQMTQSPSTLSASVGDRTVITCRASQDISNYLN 189  
QY 178 WYQORPGEAFIIFIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAAYYFCLQHDN 237  
Db 190 WYQOKPGRAPKVLITYKASTLESVPSRFSGSGSGTDFTLTISLQPEDFATYYCLQDSY 249  
QY 238 PLTFGGGKTVEIK 250  
Db 250 PLTFGGGKTVEIK 262

RESULT 10  
US-09-880-748-1049  
; Sequence 1049, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16





RESULT 13

```

US-10-293-418-1326
; Sequence 1326, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1326
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1326

```

Query Match	55.4%	Score 740.5;	DB 12;	Length 252;
Best Local Similarity	58.6%	Pred. No. 1.1e-43;		
Matches 154;	Conservation			

		Matches	56;	Indels	27;	Gaps	67;
QY	1	QVQLQQWGAAGLTKSWGTLSLTCAVSGASFSGYYWSMIRÖPPGKGLEWIGEINHRGSTTYN					
Dd	1	QVQLQQWGAAGLTKPSETLSLTCAVGGSFSGYYWSMIRÖPPGKEPWIGIKITHSGSTTYN					
QY	61	PSLDGRVTISLDTSTNQISLKLTSMTADPAVYYCARTVAGTS-----DYWGCGT					
Dd	61	PSLKSRVTMSVDSTNQFSLKLNSTPADTAVVYYCARERADYDILTGYYFGMDVWGQT					
QY	111	LVTVS <del>SGSASAP</del> TGGGGSGGGSGGGSGGGSKITLTQS <del>PAFMSATPGDKVISCK-AS</del>					
Dd	121	MVTVS-----S <del>GGGGSGGGSGGGSGGG</del> SGLTQ-PASVSGSPGGSITISCTGTS					
QY	170	RDVD--DDVNMYÖÖRPGEA <del>PIFIIEDATTLVPGISPRFSGSGYGTFDLTINNIDSEDA</del>					
Dd	168	SDVGGYNYVSMYÖQH <del>PKAKPLMIYEGSKRPSPGVENRFSGSKSGNTASLTISGLQAEDFA</del>					
QY	228	YVFCLQH-DNFPLTFGGGKTVEI 249					
Dd	228	DYCCSSYTTRSTRVFGGKITLV 250					

## RESULT 14

US-09-880-748-1360  
; Sequence 1360, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PFS23  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816

```

/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1360
/ LENGTH: 248
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-1360

```

Query Match	55.3%	Score 738.5;	DB 10;	Length 248;
Best Local Similarity	58.9%	Pred. No. 1.5e-43;		
Matches 152;	Conservation 30			

QY	1	QVQLQOMGAGLIKSWGTLISLTCAVSGA	SPSGYYTWSWIRQPPGKGIEMI	NHRGSTTN	60
		:	:	:	
Db	1	QVQLQESGPGILVKPSETTSLISCTVSGS	IRSYTWSWIRQSPGRGLEWIGHI	YHSGSTDVN	60
		:	:	:	
QY	61	PSLDGRVTISLDTSTNQISLKLTSMTA	DVAVYYCAR	-----TVAGT-----SDYWGQGT	112
		:	:	:	
Db	61	PSLRSRVTWSIDTSKNQFSLNLT	SVTADTAVYYCAR	HYDVLTGSYLQAFDVMGCGT	120
		:	:	:	
QY	113	TVSSGSASAP	TGGGGSGGGSGGGSGGGSGGSKTIL	TQSPAFMSATPGDKVSI	SCKASRDV 172
		:	:	:	
Db	121	TVSS-----	GGGGSGGGSGGGSGGGSGG	-----ALDILQLTQSP	SSLASVGDRTVITCRASQSI 170
		:	:	:	
QY	173	DDDVNMYYQRPGEAP	IFIIEDATTLVPGISPRFSGSGYGT	DFTLTINNI	DSEDAAYFCL 232
		:	:	:	
Db	171	GRYLNMYQOKPGRAP	RLLI	FVTSSLHSDVPSRFSGSGGT	DFSLTISNLQPEDFATYYCQ 230
		:	:	:	
QY	233	QHDFNPLTFGGG	TKVEIK	250	
		:	:	:	
Db	231	QSYTDP	-TFGGGTRLEIK	247	

RESULT 15

```

US-10-293-418-1360
; Sequence 1360, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1360
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1360

```

	Query Match	55.3%;	Score 738.5;	DB 12;	Length 248;	
	Best Local Similarity	58.9%;	Pred. No. 1.5e-43;			
	Matches 152;	Conservative 30;	Mismatches 57;	Indels 19;	Gaps 5;	
OY	1 QVQLQGWAGLTKSWGTSILTCAVSGASFSGYYWMIROBPCKGLEWIGEINHRRGSTTNN	60				
	:       :       :       :       :       :					
Dd	1 QVQLQGSPGLVKPSETLSISCTVSGSIRSYWSWIRQSPGRGLEWIGHIYHSGSTDYN	60				
OY	61 PSIDGRTVISLDSTNQISLKLTSMATAADTAIVYYCAR---TVAGT---SDYWGGGTLY	112				
	:       :       :       :       :       :					
Dd	61 PSLRSRVMTSIDTSKNQFSLNLTSVTAADTAIVYYCARDHYDVLTGSYLQAFDVMWGQTLY	120				
OY	113 TVSSGSASAPTTGGSGSGGGSGGGSKTTLTQSPAFMSATPGDKVISISKASRDV	172				
	:       :       :       :					
Dd	121 TVSS-----GGGSGGGSGGGSG--ALDIQLTQSPSSLASAVGDRTVITCRASQSI	170				
OY	173 DDDVNMYQQRPGEAFPIIEDATTLVPGISPRFSGSGYTDFTLTINNIDSEDAAYFCFL	232				
	:       :       :       :       :       :       :					
Dd	171 GRYLNMYQQKPKRAPRLLIFVTSSLHSADVPSRFSGSGSGTDFTLTISNLQPEDFAITYCQ	230				
OY	233 QHDNFPLTFGGGTKEIK	250				
	- - - - -               :       :					
Dd	231 QSYPD-TFGGTRLEIK	247				

Search completed: May 13, 2004, 15:43:31  
Job time : 37.0146 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:50:27 ; Search time 11.2864 Seconds  
(without alignments)  
2130.694 Million cell updates/sec

Title: US-10-072-301-21

Perfect score: 1336

Sequence: 1 QVQLQQWGAGLLKSWGTLSTL.....CLQHDNFPPLTFGGGTKVEIK 250

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pirl:\*  
2: pirl2:\*  
3: pirl3:\*  
4: pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	611	45.7	249	2	S41374	single chain Fv an
2	601.5	45.0	268	2	A56446	Ig heavy chain V r
3	532	39.8	233	2	JC5322	p53 specific singl
4	506	37.9	231	2	B23746	Ig Fab region IV-J
5	502.5	37.6	140	2	A49045	Ig heavy chain V r
6	498.5	37.3	143	2	B49028	Ig heavy chain V-I
7	490	36.7	140	2	S78052	Ig heavy chain pre
8	478	35.8	126	2	S47010	Ig heavy chain V4.
9	468	35.0	115	1	K3HU15	Ig kappa chain pre
10	452	33.8	146	1	G1HUH2	Ig heavy chain pre
11	442.5	33.1	122	2	JL0047	Ig heavy chain V r
12	439	32.9	97	2	S26898	Ig heavy chain V r
13	436.5	32.7	140	2	I37782	Ig variable region
14	431.5	32.3	130	2	S31690	Ig heavy chain V r
15	431	32.3	129	2	S44114	Ig heavy chain V r
16	430	32.2	97	2	S14474	Ig heavy chain V r
17	429	32.1	97	2	G34964	Ig heavy chain V-I
18	429	32.1	145	2	S78055	Ig heavy chain pre
19	425.5	31.8	114	2	I72667	cold agglutinin FS
20	420	31.4	118	2	S24443	Ig heavy chain V r
21	419.5	31.4	147	2	S13519	Ig heavy chain V r
22	418	31.3	139	2	S31586	Ig heavy chain V r
23	416	31.1	220	2	A49444	Ig gamma-1 heavy c
24	415.5	31.1	155	2	S31511	Ig heavy chain - h
25	414	31.0	97	2	S26805	Ig heavy chain V r
26	413.5	31.0	155	2	S31512	Ig heavy chain - h
27	411.5	30.8	123	2	S30530	Ig heavy chain V r
28	410	30.7	137	2	S31676	Ig heavy chain V r
29	409.5	30.7	134	2	S54906	Ig heavy chain V r

30	409	30.6	97	2	JH0428	Ig gamma chain V r
31	408	30.5	130	2	S30534	Ig heavy chain V r
32	406	30.4	118	2	S20780	Ig heavy chain V r
33	405.5	30.4	121	2	S44113	Ig heavy chain V r
34	404	30.2	97	2	S26806	Ig heavy chain V r
35	401.5	30.1	139	2	S31696	Ig heavy chain V r
36	400.5	30.0	127	2	S19668	Ig heavy chain V r
37	398.5	29.8	135	2	S78051	Ig heavy chain pre
38	396.5	29.7	146	2	S09711	Ig heavy chain V r
39	393	29.4	97	2	S26808	Ig heavy chain V r
40	391.5	29.3	123	2	S30529	Ig heavy chain V r
41	385.5	28.9	146	2	S09710	Ig heavy chain V r
42	385	28.8	106	2	S37454	Ig mu chain - huma
43	385	28.8	139	2	A41287	Ig heavy chain pre
44	384	28.7	97	2	S12416	Ig heavy chain V r
45	383.5	28.7	140	2	A24770	hypothetical hybr

ALIGNMENTS

RESULT 1

S41374  
single chain Fv antibody - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C:Accession: S41374  
R:Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.  
submitted to the EMBL Data Library, January 1994  
A:Description: Construction and functional characterization of a single chain Fv antibod  
A:Reference number: S41374  
A:Accession: S41374  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-249 <ART>  
A:Cross-references: EMBL:Z29480

Query Match 45.7%; Score 611; DB 2; Length 249;  
Best Local Similarity 48.1%; Pred. No. 2.3e-32;  
Matches 124; Conservative 39; Mismatches 75; Indels 20; Gaps 4;

Qy	1	QVQLQQWGAGLLKSWGTLSTLTCAVSGASFGYWSWIRQPGKLEWIGEI-NHRGSTTY 59
Db	1	QVQLQSGAELVRPGASVKLSCTASGFNFKDYLHWVKQRPKGLFIARIAPASGNVXY 60
Qy	60	NPSLDGRVTISLDTSTNQISLKLTSMTAADTAVYYCAR--TVAGTSDYWGQGLTVTVSSG 117
Db	61	VPRFQPKATITADTSSNTAYLLSLTSEDTAVYYCARRDITLSLGYWGQGSTVTVS-- 118
Qy	118	SASAPRTGGSGSGGSGGSGGSKTTLTQSPAFMSATPGDKVISISCKASR-----DV 172
Db	119	-----SRGGSGGGSGGSGGSDIELTQSPSPVVPIPGESVISICRSSKSLYSDG 168
Qy	173	DDVVMYQQRPGEPAPIFIIEDATTLVPGISPRFSGSGYGTDFLLTINNIDSEDAAYFCL 232
Db	169	DSYLFWMFLQRPQOSPQLLYRMSNLASGVPPDRFSGSGGTFTLIRISVBAEDVGVTYCM 228
Qy	233	QHDNFPPLTFGGGTKVEIK 250
Db	229	QHREYPLTFGAGTKLELK 246

RESULT 2

A56446  
Ig heavy chain V region (3H-3H bcFv) - mouse (strain BALB/C)  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996  
C:Accession: A56446  
R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.  
J. Biol. Chem. 270, 7829-7835, 1995  
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally identi  
A:Reference number: A56446; MUID:95229583; PMID:7713873  
A:Accession: A56446

A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-268 <TAN>  
A:Cross-references: GB:U20617  
C:Keywords: heterotetramer; immunoglobulin

Query Match 45.0%; Score 601.5; DB 2; Length 268;  
Best Local Similarity 48.8%; Pred. No. 1e-31;  
Matches 123; Conservative 41; Mismatches 73; Indels 15; Gaps 4;  
QY 1 QVQLQOWGAGLLKSWGTLSTLCAVSGASFSGYWMSWIRQPPGKLEWIGEINHRGSTTY 59  
DB 3 QVQLQESGAEIVKPGASVKLSCTTSGFNIKDTYMAWVKQRPQGLEWIGRIAPANGITKY 62  
QY 60 NPSLDGRVTISLDTSTNQISLKLTSMTADTAIVYCAR-TVAGTSDYWGQGLTVTVSSGS 118  
DB 63 DPKFGKATIAADTSSNTAYLQLSLTSEDTAVYICASYLTRYENYWGQGLTVTVS--- 119  
QY 119 ASAPTGGGSGGGSGGGSGGGSKTTLTQSPAFMSATPGDKVISCKASRDVDDVNM 178  
DB 120 -----SGGGSGGGSGGGSGGGSDIELTQSPAIMSASLGEKVTMSCRASSSV-NFIYW 169  
QY 179 YQORPGEAFIILEDATTLVPGISPRFSGSGYGTDTFTLTINNIDSEDAAYFCLQHDNFP 238  
DB 170 YQOKSDASPKLMVYYTSHLPQVPARFSGSGSGNSYSLTSSMEGEDAATYYCCQQTSSP 229  
QY 239 LTFGGGTKEIK 250  
DB 230 FTFGSGTKLEIK 241

RESULT 3

p53 specific single-chain antibody Pab421 - human  
JC5322  
C/Species: Homo sapiens (man)  
C/Date: 15-May-1997 #sequence\_revision 15-May-1997 #text\_change 18-Jul-1997  
C/Accession: JC5322  
R/Jannot, C.B.; Hynes, N.E.  
Biochem. Biophys. Res. Commun. 230, 242-246, 1997  
A/Title: Characterization of scFv-421, a single-chain antibody targeted to p53.  
A/Reference number: JC5322; MUID:97168950; PMID:9016757  
A/Accession: JC5322  
A:Molecule type: mRNA  
A:Residues: 1-233 <JAN>  
A:Experimental source: hybridoma cell  
C/Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 39.8%; Score 532; DB 2; Length 233;  
Best Local Similarity 45.6%; Pred. No. 2.4e-27;  
Matches 114; Conservative 40; Mismatches 74; Indels 22; Gaps 6;  
QY 5 QQWGAAGLLKSWGTLSTLCAVSGASFSGYWMSWIRQPPGKLEWIGEIN-HRGSTTYNPSL 63  
DB 1 QESGAELVRSASVYKLSCTTSGFNINDYMHVWKRPQGLEWIGRIDPENGDADMTRSS 60  
QY 64 DGRVTISLDTSTNQISLKLTSMTADTAIVYCAR-TVAGTSDYWGQGLTVTVSSGSASAPT 123  
DB 61 GVKATMTADTSSNTAYLQLSLTSEDTAVYCN--AG-MDYWGQGLTVTVS----- 108  
QY 124 GGGSGGGSGGGSGGGSGGGSKTTLTQSPAFMSATPGDKVISCKASRDVDD---VNMWY 179  
DB 109 -----SGGGSGGGSGGGSGGGSDIELTQSPALAVSLGQRATISCRASKSVSTSGYSYMAWN 164  
QY 180 QORPGEAFIILEDATTLVPGISPRFSGSGYGTDTFTLTINNIDSEDAAYFCLQHDNFP 239  
DB 165 QOKPQPPRLILYLVSNLSGVPARFSGSGSGTDTFTLNHPVEEDATYYC-QHIRELT 223  
QY 240 TFGGGTKVEI 249  
DB 224 RSEGGTKLEI 233

RESULT 4

B23746  
Ig Fab region IV-J(H4)-C (KAV cold agglutinin) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
C/Accession: B23746  
R/Leon, J.; Ghiso, J.; Goni, F.; Frangione, B.  
J. Biol. Chem. 266, 2836-2842, 1991  
A/Title: The primary structure of the Fab fragment of protein KAV, a monoclonal immuno-  
A/Reference number: A23746; MUID:91131575; PMID:1993660  
A/Accession: B23746  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-231 <LEO>  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
F,140-209/Domain: immunoglobulin homology <IMM>

Query Match 37.9%; Score 506; DB 2; Length 231;  
Best Local Similarity 80.2%; Pred. No. 1.1e-25;  
Matches 101; Conservative 4; Mismatches 17; Indels 4; Gaps 1;  
QY 2 VQLQOWGAGLLKSWGTLSTLCAVSGASFSGYWMSWIRQPPGKLEWIGEINHRGSTTYNP 61  
DB 1 VQLQOWGAGLLKPSSETLSLTCAVYGGSFSDYWMSWIRQPPGKLEWIGEINHSSTYNP 60  
QY 62 SLDRVTISLDTSTNQISLKLTSMTADTAIVYCAR-TVAGTSDYWGQGLTVTVSSG 117  
DB 61 SLKSRVTISVDTSKNQFSLKLSVTADTAIVYCARPPHDTSGHYWNYWGQGLTVTVSSG 120  
QY 118 SASAPT 123  
DB 121 SASAPT 126

RESULT 5

A49045  
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999  
C/Accession: A49045  
R/Grillot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silverma  
Eur. J. Immunol. 22, 1781-1788, 1992  
A/Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes 1 b1  
A/Reference number: A49045; MUID:92324290; PMID:1623923  
A/Accession: A49045  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-140 <GRI>  
A:Cross-references: GB:S39381; NID:9250899; PIDN:AAB22441.1; PID:9250900  
A/Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBIIP:108089)  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F,34-116/Domain: immunoglobulin homology <IMM>

Query Match 37.6%; Score 502.5; DB 2; Length 140;  
Best Local Similarity 80.2%; Pred. No. 1.1e-25;  
Matches 97; Conservative 5; Mismatches 14; Indels 5; Gaps 1;  
QY 1 QVQLQOWGAGLLKSWGTLSTLCAVSGASFSGYWMSWIRQPPGKLEWIGEINHRGSTTYN 60  
DB 20 QVQLQOWGAGLLKPSSETLSLTCAVYGGSFSDYWMSWIRQPPGKLEWIGEINHSSTYNY 79  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAIVYCAR-TVAGTSDYWGQGLTVTVS 115  
DB 80 PSLSKRVTVISVDTSKNQFSLKLSVTADTAIVYCARGGFAATIVESFDYWGQGLTVTVS 139  
QY 116 S 116  
DB 140 S 140

RESULT 6

B49028  
Ig heavy chain V-IV region - human (fragment)





F;44-54/Region: complementarity-determining 1  
F;55-69/Region: framework 2  
F;70-76/Region: complementarity-determining 2  
F;77-108/Region: complementarity-determining 3  
F;109-115/Region: complementarity-determining 3  
F;43-108/Disulfide bonds: #status predicted

Query Match 35.0%; Score 468; DB 1; Length 115;  
Best Local Similarity 87.5%; Pred. No. 1.4e-23;  
Matches 84; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 143 SKTTLTQSPA FMSATP GDKVSI SCASRDVDDVNMVQQRPGEA PFIETDATTLPGIS 202  
Db :|||||  
20 AETTLTQSPA FMSATP GDKVNI SCASQDIDDDNMVQQRPGEA AIFIIQEATTLVPGIP 79  
:|||||

QY 203 PRFSGSGYGTDFTLTINNISEDAAYYFCLQHDNFP 238  
Db |||||||  
80 PRFSGSGYGTDFTLTINNISEDAAYYFCLQHDNFP 115  
|||||

RESULT 10

GIH0H2

Ig heavy chain precursor V-II region (ARH-77) - human  
C/Species: Homo sapiens (man)

C/Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 02-Sep-1997  
C/Accession: A02101

R;Kudo, A.; Ishihara, T.; Nishimura, Y.; Watanabe, T.  
Gene 33, 181-189, 1985

A/Title: A cloned human immunoglobulin heavy chain gene with a novel direct-repeat seque

A/Reference number: A02101; MUID:85205332; PMID:3922855  
A/Accession: A02101  
A/Molecule type: mRNA

A/Residues: 1-146 <KUD>  
A/Note: the sequence was determined from the differentiated gene

C/Genetics: the authors translated the codon GGG for residue 17 as Arg  
A/Note: the authors translated the codon GGG for residue 17 as Arg

A/Genes: GDB:IGHV@

A/Cross-references: GDB:128528; OMIM:147070  
A/Map position: 14q32.33-14q32.33

A/Introns: 16/3  
C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-146/Product: Ig heavy chain V-II region (ARH-77) #status predicted <MAT>

F;20-117/Region: V segment  
F;35-117/Domain: immunoglobulin homology <IMM>  
F;118-127/Region: D segment  
F;128-146/Region: J segment

F;42-115/Disulfide bonds: #status predicted

Query Match 33.8%; Score 452; DB 1; Length 146;  
Best Local Similarity 72.2%; Pred. No. 1.9e-22;  
Matches 91; Conservative 6; Mismatches 19; Indels 10; Gaps 2;

QY 1 QVQLQQWAGAGL KSWGTL SLTCAVSGASFSGYWMSWIRQPPGKGLEWIGETINHRGSTTYN 60  
Db |||||||  
21 QVQLQQWAGAGL KPSSETL SLTCAVFGSFGYMSWIRQPPGKLEWIGETINHRGSTNYK 80  
:|||||

QY 61 PSLDGRVTISLDTSTNQISLKLTSMTAADTA VYVCARTV--AGTS-----DYMGGGT 110  
Db |||||||  
81 TSLKSRVTISLDTSKNLFSLKLSVTAAADTA VYVCARGILRGWMDVDYGYGMDVMGGGT 140  
:|||||

QY 111 LVTVSS 116  
Db |||||||  
141 TVTVSS 146  
|||||

RESULT 11

JU0047

Ig heavy chain V region precursor (clone CR18) - human  
C/Species: Homo sapiens (man)

C/Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 16-Aug-1996  
C/Accession: JU0047

R;Baer, R.; Forester, A.; Lavenir, I.; Rabbits, T.H.  
J. Exp. Med. 167, 2011-2016, 1988  
A/Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new

A/Reference number: JU0047; MUID:88258392; PMID:3133445  
A/Accession: JU0047  
A/Molecule type: mRNA  
A/Residues: 1-122 <BAE>  
A/Experimental source: T-cell line RPMI 8402  
A/Note: the authors translated the reading frame which extends to the stop codon; the s

Query Match 33.1%; Score 442.5; DB 2; Length 122;  
Best Local Similarity 84.3%; Pred. No. 6.4e-22;  
Matches 86; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 1 QVQLQQWAGAGL KSWGTL SLTCAVSGASFSGYWMSWIRQPPGKLEWIGETINHRGSTTYN 60  
Db |||||||  
9 QVQLQQWAGAGL KPSSETL SLTCAVYGGSGYWMSWIRQPPGKLEWIGETINHRGSTTYN 68  
:|||||

QY 61 PSLDGRVTISLDTSTNQISLKLTSMTAADTA VYVCAR--TVAG 101  
Db |||||||  
69 PSLKSRVTISVDTSKNQPSLKLSSVTAAADTA VYVCARGTVRG 110  
:|||||

RESULT 12

S26898

Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)  
C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S26898; S12420

R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992

A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A/Reference number: S26885; MUID:93021117; PMID:1404388  
A/Accession: S26898

A/Molecule type: DNA  
A/Residues: 1-97 <TOM>

A/Cross-references: EMBL:Z12363; NID:g32944; PIDN:CAA78233.1; PID:g32945  
A/Experimental source: clone DP-63

R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.  
EMBO J. 8, 3741-3748, 1989

A/Title: The smaller human V(H) gene families display remarkably little polymorphism.

A/Reference number: S09421; MUID:90059975; PMID:2511001  
A/Accession: S12420

A/Status: translation not shown  
A/Molecule type: DNA

A/Residues: 1-97 <SAN>  
A/Cross-references: EMBL:X56364

A/Experimental source: V(H)4.2  
C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin  
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 32.9%; Score 439; DB 2; Length 97;  
Best Local Similarity 85.6%; Pred. No. 8.5e-22;  
Matches 83; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 QVQLQQWAGAGL KSWGTL SLTCAVSGASFSGYWMSWIRQPPGKLEWIGETINHRGSTTYN 60  
Db |||||||  
1 QVQLQQWAGAGL KPSSETL SLTCAVYGGSGYWMSWIRQPPGKLEWIGETINHRGSTTYN 60  
:|||||

QY 61 PSLDGRVTISLDTSTNQISLKLTSMTAADTA VYVCAR 97  
Db |||||||  
61 PSLKSRVTISVDTSKNQPSLKLSSVTAAADTA VYVCAR 97  
:|||||

RESULT 13

I37782

Ig variable region (VDJ) (clone T23-9) - human (fragment)  
C/Species: Homo sapiens (man)



C/Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
C/Accession: I37782; S25476  
R/Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A/Title: Somatic diversification in the heavy chain variable region genes expressed by thymocytes  
A/Reference number: A36876; MUID:94119917; PMID:8290556  
A/Accession: I37782  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-140 <RES>  
A/Cross-references: EMBL:X67906; NID:g33582; PIDD:CAA48104.1; PID:g33583  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
F;46-128/Domain: immunoglobulin homology <IMM>

	Query Match	Best Local Similarity	Matches	Score	DB 2;	Length	Gaps
Qy	1	QVQLQQWAGLLKSWGTLSTLTCAVSGASFSGYYWSWIROPFGKLEWIGEINHRGSTTYN	87; Conservative	32.7%;	436.5;	140;	1;
Dd	20	QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIROPFGKLEWIGIYYSGSTYNN	8; Mismatches	71.9%;	Pred. No. 1.8e-21;	Indels 5;	
Qy	61	PSLDGRVTISLDTSTNQISLKLTSMTADTAVVYYCARTVAGT-----SDYWGGGLTVTVS					
Dd	80	PSLKSRTVISVDTSKNQFSLKLSSVTADTAVVYYCARHNSSSWYGRYFDYWGQGTLVTVS					
Qy	116	S 116					
Dd	140	S 140					

RESULT 14  
S31690

Ig heavy chain V region - human (fragment)

C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31690  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31690  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-130 <CUI>  
A;Cross-references: EMBL:214199; NID:g30984; PIDN:CA78568.1; PID:g30985  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;20-102/Domain: immunoglobulin homology <IMM>

Query Match	32.3%	Score 431.5;	DB 2;	Length 130;
Best Local Similarity	68.8%;	Pred. No. 3.5e-21;		
Matches	88;	Conservative	7;	Mismatches 18;
			Indels	15;
			Gaps	2;

QY	1 QVQLQQMGAGLLKSKWGTLSLTCAVSGASFSGYYMSWIRQPPGKGLEWIGELINHRGSTTYN	60
	:	
Db	6 QVQLQESGPGLVKPSSETLSLTCTVSGSISISYYMSWSRQPPGKGLEWIGIYISGSTNYN	65
QY	61 PSLDGRVTISLDSTSTNQISLKLTSMTADTAIVYYCARTVAGTS-----DYWGQ	108
	:	
Db	66 PSLKSRVTISVDTSKNQFSLKLSSVTADTAIVYYCAR---GSSVLLMFGEIYYFDYWGQ	122
QY	109 GTLVTVSS	116
Db	123 GTLVTVSS	130

## RESULT 15

**S44114**

Ig heavy chain V region - human

C;Species: Homo sapiens (man)

C:\Date: 13-Jan-1995 #sequence\_ revision 13-Jan-1995 #text\_change 24-May-2001

**C;Accession: S44114**

R; Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K. submitted to the EMBL Data Library, March 1994  
A; Description: Idiotypic vaccination against human B-cell lymphoma: rescue of vA; Reference number: S44105

A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-129 <HAW>  
A/Cross-references: EMBL:Z31579; NID:g4729668; PIDN:CAA83451.1; PID:g9405255  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
E/15-98/Domain: immunoglobulin homology <IMM>

Query Match	32.3%;	Score 431;	DB 2;	Length 129;
Best Local Similarity	69.8%;	Pred. No. 3.7e-21;		
Matches	88;	Conservative	6;	Mismatches 24; Indels 8; Gaps 2;
QY	1 QVQLQQMGAGLLKSWGTLSTLTCAVSGASF-SGYYSWMIROPPKGLEWIGEINHRGSTTY	59		
	:			
Db	1 QVQLQESGPGLVKPISGTLSTLTCAVSGSGSISSSNMWSWVRQPPKGLEWIGEIYHSGSTNY	60		
QY	60 NPSLDGRVTIISLPDSTNQISLKLTSMTADPAFVYYCART-----VAGTSDYWGOGTLY	112		
Db	61 NPSPFKSRVTIISADTSKNQFSCLKVNSVTADTAFAVYCARRNYDFWMSGGDGPFDDYWGQGTLV	120		
QY	113 TVSSGS	118		
Db	121 TVSSAS	126		

Search completed: May 13, 2004, 15:08:42  
Job time : 11.2864 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:01 ; Search time 7.03884 Seconds  
(without alignments)  
1849.388 Million cell updates/sec

Title: US-10-072-301-21  
Perfect score: 1336  
Sequence: 1 QVQLQQWAGALLKSMGTLSTL.....CLQHDNPLTFGGGTKEIK 250

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	468	35.0	115	1	KV5A_HUMAN P06315 homo sapien
2	452	33.8	146	1	HV2I_HUMAN P06331 homo sapien
3	374.5	28.0	129	1	HV2F_HUMAN P01824 homo sapien
4	365.5	27.4	117	1	HV2G_HUMAN P01825 homo sapien
5	334.5	25.0	137	1	HV46_MOUSE P01822 mus musculu
6	333	24.9	108	1	KV1Y_HUMAN P80362 homo sapien
7	330	24.7	108	1	KV1P_HUMAN P01608 homo sapien
8	326	24.4	108	1	KV1R_HUMAN P01610 homo sapien
9	317	23.7	108	1	KV1Q_HUMAN P01609 homo sapien
10	316.5	23.7	144	1	HV43_MOUSE P01819 mus musculu
11	316	23.7	108	1	KV1A_HUMAN P01593 homo sapien
12	315	23.6	108	1	KV1B_HUMAN P01594 homo sapien
13	313	23.4	108	1	KV5S_MOUSE P01652 mus musculu
14	313	23.4	128	1	KV5E_MOUSE P01637 mus musculu
15	313	23.4	149	1	KV5A_MOUSE P01633 mus musculu
16	312	23.4	108	1	KV5Q_MOUSE P01650 mus musculu
17	312	23.4	108	1	KV5T_MOUSE P01653 mus musculu
18	311.5	23.3	113	1	HV47_MOUSE P01823 mus musculu
19	310	23.2	119	1	HV37_MOUSE P01807 mus musculu
20	307	23.0	108	1	KV1G_HUMAN P01599 homo sapien
21	306	22.9	108	1	KV1M_HUMAN P01605 homo sapien
22	305	22.8	119	1	HV40_MOUSE P01810 mus musculu
23	304.5	22.8	129	1	KV3H_HUMAN P04207 homo sapien
24	304	22.8	135	1	HV02_XENLA P20957 xenopus lae
25	303	22.7	108	1	KV1V_HUMAN P04430 homo sapien
26	302	22.6	108	1	KV1C_HUMAN P01595 homo sapien
27	302	22.6	111	1	KV3N_MOUSE P01666 mus musculu
28	301.5	22.6	116	1	HV60_MOUSE P18531 mus musculu
29	301	22.5	108	1	KV5R_MOUSE P01651 mus musculu
30	300	22.5	111	1	KV3M_MOUSE P01665 mus musculu
31	299.5	22.4	117	1	HV41_MOUSE P01811 mus musculu
32	299	22.4	108	1	KV1S_HUMAN P01611 homo sapien
33	299	22.4	111	1	KV3L_MOUSE P01664 mus musculu

34	299	22.4	111	1	KV3O_MOUSE	P01667 mus musculu
35	299	22.4	119	1	HV38_MOUSE	P01808 mus musculu
36	299	22.4	129	1	KV1W_HUMAN	P04431 homo sapien
37	298	22.3	108	1	KV1O_HUMAN	P01607 homo sapien
38	298	22.3	108	1	KV5P_MOUSE	P01649 mus musculu
39	296	22.2	111	1	KV3Q_MOUSE	P01669 mus musculu
40	296	22.2	122	1	HV3A_HUMAN	P01762 homo sapien
41	294.5	22.0	117	1	HV42_MOUSE	P01812 mus musculu
42	294	22.0	122	1	HV3H_HUMAN	P01769 homo sapien
43	293.5	22.0	117	1	HV17_MOUSE	P01786 mus musculu
44	293.5	22.0	129	1	KV3L_HUMAN	P18135 homo sapien
45	293	21.9	122	1	HV20_MOUSE	P01789 mus musculu

ALIGNMENTS

```
RESULT 1
KV5A_HUMAN
ID KV5A_HUMAN STANDARD; PRT; 115 AA.
AC P06315;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V region EV15 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85242052; Pubmed=3925437;
RA Stavnezer J., Kekish O., Batter D., Grenier J., Balazs I.,
RA Henderson E., Zegers B.J.M.;
RT "Aberrant recombination events in B cell lines derived from a kappa-
RT deficient human.";
RL Nucleic Acids Res. 13:3495-3514(1985).
CC -1- MISCELLANEOUS: THIS SEQUENCE DOES NOT BELONG TO ANY OF THE
CC PREVIOUSLY DESCRIBED V-KAPPA SUBGROUPS. ALTHOUGH THE GENE IS
CC LOCATED IN THE SAME REGION AS OTHER V-KAPPA GENES, IT APPEARS TO
CC BE THE ONLY ONE OF ITS TYPE.
CC -1- MISCELLANEOUS: THE GENE WAS FOUND TO BE ABERRANTLY REARRANGED IN
CC AN INDIVIDUAL WHO DOES NOT SYNTHESIZE ANY KAPPA LIGHT CHAINS. IT
CC HAS NOT BEEN SHOWN TO BE EXPRESSED.
DR PIR; A01906; KAHU15.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 20
FT DOMAIN 1 21
FT DOMAIN 2 44
FT DOMAIN 3 55
FT DOMAIN 4 69
FT DOMAIN 5 76
FT DOMAIN 6 108
FT DOMAIN 7 109
FT DISULFID 43 108
FT NON_TER 115
SQ SEQUENCE 115 AA; 12728 MW; A5EA515BA2F11A29 CRC64;

Query Match 35.0%; Score 468; DB 1; Length 115;
Best Local Similarity 87.5%; Pred. No. 6.7e-28;
Matches 84; Conservative 10; Mismatches 2; Indels 0; Gaps 0;
OY 143 SKTLTQSPAFMSATPGDKVSIISCKASRDVDDVNMVYQDRPGEAFIFIIEDATTLVPGIS 202
:::|||||
```

Db 20 AETLTGSPAFMSATPGDKVNISCKASQDIDDDMMWYQOKPGEAIFITQEAATLVPGIP 79  
QY 203 PRFSGSGYGTDFTLTINNIDSEDAAYFYCLQHDNFP 238  
Db 80 PRFSGSGYGTDFTLTINNIDSEDAAYFYCLQHDNFP 115

## RESULT 2

HV2I\_HUMAN  
ID HV2I\_HUMAN STANDARD; PRT; 146 AA.  
AC P06331;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V-II region ARH-77 precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85205332; PubMed=3922855;  
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;  
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-  
RT repeat sequence in 5' flanking region."  
RL Gene 33:181-189(1985).  
DR PIR; A02101; GIHU2.  
DR HSSP; P01825; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT CHAIN 1 19  
FT DOMAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.  
FT DOMAIN 118 127 V SEGMENT.  
FT DOMAIN 128 146 D SEGMENT.  
FT DISULFID 42 115 J SEGMENT.  
FT NON TER 146 146 BY SIMILARITY.  
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Query Match 33.8%; Score 452; DB 1; Length 146;  
Best Local Similarity 72.2%; Pred. No. 1.3e-26;  
Matches 91; Conservative 6; Mismatches 19; Indels 10; Gaps 2;

QY 1 QVQLQOMGAGLILKSWGTLSTLCVAGSAGSFQYYSWIRQPPGKLEWIGEINRGSTTYN 60  
Db 21 QVQLQOMGAGLVKPSSETLSTLCVAFGSGFSGYYSWIRQPPGKLEWIGEINRGSTNYK 80  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTAADTAVYYCARV--AGTS-----DYWGQGT 110  
Db 81 TSLKSRVTISLDTSKVLFSKLTSYTAADTAVYYCARGLRGGMNDVDYGYGMDVWGQGT 140  
QY 111 LVTYSS 116  
Db 141 TTVVSS 146

## RESULT 3

HV2F\_HUMAN  
ID HV2F\_HUMAN STANDARD; PRT; 129 AA.  
AC P01824;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-II region WAH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.

RX MEDLINE=82222235; PubMed=6806818;  
RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;  
RT "Complete amino acid sequence of the delta heavy chain of human  
RT immunoglobulin D."  
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).  
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA  
CC PROTEIN.

CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A02099; D2HWA.  
DR HSSP; P01825; 7FAB.

DR GlycoSuiteDB; P01824;  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 113  
FT NON TER 129 129 IG-LIKE.  
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 28.0%; Score 374.5; DB 1; Length 129;  
Best Local Similarity 61.2%; Pred. No. 5.2e-21;  
Matches 79; Conservative 10; Mismatches 27; Indels 13; Gaps 3;

QY 1 QVQLQOMGAGLILKSWGTLSTLCVAGSAGF--SGYYSWIRQPPGKLEWIGEINRGSTT 58  
Db 1 RLQLQESGPGVLKPSSETLSTLCIVSGPIRTGTGYWGIRQPPGKLEWIGVYTGSIY 60  
QY 59 YNPSLDGRVTISLDTSTNQISLKLTSMTAADTAVYYCAR-----TVAGTS-----DYWG 107  
Db 61 YNPSLDGRVTISVDTSRNQPSLNLRSMSAADTAVYYCARGNPPPYDIDGTGSDGIDVWG 120  
QY 108 QGTVTVSS 116  
Db 121 QGTVTVSS 129

## RESULT 4

HV2G\_HUMAN  
ID HV2G\_HUMAN STANDARD; PRT; 117 AA.  
AC P01825;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-II region NEMW.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=77242302; PubMed=407927;  
RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;  
RT "Amino acid sequence of the VH region of a human myeloma  
RT immunoglobulin (IgG New)."  
RL Biochemistry 16:3412-3420(1977).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.  
RX MEDLINE=78066916; PubMed=618887;  
RA Saul F.A., Amzel L.M., Poljak R.J.;  
RT "Preliminary refinement and structural analysis of the Fab fragment  
RT from human immunoglobulin new at 2.0-A resolution."  
RL J. Biol. Chem. 253:585-597(1978).  
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA  
CC PROTEIN.



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CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90404; G1HUM.
DR PDB; 7FAB; 31-JAN-94.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
FT DOMAIN 1 111 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT TURN 30 31
FT STRAND 33 39
FT TURN 41 42
FT STRAND 46 51
FT TURN 53 54
FT STRAND 57 59
FT HELIX 61 63
FT TURN 64 66
FT STRAND 67 72
FT TURN 73 76
FT STRAND 77 82
FT HELIX 87 89
FT STRAND 91 98
FT STRAND 104 107
FT STRAND 111 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;

Query Match 27.4%; Score 365.5; DB 1; Length 117;
Best Local Similarity 60.7%; Pred. No. 2.1e-20;
Matches 71; Conservative 20; Mismatches 25; Indels 1; Gaps 1;

Qy 1 QVQLQOMGAGLLKSWGTLSTLCAVSGASFSGYVSWITROPKGLWIGELINHRGSTYNN 60
Db 1 QVQLLEQSGPGLVPRSQTLSTLCTVSGSTFSDNYTWTWRQPPGRGLEWIGYVFYHGTSDT 60
Qy 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAVYYCART-VAGTSDYWGQGLVTVSS 116
Db 61 TPLRSRVMTMLVDTSKNQFSLRLSSVTAADTAVYYCARNLIAGCIDVWGQGLVTVSS 117

RESULT 5
HV46_MOUSE
ID HV46_MOUSE STANDARD; PRT; 137 AA.
AC P01822;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig heavy chain V region MOPC 315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89238351; PubMed=2497341;
RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
RT gene segment.";
RL Mol. Immunol. 26:431-434(1989).
RN [2]
RP SEQUENCE OF 1-31.
RX MEDLINE=78094475; PubMed=414225;
RA Jilka R.L., Pestka S.;
RT "Amino acid sequence of the precursor region of MOPC-315 mouse

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RT immunoglobulin heavy chain.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977).  
 RN [3]  
 RP SEQUENCE OF 1-21.  
 RX MEDLINE=79148758; PubMed=428562;  
 RA Schechter I., Wolf O., Zemell R., Burstein Y.;  
 RT "Structure and function of immunoglobulin genes and precursors.";  
 RL Fed. Proc. 38:1839-1845 (1979).  
 RN [4]  
 RP SEQUENCE OF 19-136.  
 RX MEDLINE=74170779; PubMed=4524622;  
 RA Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;  
 RT "Amino-acid sequence of the variable region of the heavy (alpha)  
 chain of a mouse myeloma protein with anti-hapten activity.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127 (1974).  
 RN [5]  
 RP REVISION TO 53.  
 RX MEDLINE=77244979; PubMed=268248;  
 RA Hood L., Margolies M.N., Givol D., Zakut R.;  
 RL Unpublished results, cited by:  
 RL Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;  
 RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637 (1977).  
 CC -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA  
 CC PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.

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DR EMBL; M27638; AAA61337.1; -.  
DR EMBL; X07880; CAA30727.1; -.  
DR PIR; P10102; AVMS35.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; ig; 1.

DR PROSITE; PS50835; IG\_LIKE; 1.

[illegible]

11	20	IG HEAVY CHAIN V REGION MOPC 315.
FT	19	137
CHAIN		

FT	DOMAIN	COMPLEMENTARITY-DETERMINING-1.
1	DOMAIN	COMPLEMENTARITY-2.
49		
54		

FT	DOMAIN	COMPLEMENTARITY-DETERMINING-2.
69	84	

FT	DOMAIN	117	126	COMPLEMENTARITY-DETERMINING-3.
F1	DOMAIN	83	118	INTERDOMAIN-3.

FT	DISU.FID	40	114	BY SIMILARITY.
F1	DOUAIN	127	137	EXTRAMORNA-4.

FT	CONFLICT	15	15	G -> H (IN REF. 2).
F1	CONFLICT	15	15	G -> G8 (IN REF. 1, CASSO/2/1)
F1	CONFLICT	15	15	G -> G8 (IN REF. 1, CASSO/2/1)

FT	CONFLICT	102	102	N -> D (IN REF. 4).
F1	CONFLICT	11	18	G1 -> 18 (IN REF. 2/)

	CONFID	NON TER	FT	MISSING (IN REF. 1)
F1	123	123		
FT	137	137		

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Query Match	25.0%;	Score 334.5;	DB 1;	Length 137;
Best Local Similarity	57.4%;	Pred. No. 4.7e-18;		
Matches 70; Conservative	14;	Mismatches 27;	Indels 11;	Gaps 3;

```

Oy      2 VQLOQWAGLLKSWGTLSTCAVSGASF-SCYYWSMIRQPPGKGLEWIGELNHRGSTTYN 60
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      20 VQLOESGPGLVKPSQSLSTCSVTGYSTSGTFMNWIRQFPGNKLEWLGFICKDGSNGYN 79

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```
Qy      61 PSLDGRVTISLDTSTNQSLKLTSMATDAVYVCARTVAGTS-----DYWGCGTLTV    114  
        ||| :||: ||| | ||| | ||| : ||| : ||| : ||  
Db      80 PSLKNRVSITRDTSENQFLKLNVSFTTEDTATYYC---AGNDNHL YFDYWGCGSTLLTV   135
```



Db 4 MTQSPSSLSASVGDRTVITCQASQDISIFLNWYQOKPGKAPKLLIYDASKLEAGVPSRFS 63

Qy 207 GSGYGTDFLTINNIDSEDAAYFYCLOHNPFLTGGGTKEIK 250

Db 64 GTGSGTDFLTITSLQPEDIATYCCQFDNLPFLTGGGTKEIK 107

RESULT 8

KVIR\_HUMAN

ID\_KVIR\_HUMAN STANDARD; PRT; 108 AA.

AC P01610;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-I region WEA.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=83273707; PubMed=6410398;

RA Goni F., Frangione B.;

RT "Amino acid sequence of the Fv region of a human monoclonal IgM (protein WEA) with antibody activity against 3,4-pyruvylated

RT galactose in Klebsiella polysaccharides K30 and K33.";

RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

CC -I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH WALDENSTROM'S MACROGLOBULINEMIA.

CC PIR; A01876; KIHUWE.

DR HSSP; P80362; 1WTL.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG\_LIKE; 1.

KW Immunoglobulin V region; Monoclonal antibody.

FT DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 35 49 FRAMEWORK-2.

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 57 88 FRAMEWORK-3.

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 98 107 FRAMEWORK-4.

FT DISULFID 23 88 BY SIMILARITY.

FT NON TER 108 108

SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match 24.4%; Score 326; DB 1; Length 108;

Best Local Similarity 56.7%; Pred. No. 1.5e-17;

Matches 59; Conservative 23; Mismatches 22; Indels 0; Gaps 0;

Qy 147 LTQSPAFMSATPGDKVISICKASRDVDDVNMWYQORPGEAPFIIEDATTLVPGISPRFS 206

Db 4 MTQSPSSLSASVGDRTVITCQASQDIRKHLNMYDQKPGKAPRLLIYGASTLETGVPSPRFS 63

Qy 207 GSGYGTDFLTINNIDSEDAAYFYCLOHNPFLTGGGTKEIK 250

Db 64 GSGSGTDFLTITSLQPEDFATYCYCLOYSFPWTFGGGTKEIVK 107

RESULT 9

KV1Q\_HUMAN

ID\_KV1Q\_HUMAN STANDARD; PRT; 108 AA.

AC P01609;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-I region Scw.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=75059271; PubMed=4435756;

RA Eulitz M., Hilschmann N.;

RT "The primary structure of a human immunoglobulin L-chain of kappa-type (Bence-Jones protein Scw.), II: The chymotryptic peptides and the complete amino acid sequence.";

RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).

CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.

CC -I- MISCELLANEOUS: This is a Bence-Jones protein.

DR PIR; A01875; KIHUSW.

DR HSSP; P01607; 1REI.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG\_LIKE; 1.

KW Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 35 49 FRAMEWORK-2.

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 57 88 FRAMEWORK-3.

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 98 107 FRAMEWORK-4.

FT DISULFID 23 88 BY SIMILARITY.

FT NON TER 108 108

SQ SEQUENCE 108 AA; 11764 MW; 32CECDDDF9644414 CRC64;

Query Match 23.7%; Score 317; DB 1; Length 108;

Best Local Similarity 54.8%; Pred. No. 6.9e-17;

Matches 57; Conservative 22; Mismatches 25; Indels 0; Gaps 0;

Qy 147 LTQSPAFMSATPGDKVISICKASRDVDDVNMWYQORPGEAPFIIEDATTLVPGISPRFS 206

Db 4 MTQSPSSLSASVGDRTVITCQASQDIRKHLNMYDQKPGKAPRLLIYGASTLETGVPSPRFS 63

Qy 207 GSGYGTDFLTINNIDSEDAAYFYCLOHNPFLTGGGTKEIK 250

Db 64 GSGSGTDFLTITSLQPEDIGNYCCQYDNVPITFGGTKEVKNK 107

RESULT 10

HV43\_MOUSE

ID\_HV43\_MOUSE STANDARD; PRT; 144 AA.

AC P01819;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V region MOPC 141 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=81012133; PubMed=6774258;

RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;

RT "Two types of somatic recombination are necessary for the generation of complete immunoglobulin heavy-chain genes.";

RL Nature 286:676-683(1980).

CC -I- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.

CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.



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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; V00768; CAA24149.1; -  
DR PIR; A02094; G2MS14.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
DR Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.  
FT DOMAIN 20 130 IG-LIKE.  
FT NON TER 144 144  
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match 23.7%; Score 316.5; DB 1; Length 144;  
Best Local Similarity 52.0%; Pred. No. 1e-16;  
Matches 65; Conservative 16; Mismatches 35; Indels 9; Gaps 1;

QY 1 QVQLQWAGLKLKSGTSLTCAVSGASFGSYWYMWIRPPGKLEWIGEINRGSTTYN 60  
DB 20 QVQLKESGPGLVAPSSQSLITCTVSGFSLTGYGVNWRQPPGKLEWLTGTMNGSTDYN 79  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAIVYVCARTVA-----GTSIYWGQGL 111  
DB 80 STLKSLRTITKDNSSKQVFLKMSLQTDRTARYCASVSIYYGRSDKYFTLDYWGQGT 139  
QY 112 VTWSS 116  
DB 140 VTWSS 144

## RESULT 11

KV1A HUMAN  
ID KV1A HUMAN STANDARD; PRT; 108 AA.  
AC P01593;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region AG.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE.  
RX MEDLINE=69234734; PubMed=4893682;  
RA Tiltani K., Shinoda T., Putnam F.W.;  
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The  
RT complete sequence and the location of the disulfide bridges.";  
RL J. Biol. Chem. 244:3550-3560(1969).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
DR PIR; A01861; K1HUG.  
DR HSSP; P01607; IREI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DISULFID 98 107 FRAMEWORK-4.  
FT NON TER 23 88  
FT SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0CAF CRC64;

Query Match 23.7%; Score 316; DB 1; Length 108;  
Best Local Similarity 54.8%; Pred. No. 8.1e-17;  
Matches 57; Conservative 22; Mismatches 25; Indels 0; Gaps 0;

QY 147 LTQSPAFMSATPGDKVISICKASRDVDDVWYQRPGEAPFIIDATTVPGISPRFS 206  
DB 4 MTQSPSLASVGDRTITQASQDINHLYNQGPCKAPKILYDASNLETGVPSPRFS 63  
QY 207 GSGYGTDTLTINNIDSEDAAYFCLQHDNFPFLFGCGTKVEIK 250  
DB 64 GSGGFTDTFTISGLQPEDIAITYCQGYDTLPRTFGQGTKEIK 107

## RESULT 12

KV1B HUMAN  
ID KV1B HUMAN STANDARD; PRT; 108 AA.  
AC P01594;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig kappa chain V-I region AU.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE.  
RX MEDLINE=72189444; PubMed=5028201;  
RA Schlechl H., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
RL protein Au).";  
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).  
RN [2]

RP X-RAY CRYSTALLOGRAPHY.  
RX MEDLINE=77022433; PubMed=1234024;  
RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,  
RT "The structure determination of the variable portion of the  
RT Bence-Jones protein Au.";  
RL Biophys. Struct. Mech. 1:139-146(1975).  
CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY  
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V  
CC REGION OF THE KAPPA CHAIN REI.  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
DR PIR; A91653; K1HUV.  
DR PDB; 1UV5; 30-JAN-02.

DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.







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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:31 ; Search time 33.6165 Seconds  
(without alignments)  
2346.453 Million cell updates/sec

Title: US-10-072-301-21  
Perfect score: 1336  
Sequence: 1 QVQLQQWGAGLLKSWGTLSTL.....CLQHDFPLTFGGGKVEIK 250

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: SPTRMBL.25:\*
- 2: sp\_archaea:\*
- 3: sp\_bacteria:\*
- 4: sp\_fungi:\*
- 5: sp\_human:\*
- 6: sp\_invertebrate:\*
- 7: sp\_mammal:\*
- 8: sp\_mhc:\*
- 9: sp\_organelle:\*
- 10: sp\_phage:\*
- 11: sp\_plant:\*
- 12: sp\_rodent:\*
- 13: sp\_virus:\*
- 14: sp\_vertebrate:\*
- 15: sp\_unclassified:\*
- 16: sp\_virus:\*
- 17: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	667	49.9	298	11	Q9QYF0	Q9QYF0 mus musculu
2	603.5	45.2	241	11	Q921A6	Q921A6 mus musculu
3	585.5	43.8	243	11	Q7TQM2	Q7TQM2 mus musculu
4	509	38.1	588	4	Q8WUX4	Q8WUX4 homo sapien
5	509	38.1	597	4	Q9BU10	Q9BU10 homo sapien
6	509	38.1	618	4	Q96AA6	Q96AA6 homo sapien
7	503	37.6	597	4	Q9BQB8	Q9BQB8 homo sapien
8	453	33.9	218	11	Q925S1	Q925S1 mus musculu
9	443.5	33.2	613	4	Q96EY0	Q96EY0 homo sapien
10	437.5	32.7	116	4	Q7Z3Y6	Q7Z3Y6 homo sapien
11	437	32.7	150	4	Q95973	Q95973 homo sapien
12	416.5	31.2	119	4	Q9UL73	Q9UL73 homo sapien
13	415.5	31.1	496	4	Q96KX8	Q96KX8 homo sapien
14	403.5	30.2	478	4	Q7Z379	Q7Z379 homo sapien
15	398	29.8	492	4	Q7Z374	Q7Z374 homo sapien
16	386.5	28.9	139	4	Q86SX2	Q86SX2 homo sapien

17	378.5	28.3	479	11	Q99M22	Q99M22 mus musculu
18	369	27.6	473	4	Q8TC63	Q8TC63 homo sapien
19	362	27.1	130	4	Q81ZD7	Q81ZD7 homo sapien
20	361	27.0	234	11	Q8R028	Q8R028 mus musculu
21	352	26.3	597	4	Q96BB9	Q96BB9 homo sapien
22	339	25.4	482	11	Q91X92	Q91X92 mus musculu
23	334	25.0	487	11	Q99KA4	Q99KA4 mus musculu
24	332	24.9	122	4	Q9UL75	Q9UL75 homo sapien
25	327.5	24.5	613	4	Q8WUK1	Q8WUK1 homo sapien
26	325	24.3	108	11	Q8VJU0	Q8VJU0 mus musculu
27	323	24.2	143	11	Q924P9	Q924P9 mus musculu
28	319.5	23.9	142	11	Q924Q2	Q924Q2 mus musculu
29	314	23.5	488	11	Q91WR1	Q91WR1 mus musculu
30	313.5	23.5	140	11	Q924R2	Q924R2 mus musculu
31	312	23.4	108	4	Q9UL79	Q9UL79 homo sapien
32	312	23.4	236	11	Q7TS98	Q7TS98 mus musculu
33	312	23.4	482	11	Q8KI72	Q8KI72 mus musculu
34	312	23.4	484	11	Q8VEA0	Q8VEA0 mus musculu
35	311.5	23.3	109	4	Q9UL85	Q9UL85 homo sapien
36	311.5	23.3	142	11	Q924Q1	Q924Q1 mus musculu
37	311.5	23.3	146	11	Q924R8	Q924R8 mus musculu
38	311.5	23.3	170	11	Q925S2	Q925S2 mus musculu
39	310.5	23.2	109	4	Q9UL78	Q9UL78 homo sapien
40	310.5	23.2	480	11	Q91XE1	Q91XE1 mus musculu
41	310	23.2	214	11	Q9RLA5	Q9RLA5 mus musculu
42	309.5	23.2	479	11	Q91WP5	Q91WP5 mus musculu
43	309.5	23.2	480	11	Q8K0Z4	Q8K0Z4 mus musculu
44	309	23.1	108	4	Q9UL83	Q9UL83 homo sapien
45	309	23.1	469	11	Q8R3V9	Q8R3V9 mus musculu

ALIGNMENTS

RESULT 1		PRELIMINARY;		PRT;		298 AA.	
ID	Q9QYF0						
AC	Q9QYF0;						
DT	01-MAY-2000 (Tremblrel. 13, Created)						
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)						
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)						
DE	CN 8 scfv.						
GN	CN 8.						
OS	Mus musculus (Mouse).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
OX	NCBI_TaxID=10090;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=Balb/c; TISSUE=Spleen;						
RX	MEDLINE=20183931; PubMed=10706631;						
RA	Shinohara N., Demura T., Fukuda H.;						
RT	"Isolation of a vascular cell wall-specific monoclonal antibody						
RT	recognizing a cell polarity by using a phage display subtraction						
RT	method."						
RL	Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590 (2000).						
DR	EMBL; AB036341; BAA8633.1; -.						
DR	PIR; A33933; A33933.						
DR	PIR; S19112; S19112.						
DR	HSSP; P01607; IREI.						
DR	InterPro; IPR007110; Ig-like.						
DR	InterPro; IPR003596; Ig_v.						
DR	Pfam; PF00047; Ig; 2.						
DR	SMART; SM00406; IGV; 2.						
DR	PROSITE; PSS0835; IG_LIKE; 2.						
SO	SEQUENCE 298 AA; 31867 MW; EOF96B8A17004317 CRC64;						
Query Match 49.9%; Score 667; DB 11; Length 298;							
Best Local Similarity 52.4%; Pred. No. 2.2e-44;							
Matches 132; Conservative 40; Mismatches 66; Indels 14; Gaps 3;							
QY	1 QVQLQQWGAGLLKSWGTLSTLCAVSGASFSGYWMIROPPGKLEWIGGINRGST-TV 59						

```

Db      40 QVKLQQSGGGLVKKPGGSLKLSCAASGSDFSRYMSWVRQAPKGLEWIGEINPDSSTINY 99
QY      60 NPSLDGRVTISLDSTNQISLKLTSMTADTAVYYCAR-TVAGTSDYWGQGLVTVSSGS 118
      ||| : ||| : : : : : ||| : ||| ||| |||
Db      100 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARASYGHSAYWGQTTVTVS --- 156
QY      119 ASAPTGGGSGGGSGGGSGGGSGGSKTTLTQSPAFMSATPGDKVYSISCKASRDVDDVNW 178
      ||| ||| ||| ||| ||| ||| ||| ||| : ||| : : : : :
Db      157 -----SGGGSGGGSGGGSGGGSGDIELTQSPALSASVGETVITTCRASGNINXYLAW 207
QY      179 YQQRPEAPFIETEDATTLVPGISPRFSGSGYGTDFTLTININIDSEDAAYFCLQHDNFP 238
      ||| : : : : : ||| : ||| ||| : : ||| : : : |||
Db      208 YQQKQKSPOLLVYNNAKTLADGVPRFRFSGSGSGTQYSLKINSIQPEDFGSYQCWFWTTP 267
QY      239 LTFGGGTVEIK 250
      ||| ||| ||| ||| |||
Db      268 YTFGGGTLEIK 279

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RESULT 2
Q921A6
ID Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Anti-CEA 79 single chain Fv fragment (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL; U88067; AAB48044.1; -.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IGV_LIKE; 2.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

```

Query Match	45.2%	Score 603.5	DB 11	Length 241
Best Local Similarity	48.4%	Pred. No. 1.6e-39		
Matches 124	Conservative 41	Mismatches 68	Indels 23	Gaps 6
QY	1 QVQLQQWAGLLKSWGTLSTLCAVSGASFSGYYMSWIRQPGKLEWIGEIN-HRGSTTY	59		
Dp	1 QVTLQOQSGPELKKPGETVKISCKASGYTFDYGMMNWKQAPGKCLKMMGMINTYTGEPY	60		
QY	60 NPSLDGRVTISLDTSTNOISLKLTSMTAADTAVYYCAR-TVAGTSDYWGQGLTVTVSSGS	118		
Dp	61 ADDDFKGRFAFSLFETSASTAYLQINLNKEDTATYFCARKDILRYFDYWGQGTIVTVS---	117		
QY	119 ASAPTGGGSGGGSGGGSGGGSGGSKTTLTQSPAFMSATPGDKVISISCKASRDVDDVNW	178		
Dp	118 -----SGGGSGGGSGGGSGGGSDIELTQSPSSLSASLGKVTITCKASQDINKRIYAW	168		
QY	179 YQQRPGEAPIFIIEDATTL-----VPGISPRFSGSGYNDFTLTINNIDSEDAVYFCLOH	234		
Dp	169 YQHKPGKGP---RSAHTLHIYIQGIPSRFSGSGSGRDYSFSISNLEPEDIAITYYCLHY	224		
QY	235 DNFPLTFGGGKTVKVEIK	250		
Dp	225 DNLH-TFPGGKTVLELK	239		

```

RESULT 3
O7QM2
ID O7QM2 PRELIMINARY; PRT; 243 AA.
AC O7QM2;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SCFV 6H8 protein (Fragment).
GN SCFV 6H8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/C;
RA Peter J.C., Eftekhari P., Billiard P., Wallukat G.;
RT "scfv single chain antibody variable fragment as inverse agonist for
RT the beta-2 adrenergic receptor.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ574851; CAE00495.1; -.
FT NON_TER 1 1
SQ SEQUENCE 243 AA; 25976 MW; BEEFF64D2DCFAF76 CRC64;

```

Query Match	Best Local Similarity	43.8%;	Score 585.5;	DB 11;	length 243;
Matches 118;	Conservative 47;	Mismatches 71;	Indels 15;	Gaps 4;	
QY	1 QVQLQQWAGLLKSWGTLISLTCAVSGASFSGYYMSWIRQPPGKLEWIGEI-NHRGSTTY	59			
Db	1 QVQLQQSGSELVVRPGASAVKLSCASGYFTFTYMHMWVKRHHQGLEWIGNIYPGSGITNY	60			
QY	60 NPSLDGRVTISLDTSTNQISLKLTSMTADTAVVYCARTVAGTSDYWGQGLTVTVSSGSA	119			
Db	61 DEKFNKKGILTVDTSSSTAYMHLISLASEDSAVVYCARGRGL-DVMGAGTTLTVS----	115			
QY	120 SAPTGGGGSGGGSGGGSGGGSKTTLTQSPAFMSATPGDKVISICKASRDVDDVNWY	179			
Db	116 -----SGGGSGGGSGGGSGGGSDIQMTQSSSSPSVSLGDRVTITCKASEDIYNRLAWY	167			
QY	180 QQRPGEAIFIFIIDATTLVPGISPRFSGSGYTDFTLLTINNIDSEDAAYFCLQHDNFP	239			
Db	168 QQKPGNAPRLISGATSLETGVPSRFSGSGSGKDYTLISLTQTEDVATYYCOQYWS-TR	226			
QY	240 TFGGGTKVEIK 250				
Db	227 TFGGGTKLEIK 237				

```

RESULT 4
OSWUX4
ID Q8WUX4 PRELIMINARY; PRT; 588 AA.
AC Q8WUX4;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DS Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1] _
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.1; -
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_5.

```



DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;

Query Match 38.1%; Score 509; DB 4; Length 588;  
Best Local Similarity 41.0%; Pred. No. 1.2e-31;  
Matches 136; Conservative 23; Mismatches 81; Indels 92; Gaps 11;

QY 1 QVQLQWGAQLKSWGTLSTCAVSGASFSGYWMIROPPGKLEWIGEINHRGSTTN 60  
DB 20 QVQLQWGAQLKPSSETLSLTGCVYGSFSGYWMIROPPGKLEWIGEINHSSTNN 79  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAVYVCARTVAGTS-----DYGQGITL 111  
DB 80 PSLKSRVTISVDTSKQLSLKLSVNAADTAVYVCARVITRASPGTDRYGMVWGQGIT 139  
QY 112 VTVSSGSASAPT-----GGGSGGGSGGG-----GSGGGSKTTLTQSPA 152  
DB 140 VTVSSGSASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG 199  
QY 153 FMSATPGDKVISISCKA---SRDV---DDVNMWYQORPG-----EAPIFIID---ATT 196  
DB 200 FPSVLRGKKAATSQVLLPSKDVMOGTDEHVCKVQHPNGNKEKNVPLPVIAELPKVSV 259  
QY 197 LVP-----GISPR-----FSGSGYGTD----- 213  
DB 260 FVPPRDGFFGNPRKSKLICQATGFSFRQIQVSWLREGKQVSGVTTDQVQAEAKESGPTT 319  
QY 214 ----FTLTINNIDSEDAAYFCLQHDNFPPLTF 241  
DB 320 YKVTSTLTIKESDWLSQSMFTC-RVDHRLTLF 350

## RESULT 5

Q9BU10 PRELIMINARY; PRT; 597 AA.  
AC Q9BU10;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BC002963; AAH02963.1; -.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match 38.1%; Score 509; DB 4; Length 597;  
Best Local Similarity 41.0%; Pred. No. 1.2e-31;  
Matches 136; Conservative 23; Mismatches 81; Indels 92; Gaps 11;

QY 1 QVQLQWGAQLKSWGTLSTCAVSGASFSGYWMIROPPGKLEWIGEINHRGSTTN 60  
DB 20 QVQLQWGAQLKPSSETLSLTGCVYGSFSGYWMIROPPGKLEWIGEINHSSTNN 79  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAVYVCARTVAGTS-----DYGQGITL 111

DB 80 PSLKSRVTISVDTSKQLSLKLSVNAADTAVYVCARVITRASPGTDRYGMVWGQGIT 139  
QY 112 VTVSSGSASAPT-----GGGSGGGSGGG-----GSGGGSKTTLTQSPA 152  
DB 140 VTVSSGSASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG 199  
QY 153 FMSATPGDKVISISCKA---SRDV---DDVNMWYQORPG-----EAPIFIID---ATT 196  
DB 200 FPSVLRGKKAATSQVLLPSKDVMOGTDEHVCKVQHPNGNKEKNVPLPVIAELPKVSV 259  
QY 197 LVP-----GISPR-----FSGSGYGTD----- 213  
DB 260 FVPPRDGFFGNPRKSKLICQATGFSFRQIQVSWLREGKQVSGVTTDQVQAEAKESGPTT 319  
QY 214 ----FTLTINNIDSEDAAYFCLQHDNFPPLTF 241  
DB 320 YKVTSTLTIKESDWLSQSMFTC-RVDHRLTLF 350

## RESULT 6

Q96AA6 PRELIMINARY; PRT; 618 AA.  
AC Q96AA6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BC017356; AAH17356.1; -.  
DR PIR; S15590; S15590.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;

Query Match 38.1%; Score 509; DB 4; Length 618;  
Best Local Similarity 41.0%; Pred. No. 1.3e-31;  
Matches 136; Conservative 23; Mismatches 81; Indels 92; Gaps 11;

QY 1 QVQLQWGAQLKSWGTLSTCAVSGASFSGYWMIROPPGKLEWIGEINHRGSTTN 60  
DB 20 QVQLQWGAQLKPSSETLSLTGCVYGSFSGYWMIROPPGKLEWIGEINHSSTNN 79  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAVYVCARTVAGTS-----DYGQGITL 111  
DB 80 PSLKSRVTISVDTSKQLSLKLSVNAADTAVYVCARVITRASPGTDRYGMVWGQGIT 139  
QY 112 VTVSSGSASAPT-----GGGSGGGSGGG-----GSGGGSKTTLTQSPA 152  
DB 140 VTVSSGSASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG 199  
QY 153 FMSATPGDKVISISCKA---SRDV---DDVNMWYQORPG-----EAPIFIID---ATT 196  
DB 200 FPSVLRGKKAATSQVLLPSKDVMOGTDEHVCKVQHPNGNKEKNVPLPVIAELPKVSV 259  
QY 197 LVP-----GISPR-----FSGSGYGTD----- 213  
DB 260 FVPPRDGFFGNPRKSKLICQATGFSFRQIQVSWLREGKQVSGVTTDQVQAEAKESGPTT 319

QY 214 ----FTLTNNIDSEDAAYFCLQHDNFPLTF 241  
Db 320 YKVTSTLTIKESDWLSQSMFTC-RVDHRLTLP 350

## RESULT 7

Q9BQB8 PRELIMINARY; PRT; 597 AA.  
AC Q9BQB8;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Muscle, and Lymph;  
RA Strausberg R.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC006180; AAH06180.1; -  
DR EMBL; BC001872; AAH01872.1; -  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-1like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 37.6%; Score 503; DB 4; Length 597;  
Best Local Similarity 40.7%; Pred. No. 3.6e-31;  
Matches 135; Conservative 23; Mismatches 82; Indels 92; Gaps 11;

QY 1 QVQLQQMGAGLLKSWGTLISLTCAVSGASFSGYWMIROPPGKLEWIGEINHRGSTTYN 60  
Db 20 QVQLQQMGAGLLKPSSETLSLTGCVYGSFSGYWSWIRQPPGKLEWIGEINHSGITNYN 79  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAAYVYCAATVAGTS-----DYMGGTL 111  
Db 80 PSLKSRVTISVDTSKQSLKLSSVNADTAAYVYCAVITRASPGIDGRYGMVWGQTT 139  
QY 112 VTVSSGSASAPT-----GGGGSGGGSGGG-----SGGGGSKTTLTQSPA 152  
Db 140 VTVSSGSASAPTLPLVSCENSPSDTSSVAVGLAQDFLPDSTFSSWKYKNSDISSTRG 199  
QY 153 FMSATPGDKVSIKRA---SRDV---DDVWVYQQRPG---EAFIFIED---ATT 196  
Db 200 FPSVLRGKGYAATSQVLLPSKDVWGCTDEHYVCKVQHPNGKKNVPLPVIAELPKVSV 259  
QY 197 LVP-----GISPR-----FSGSGYGT----- 213  
Db 260 FVPPRDGFFGNPRKSKLICQATGFSRQIQVSWLRBKGQVSGVTTDQVQAEAKESGPTT 319  
QY 214 ----FTLTNNIDSEDAAYFCLQHDNFPLTF 241  
Db 320 YKVTSTLTIKESDWLSQSMFTC-RVDHRLTLP 350

## RESULT 8

Q925S1 PRELIMINARY; PRT; 218 AA.  
AC Q925S1;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE MRP5 (Fragment).  
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX PubMed=11819679;  
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,  
RA Su C.;  
RT "Mechanism of exogenous nucleic acids and their precursors improving  
RT the repair of intestinal epithelium after irradiation in mice.";  
RL World J. Gastroenterol. 6:709-717(2000).  
RN [2]

RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Cui D., Zeng G., Yan X., Li X., Su C.;  
RT "Cloning of mouse genes related to repairing of intestinal epithelium  
RT of the irradiated mice by treatment with the intestinal RNA of mice of  
RT the same strain.";  
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
DR EMBL; AF240168; AAK43733.1; -  
DR InterPro; IPR007110; Ig-1like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
DR NON TER 218 218  
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 33.9%; Score 453; DB 11; Length 218;  
Best Local Similarity 43.8%; Pred. No. 8.7e-28;  
Matches 98; Conservative 33; Mismatches 75; Indels 18; Gaps 4;

QY 1 QVQLQQMGAGLLKSWGTLISLTCAVSGASFSGYWMIROPPGKLEWIGEIN-HRGSTTY 59  
Db 3 QVQLQQSGPELKKPGETVRISCKASGYFTTAGMQWVQKMPGKGLKWIGINTHSQVPKY 62  
QY 60 NPSLDGRVTISLDTSTNQISLKLTSMTADTAAYVYCAR-ITVAGTSDYWGQTLVTVSSGS 118  
Db 63 ABEFKGRFAPSLSTASTAYVLQISLNKNEIDTATYFCMRNDYDGGFAYWGQTYTVVS--- 119  
QY 119 ASAPTGGGGSGGGSGGGSGGGSKTTLTQSPAFMSATPGDKVISICKASRDVDD---- 174  
Db 120 -----SGGGSGGGSGGSDIVLTQSPASLAVSLGQRTATISCRASSVDNIGIS 170  
QY 175 DVNMYQQRPEAPFIIFIEDATTLVPGISPRFSGSGYGTDTLTI 218  
Db 171 FNNWFQOKPGQPKLLIYAASKQSGSVPAGLAAGSGGTDFSLNI 214

## RESULT 9

Q96EY0 PRELIMINARY; PRT; 613 AA.  
AC Q96EY0;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011857; AAH11857.1; -  
DR PIR; S15590; S15590.  
DR InterPro; IPR007110; Ig-1like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 5.

DR SMART, SM00406; IGv, 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KM Hypothetical protein.  
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match 33.2%; Score 443.5; DB 4; Length 613;  
Best Local Similarity 39.2%; Pred. No. 1.7e-26;  
Matches 129; Conservative 24; Mismatches 85; Indels 91; Gaps 12;

QY 1 QVQLQWAGLGLKSWGTLTLTCAVSGASFSGYWMIROPPGKLEWIGELINHRGSTTN 60  
DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGSISSTYWSWIRQPAKGLEWIGRIYTSGSTNN 79  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTAADTAVYYCAR-----TVAGTSDYWGQGLVTV 114  
DB 80 PSLKSRVTMSVDTSKNQFSLKLSSVTAAADTAVYYCASQPMELPTVG--LFYWGQGLVTV 137  
QY 115 SSGSASAPT-----GGGSGGGSGGG-----GSGGGSKTTLTQSPAFMS 155  
DB 138 SSGSASAPTLFPLVSCENSPSDTSSVAVGLAQDFLPDSITFSWKYKXNSDISSTRGFP 197  
QY 156 ATPGDKVSIACKA---SRDV---DDVVMYQQRPG-----EAPFIED---ATTLVP 199  
DB 198 VLRGSKYAATSOVLLPSKDVMGTDENVCKVQHNGNKKVPLVIAELPKVSVFVP 257  
QY 200 -----GISPR-----FSGSGYGTD----- 213  
DB 258 PRDGFEGNPKRSKLICQATGFSPRQIQVSWLRGKQVGSVTTDQVAEAKESGPTTYKV 317  
QY 214 -FTLTINNIDSEDAVYFCLQHDNPLTF 241  
DB 318 TSTLTIKESDWLSQSMFTC-RVDHRLGTF 345

RESULT 10

Q723Y6 PRELIMINARY; PRT; 116 AA.  
AC Q723Y6; 25, Created  
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Rearranged VH4-34 V gene segment (Fragment).  
GN VH4-34.  
OS Homo sapiens (Human).  
OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TRISSE=Hodgkin lymphoma;  
RA Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuipers R.,  
RA Hansmann M.L., Brauning A.;  
RT "Analysis of a clonally related mantle cell and Hodgkin lymphoma  
RT indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg  
RT cell precursor in a germinal center."  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ564425; CAD92032.1; -.  
FT NON\_TER 1  
FT NON\_TER 116  
SQ SEQUENCE 116 AA; 12902 MW; CE3DBA846616C908 CRC64;

Query Match 32.7%; Score 437.5; DB 4; Length 116;  
Best Local Similarity 72.0%; Pred. No. 6.5e-27;  
Matches 85; Conservative 8; Mismatches 14; Indels 11; Gaps 1;

QY 1 QVQLQWAGLGLKSWGTLTLTCAVSGASFSGYWMIROPPGKLEWIGELINHRGSTTN 60  
DB 1 QVQLQWAGLGLKPSSETLSLSCAVYGSFSGYWMWIRQPPGKLEWIGELINHSSTNN 60  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTAADTAVYYCARTVAGTSDYWGQGLVTVSSGS 118  
DB 61 PSLKSRVTISVDTSKNQSLKLSSVTAAADTAVYYCAR-----GEIVVPAAS 107

RESULT 11

ID 095973 PRELIMINARY; PRT; 150 AA.  
AC 095973;  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE VH4 heavy chain variable region precursor (Fragment).  
GN IGM.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;  
RT "Clonal proliferation of Igm secreting B cell in the synovium of  
RT Behcet's patient with arthritis."  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF103795; AAC79084.1; -.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW signal.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 >150 VH4 HEAVY CHAIN VARIABLE REGION.  
FT NON\_TER 150 150  
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 32.7%; Score 437; DB 4; Length 150;  
Best Local Similarity 68.0%; Pred. No. 9.8e-27;  
Matches 85; Conservative 13; Mismatches 25; Indels 2; Gaps 1;

QY 1 QVQLQWAGLGLKSWGTLTLTCAVSGASFS--GYWMIROPPGKLEWIGELINHRGSTT 58  
DB 20 QVQLQESGPGLVKPSSETLSLSCYVSGSISSTNYWGWIRQPPGKLEWIGSLHNSGSDY 79  
QY 59 YNPSLDGRVTISLDTSTNQISLKLTSMTAADTAVYYCARTVAGTSDYWGQGLVTVSSGS 118  
DB 80 YNPSLKRVTISVDTSKNQFSLKLSSVTAAADTAVYYCARLGMGAFDFWGHGTMVTSSGS 139  
QY 119 ASAPT 123  
DB 140 ASAPT 144

RESULT 12

Q9UL73 PRELIMINARY; PRT; 119 AA.  
AC Q9UL73;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; Pubmed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus."  
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
DR EMBL; AF035041; AAD56277.1; -.



DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 119  
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;

Query Match 31.2%; Score 416.5; DB 4; Length 119;  
Best Local Similarity 70.6%; Pred. No. 3e-25;  
Matches 84; Conservative 6; Mismatches 26; Indels 3; Gaps 1;

QY 1 QVQLQOMGAGLLKSWGTLSTLCAVSGASFSGYYMSWIRQPPGKLEWIGELINHRGTTYN 60  
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGISGYMSWIRQPPGKLEWIGYIYSGSTNYT 60  
QY 61 PSIDGRVTISLDTSTNQISLKLSTMTADTAVYVCARTVAGTS--DYWGQGLVTVSS 116  
DB 61 PSLKSRVTISVDRSKNQFSLKLTSLTAADTAVYFCARLSNMGPYYFDYWGQGLVTVSS 119

RESULT 13

Q96KX8 ID Q96KX8 PRELIMINARY; PRT; 496 AA.  
AC Q96KX8;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC016369; AAH16369.1; -  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 4.  
DR PROSITE; PSS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 31.1%; Score 415.5; DB 4; Length 496;  
Best Local Similarity 42.8%; Pred. No. 2.1e-24;  
Matches 101; Conservative 20; Mismatches 54; Indels 61; Gaps 7;

QY 1 QVQLQOMGAGLLKSWGTLSTLCAVSGASF--SGYYMSWIRQPPGKLEWIGELINHRGTT 58  
DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGSGISSSYYMGWIRQPPGKLEWIANITYSGITY 79  
QY 59 YNPISLDGRVTISLDTSTNQISLKLSTMTADTAVYVCAR-----TVAGTSIDYWGQGLV 112  
DB 80 YNPISLKSRYTISVDTSKNQLSLKRVSTADTAVYFCARHGYSRSGRTGALDIYWGQGLV 139  
QY 113 TVSSGSASAPPTGGGSGGGSGGGGSKTTLTQSPAFMSATPGDKVISCKASRDV 172  
DB 140 TVSSASPTSPK-----VFPLSLCSTQPDGNVYIACLVQ--- 172  
QY 173 DDVVMYQQRPGAPFIETDATTLPVGI SPRFGSGYGTDTLTINNI-DSEDA 227  
DB 173 ----GFFPQEP-----LSVTWSESQG---VTARNFPSPQDAS 203

RESULT 14

Q72379 ID Q72379 PRELIMINARY; PRT; 478 AA.  
AC Q72379;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein DKFZp686K04218 (Fragment).  
GN DKFZp686K04218.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Robo G., Han M., Wiemann S.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX538066; CAD97996.1; -  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match 30.2%; Score 403.5; DB 4; Length 478;  
Best Local Similarity 42.9%; Pred. No. 1.7e-23;  
Matches 100; Conservative 28; Mismatches 46; Indels 59; Gaps 10;

QY 1 QVQLQOMGAGLLKSWGTLSTLCAVSGASF-SGYYMSWIRQPPGKLEWIGELINHRGTT 58  
DB 19 QVQLQESGPGLVKPSQTLSTLCTVSGSGISGDFWMSWIRQPPGKLEWIGYIYSGSTY 78  
QY 59 YNPISLDGRVTISLDTSTNQISLKLSTMTADTAVYVCARTVA-GTS-DYWGQGLVTVSS 116  
DB 79 YNPISLKSRLSISIDTSKNQFSLRLNLTADTAVYFCARGVGLGTAFDIWGQGLVTVSS 138  
QY 117 GSASAPPTGGGSGGGSGGGGSKTTLTQSPAFMSATPGD-KVISCKASRDVDD 175  
DB 139 ASPTSP-----KVFPISLDTSTPDGNVYIACLVQ----- 167  
QY 176 VNMVYQQRPGAPFIETDATTLPVGI SPRFGSGYGTDTLTINNI-DSEDA 227  
DB 168 -GFFPQEP-----LSVTWSESQG---NVTARNFPSPQDAS 198

RESULT 15

Q72374 ID Q72374 PRELIMINARY; PRT; 492 AA.  
AC Q72374;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein DKFZp686C02218 (Fragment).  
GN DKFZp686C02218.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Robo G., Han M., Wiemann S.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX538077; CAD98001.1; -  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 29.8%; Score 398; DB 4; Length 492;  
Best Local Similarity 41.9%; Pred. No. 4.8e-23;  
Matches 98; Conservative 23; Mismatches 53; Indels 60; Gaps 8;

QY 1 QVQLQOMGAGLLKSWGTLSTLCAVSGASF--GYYSWIRQPPGKLEWIGELINHRGTT 58



Db	32	QLQIQESGPGLVKPSSETLSLCTVSGGSVSNRNYWGWIRQPGKGLEWIGSIYNNENTY	91
OY	59	YNPSLDGRVTISLDTSTNOISLKLTSMTAADTAVYYCARTVAGT---SDYWGQGLVTVS	115
Db	92	YSPSLKSRLLTFVDTSKNHFSRLRLTSVTAADTAVYYCVRHVEGPGYGFDPWGQGLVTVS	151
OY	116	SGSASAPTCGGGGGGGGGGGGGGGGGGGSKTTLTQSPAFMSATPGD-KVISISCKASRDVDD	174
Db	152	SASPTSP-----KVFPPLSLDSTPQDGNVVVACLVD-----	181
OY	175	DVNWYQQRPGEAPIFIEDATTLVPGISPRFSGSGYGTDFTLINNI-DSEDA	227
Db	182	--GFFPQEP-----LSVTWSESGQ---NVTARNFPSPQDAS	212

Search completed: May 13, 2004, 15:06:57  
Job time : 34.6165 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:48:56 ; Search time 52.0738 Seconds  
(without alignments)  
1372.754 Million cell updates/sec

Title: US-10-072-301-23  
Perfect score: 1348  
Sequence: 1 QVTLKSGPVLVKPTQTTLT.....CQSDYLPITFGGTRKVDIK 253

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1:	geneseqp19808:*
2:	geneseqp19908:*
3:	geneseqp20008:*
4:	geneseqp20018:*
5:	geneseqp20028:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	844	62.6	256	3	AAY55072	Aay55072 Interleuk
2	844	62.6	260	3	AAY55075	Aay55075 Single ch
3	844	62.6	367	3	AAY55078	Aay55078 Single ch
4	844	62.6	381	3	AAY55079	Aay55079 Single ch
5	844	62.6	519	3	AAY55080	Aay55080 Single ch
6	844	62.6	546	3	AAY55074	Aay55074 Single ch
7	844	62.6	626	3	AAY55081	Aay55081 Single ch
8	844	62.6	640	3	AAY55082	Aay55082 Single ch
9	822.5	61.0	259	3	AAB09778	Aab09778 Antiviral
10	822.5	61.0	259	4	AAB70885	Aab70885 TMV 54K p
11	811.5	60.2	251	5	ABP45038	Abp45038 Human Bly
12	811.5	60.2	909	2	AAR50092	Aar50092 Humanised
13	803	59.6	248	5	ABP45349	Abp45349 Human Bly
14	801.5	59.5	255	5	ABP45592	Abp45592 Human Bly
15	800.5	59.4	249	5	ABP45310	Abp45310 Human Bly
16	789	58.5	248	5	ABP45865	Abp45865 Human Bly
17	787	58.4	240	4	AAB46044	Aab46044 Human TF
18	787	58.4	240	4	AAB46045	Aab46045 Human TF
19	786	58.3	240	4	AAB46010	Aab46010 Human MUC
20	781.5	58.0	243	5	ABP45924	Abp45924 Human Bly
21	781.5	58.0	249	5	ABP45177	Abp45177 Human Bly
22	779.5	57.8	272	2	AAR21260	Aar21260 ScFv sequ
23	779.5	57.8	285	2	AAR64810	Aar64810 ScFv anti
24	779	57.8	240	4	AAB46011	Aab46011 Human MUC

26	779	57.8	240	4	AAB46012	Aab46012 Human MUC
27	777	57.6	249	5	AAU75150	Aau75150 Amino aci
28	777	57.6	250	5	ABP45163	Abp45163 Human Bly
29	775	57.5	240	4	AAB46006	Aab46006 Human MUC
30	773	57.3	240	4	AAB45996	Aab45996 Human MUC
31	772	57.3	240	4	AAB46009	Aab46009 Human MUC
32	772	57.3	240	4	AAB46039	Aab46039 Human TF
33	771	57.2	240	4	AAB45991	Aab45991 Human MUC
34	769	57.0	240	4	AAB46018	Aab46018 Human MUC
35	769	57.0	240	4	AAB46021	Aab46021 Human MUC
36	769	57.0	266	5	ABG97826	Abg97826 Human sin
37	769	57.0	266	5	ABG35329	Abg35329 Thrombopo
38	767	56.9	240	4	AAB46013	Aab46013 Human MUC
39	767	56.9	240	4	AAB45992	Aab45992 Human MUC
40	767	56.9	240	4	AAB46017	Aab46017 Human MUC
41	767	56.9	240	4	AAB46014	Aab46014 Human MUC
42	766	56.8	240	4	AAB46040	Aab46040 Human TF
43	766	56.8	667	6	ABP97414	Abp97414 Anti-huma
44	765	56.8	240	4	AAB45997	Aab45997 Human MUC
45	765	56.8	240	4	AAB46038	Aab46038 Human TF

ALIGNMENTS

RESULT 1  
ID AAY55072 standard; protein; 256 AA.  
XX AAY55072;  
AC  
XX  
DT 25-FEB-2000 (first entry)  
XX  
DE Interleukin-6 specific ScFv protein sequence.  
XX  
KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretable functional protein; antigenic protein;  
KW protein isolation; diagnosis; interleukin-6; ScFv.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9960113-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 30-APR-1999; 99WO-JP002341.  
XX  
PR 20-MAY-1998; 98JP-00138652.  
PR 01-OCT-1998; 98JP-00279876.  
XX  
PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Tsuchiya M, Saito M, Ohtomo T;  
XX  
DR WPI; 2000-039382/03.  
DR N-PSDB; AAZ40291.  
XX  
PT Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
PT production of drugs treating abnormal functions of the protein.  
XX  
PS Example 1; Page 54-56; 120pp; Japanese.  
XX  
CC This sequence represents a ScFv specific for human interleukin-6. The  
CC invention relates to a method for isolating a gene encoding a membrane-  
CC bound protein, comprising introducing a vector into a cell, contacting an  
CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the cDNA.  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for

CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein  
XX  
SQ Sequence 256 AA;

Query Match 62.6%; Score 844; DB 3; Length 256;  
Best Local Similarity 65.6%; Pred. No. 3.1e-49;  
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVGVWRQPPGKALEWLALTYWDDDKR 60  
DB 1 QVQLQESGPGLVPRPSQTLSTCTVSGYSI-TSDHAWGVRQPPGRLGIEWIGYISYGITT 59  
QY 61 YSPSLKSRLLITKDTSKQVLTMTNVPADTATYCTHEQYVYDTSQQPYFDFWGQGT 120  
DB 60 YNPSLSKSRVTMLRDTSKNQPSLRSLSSVTADTAVYYCAR-----SLARTTAMDYWGQGS 113  
QY 121 LVTYSSGGGGSGGGSGGGSGGSGNIGVTQSPSSLSASVGDRTVMTCRASQDIRKNLN 180  
DB 114 LVTYS-----SGGGSGGGSGGGSGGSDIQMTQSPSSLSASVGDRTVITTCRASQDISSYLN 168  
QY 181 WYQOKPGKAPKVLIVDASDLETGIPSRFSGSGSGTDFILITSSLOPEDIATYCCQGSDDL 240  
DB 169 WYQOKPGKAPKLLIYTSRLHSGVPSRFSGSGSGTDFTTITSSLOPEDIATYCCQGNL 228  
QY 241 PLTFGGGTQVDIK 253  
DB 229 PYTFGGGTQVEIK 241

RESULT 2  
AAVS5075  
ID AAVS5075 standard; protein; 260 AA.  
XX  
AC AAVS5075;  
XX  
DT 25-FEB-2000 (first entry)  
XX  
DE Single chain Fv protein sequence shPM1(deltaEL).

XX  
KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretable functional protein; antigenic protein;  
KW protein isolation; diagnosis; ScFv.  
XX  
OS Synthetic.  
XX  
PN WO9960113-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 30-APR-1999; 99WO-JP002341.  
XX  
PR 20-MAY-1998; 98JP-00138652.  
PR 01-OCT-1998; 98JP-00279876.  
XX  
PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Tsuchiya M, Saito M, Ohtomo T;  
XX  
DR WPI, 2000-039382/03.  
DR N-PSDB; AAZ40305.  
XX

PT Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
PT production of drugs treating abnormal functions of the protein.  
XX  
PS Example 7; Page 80-82; 120pp; Japanese.  
XX

CC This sequence represents a single chain Fv (ScFv) sequence. The invention  
CC relates to a method for isolating a gene encoding a membrane-bound  
CC protein, comprising introducing a vector into a cell, contacting an  
CC

CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the cDNA.  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for  
CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein  
XX  
SQ Sequence 260 AA;

Query Match 62.6%; Score 844; DB 3; Length 260;  
Best Local Similarity 65.6%; Pred. No. 3.1e-49;  
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVGVWRQPPGKALEWLALTYWDDDKR 60  
DB 20 QVQLQESGPGLVPRPSQTLSTCTVSGYSI-TSDHAWGVRQPPGRLGIEWIGYISYGITT 78  
QY 61 YSPSLKSRLLITKDTSKQVLTMTNVPADTATYCTHEQYVYDTSQQPYFDFWGQGT 120  
DB 79 YNPSLSKSRVTMLRDTSKNQPSLRSLSSVTADTAVYYCAR-----SLARTTAMDYWGQGS 132  
QY 121 LVTYSSGGGGSGGGSGGGSGGSGNIGVTQSPSSLSASVGDRTVMTCRASQDIRKNLN 180  
DB 133 LVTYS-----SGGGSGGGSGGGSGGSDIQMTQSPSSLSASVGDRTVITTCRASQDISSYLN 187  
QY 181 WYQOKPGKAPKVLIVDASDLETGIPSRFSGSGSGTDFILITSSLOPEDIATYCCQGSDDL 240  
DB 188 WYQOKPGKAPKLLIYTSRLHSGVPSRFSGSGSGTDFTTITSSLOPEDIATYCCQGNL 247  
QY 241 PLTFGGGTQVDIK 253  
DB 248 PYTFGGGTQVEIK 260

RESULT 3  
AAVS5078  
ID AAVS5078 standard; protein; 367 AA.  
XX  
AC AAVS5078;  
XX  
DT 25-FEB-2000 (first entry)  
XX  
DE Single chain Fv protein sequence shPM1-Kappa.

XX  
KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretable functional protein; antigenic protein;  
KW protein isolation; diagnosis; ScFv.  
XX  
OS Synthetic.  
XX  
PN WO9960113-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 30-APR-1999; 99WO-JP002341.  
XX  
PR 20-MAY-1998; 98JP-00138652.  
PR 01-OCT-1998; 98JP-00279876.  
XX  
PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Tsuchiya M, Saito M, Ohtomo T;  
XX  
DR WPI, 2000-039382/03.  
DR N-PSDB; AAZ40308.  
XX

PT Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
PT production of drugs treating abnormal functions of the protein.  
PT



XX Example 7; Page 86-89; 120pp; Japanese.

CC This sequence represents a single chain Fv (ScFv) sequence. The invention  
CC relates to a method for isolating a gene encoding a membrane-bound  
CC protein, comprising introducing a vector into a cell, contacting an  
CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the cDNA.  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for  
CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein

XX Sequence 367 AA;

Query Match 62.6%; Score 844; DB 3; Length 367;  
Best Local Similarity 65.6%; Pred. No. 4.4e-49;  
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

OY 1 QVTLKSGPTLVKPTQTLLTCTFSGFSRLRTGEGVGVWRQPPGKALEWLALYWD DDKR 60  
DB 20 QVQLQESGPGILVRPSQTLSTCTVSGYSI-TSDHAWSWVRQPPGLEWIGYISYSGIT 78  
OY 61 YSPSLKSRLLITKDTSKQVVLMTNVDPADTATYYCTHEQYVYDTSQPYFDFWGQGT 120  
DB 79 YNPSLKSRLVTLMLRDTSKNQFSRLSSVTAADTAVYYCAR-----SLARTTAMDYWGQS 132  
OY 121 LVTWSSGGGSGGGSGGGSGGGSNIQVTSPPSLASVGDRTVMTCRASQDIRKNLN 180  
DB 133 LVTVS-----SGGGSGGGSGGGSGGSDIQMTQSPSSLASVGDRTVITCRASQDISSYLN 187  
OY 181 WYQQRKPKAPKVLIDASDLETGIPSRFSGSGSCTDFILITSSLOPEDIAITYYCOQSDYL 240  
DB 188 WYQQRKPKAPKLLIYTSRLHSGVPSRFSGSGSCTDFTFTISSLOPEDIAITYYCOQGNL 247  
OY 241 PLTFGGGTGVNDIK 253  
DB 248 PYTFGGGTGVNDIK 260

RESULT 4

AAY55079 standard; protein; 381 AA.

XX AAY55079;  
DT 25-FEB-2000 (first entry)  
DE Single chain Fv protein sequence shPM1-MCH4.

KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretable functional protein; antigenic protein;  
KW protein isolation; diagnosis; ScFv.

XX Synthetic.

PN WO9960113-A1.

PD 25-NOV-1999.

PF 30-APR-1999; 99WO-JP002341.

PR 20-MAY-1998; 98JP-00138652.

PR 01-OCT-1998; 98JP-00279876.

PA (CHUS ) CHUGAI SEIYAKU KK.

PI Tsuchiya M, Saito M, Ohtomo T;

DR WPI; 2000-039382/03.

PT Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
PT production of drugs treating abnormal functions of the protein.

XX Example 7; Page 90-94; 120pp; Japanese.

CC This sequence represents a single chain Fv (ScFv) sequence. The invention  
CC relates to a method for isolating a gene encoding a membrane-bound  
CC protein, comprising introducing a vector into a cell, contacting an  
CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the cDNA.  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for  
CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein

SQ Sequence 381 AA;

Query Match 62.6%; Score 844; DB 3; Length 381;  
Best Local Similarity 65.6%; Pred. No. 4.6e-49;  
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

OY 1 QVTLKSGPTLVKPTQTLLTCTFSGFSRLRTGEGVGVWRQPPGKALEWLALYWD DDKR 60  
DB 20 QVQLQESGPGILVRPSQTLSTCTVSGYSI-TSDHAWSWVRQPPGLEWIGYISYSGIT 78  
OY 61 YSPSLKSRLLITKDTSKQVVLMTNVDPADTATYYCTHEQYVYDTSQPYFDFWGQGT 120  
DB 79 YNPSLKSRLVTLMLRDTSKNQFSRLSSVTAADTAVYYCAR-----SLARTTAMDYWGQS 132  
OY 121 LVTWSSGGGSGGGSGGGSGGGSNIQVTSPPSLASVGDRTVMTCRASQDIRKNLN 180  
DB 133 LVTVS-----SGGGSGGGSGGGSGGSDIQMTQSPSSLASVGDRTVITCRASQDISSYLN 187  
OY 181 WYQQRKPKAPKVLIDASDLETGIPSRFSGSGSCTDFILITSSLOPEDIAITYYCOQSDYL 240  
DB 188 WYQQRKPKAPKLLIYTSRLHSGVPSRFSGSGSCTDFTFTISSLOPEDIAITYYCOQGNL 247  
OY 241 PLTFGGGTGVNDIK 253  
DB 248 PYTFGGGTGVNDIK 260

RESULT 5

AAY55080 standard; protein; 519 AA.

XX AAY55080;

DT 25-FEB-2000 (first entry)

DE Single chain Fv protein sequence shPM1(deltaE)-BVGS3.

KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretable functional protein; antigenic protein;  
KW protein isolation; diagnosis; ScFv.

XX Synthetic.

PN WO9960113-A1.

PD 25-NOV-1999.

PF 30-APR-1999; 99WO-JP002341.

PR 20-MAY-1998; 98JP-00138652.



KW antigen-binding cell; secretable functional protein; antigenic protein;  
 KW protein isolation; diagnosis; ScFv.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9960113-A1.  
 XX  
 PD 25-NOV-1999.  
 XX  
 PF 30-APR-1999; 99WO-JP002341.  
 XX  
 PR 20-MAY-1998; 98JP-00138652.  
 PR 01-OCT-1998; 98JP-00279876.  
 XX  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX  
 PI Tsuchiya M, Saito M, Ohtomo T;  
 DR WPI; 2000-039382/03.  
 DR N-PSDB; AA240316.  
 XX  
 PT Efficient and selective isolation of a gene encoding membrane protein  
 PT with low or no antigenic binding activity, for diagnosis, study of, and  
 PT production of drugs treating abnormal functions of the protein.  
 XX  
 PS Example 7; Page 103-109; 120pp; Japanese.

This sequence represents a single chain Fv (ScFv) sequence. The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the cDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a cDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is efficient and selective, which is different from the prior art transmembrane trap (TMT) method wherein an epitope recognised by an antibody is carried in a fused protein

**SQ** Sequence 626 AA;

Query Match	62.6%	Score 844;	DB 3;	Length 626;
Best Local Similarity	65.6%	Pred. No. 7.4e-49;		
Matches 166;	Conservative 29;	Mismatches 46;	Indels 12;	Gaps 3;

Qy	1	QVTLKESGPTLVKPTQTLTLCTPSCGSLFTTGGEGVWVRÖPPGKALEWTLALIWDDDKR	60
Db	20	QVÖLQESGPGLVPRPSQTLSLTCTVSGYSI-TSDHAWSWVRÖPPGRGLEWIGIYSIGITT	78
Qy	61	YSPSLKSLRLLTTKDTSKKQVLLTMVDPADTATYYCTHEQYYDTSGQPYFEDWGÖGT	120
Db	79	YNPSLKSRVTMLRDTSKNQFSLRLSSTYAADTAVYYCAR-----SLARTTANDYWGÖGS	132
Qy	121	LVTVSSGGGSGGGSGGGSGGGSGGSGNIQVTQSPSSLASVGDRTVMTCRASODIRKLN	180
Db	133	LVTVS-----SGGGSGGGSGGGSGGGSGDQMTQSPSSLASVGDRTVITCRASODISSYLN	187
Qy	181	WYÖQKPGKAPKVLIIYDASDLETGIPSRFSGSGSCTDFILTISSLQPEDIAATYYCQÖSDYL	240
Db	188	WYÖQKPGKAPKVLIIYTSRLHSGVPSRFSGSGSCTDFTFTISSLQPEDIAATYYCQÖGNTL	247
Qy	241	PLTFGGGCTKVDIK	253
Db	248	PYTFGÖGTKEIK	260

RESULT	8
AAV5082	
ID	AAV5082 standard; protein; 640 AA.
XX	
AC	AAV5082;

XX	25-FEB-2000	(first entry)
DT		
XX		
DE	Single chain Fv protein sequence shPM1-MCH4-BvGS3.	
XX		
KW	Gene isolation; membrane-bound protein; fusion protein; drug production;	
KW	antigen-binding cell; secretable functional protein; antigenic protein;	
KW	protein isolation; diagnosis; ScFv.	
XX		
OS	Synthetic.	
XX		
PN	WO9960113-A1.	
XX		
PD	25-NOV-1999.	
XX		
PF	30-APR-1999; 99WO-JP002341.	
XX		
PR	20-MAY-1998; 98JP-00138652.	
PR	01-OCT-1998; 98JP-00279876.	
XX		
PA	(CHUS ) CHUGAI SEIYAKU KK.	
XX		
PI	Tsuchiya M, Saito M, Ohtomo T;	
XX		
DR	WPI; 2000-039382/03.	
DR	N-PSDB; AAZ40321.	
DR		

Efficient and selective isolation of a gene encoding membrane protein with low or no antigenic binding activity, for diagnosis, study of, and production of drugs treating abnormal functions of the protein.

WPI; 2000-039382/03.  
N-PSDB; AAZ40321.

**Example 7:** Page 111-117; 120pp; Japanese.

This sequence represents a single chain Fv (ScFv) sequence. The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the cDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a cDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is efficient and selective, which is different from the prior-art transmembrane trap (TMT) method wherein an epitope recognised by an antibody is carried in a fused protein

**SQ Sequence 640 AA;**

Query Match	62.6%;	Score 844;	DB 3;	Length 640;
Best Local Similarity	65.6%;	Pred. No. 7.6e-49;		
Matches 166; Conservative	29;	Mismatches 46;	Indels 12;	Gaps 3;

OY		1	QVTLKESGPTLVKPTQTLTILCTFSGFSLRTTGEVGWVRQPCKALEMLALIYWDDDKR	60
Dd		20	ÖVQLÖESGPGLWRPŞÖTLSTLCTIVSGYSI-TSDHAMSWMRÖPCRGLEWIGIYSISGITTT	78
OY		61	YSPSLKSRLTITKTDTSKKKOVLTMTNVDPADTATYYCTHEQQYYYDTSÇOPYFFDFWGQGT	120
Dd		79	YNPSLKSRVTMTLRDTSKNĞEŞLRLSVSVAADTAVERYCAR-----SLARTTAMDYWGQS	132
OY		121	LTVSSGGGS GGGS GGGS GGGSNİQTQSPSSLASAVGDVRTMTCRASODIRKNLN	180
Dd		133	LTVS-----SGGGSGGGSGSGGGSDİQMTOŞPSSLASAVEDRVITI CRASQDISSYLN	187
OY		181	WYÖQKP GKAPKVLIYDASDLTGIPSRFSGSGSTD FILLTSSLOPEDIAITYCCQSQDYL	240
Dd		188	WYÖQKP GKAPKLIIYTŞRLHSĞVPSRFSGSGSGTDFTPTISSLOPEDIAITYYCQCGNTL	247
OY		241	PLTFGGGTKVDIK	253
Dd		248	PYTFGGG TKVEİK	260









XX  
DR MPI; 1994-111012/14.  
XX N-PSDB; AAQ58696.

PT New fusion protein contg. enzyme for prodrug activation - coupled to  
PT antigen binding component, esp. sfv antibody fragment, partic. for  
XX treatment of tumours.

XX  
PS Claim 13; Page 12-15; 35pp; German.  
XX

CC The sequence AAR50092 comprises a humanised sfv-fragment against CEA  
CC fused to a human beta-glucuronidase. The fusion protein is useful for  
CC targeting beta-glucuronidase to cancer cells expressing CEA, where the  
CC enzyme is able to convert a prodrug into its active form. Any fusion  
CC protein not bound to tumour can be removed by internalisation via the  
CC mannose-6-phosphate and galactose receptors. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX  
XX Sequence 909 AA;

[illegible]

```

RESULT 15
ID   ABP45310 standard; protein; 249 AA.
XX   AC   ABP45310;
XX   DT   19-AUG-2002 (first entry)
XX   DE   Human Blys binding scFv SEQ ID 1321.
XX
KM   Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM   tumour necrosis factor; B cell proliferation; B cell differentiation;
KM   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KM   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 1979-1980; 3148pp; English.
XX
XX   This invention describes novel antibodies that immunospecifically bind to
XX   B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX   tumour necrosis factor (TNF) super family and induces B cell
XX   proliferation and differentiation. The antibodies of the invention have
XX   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX   antirheumatic and antiAIDS activity and can be used in vaccines to
XX   inhibit the expression and activity of Blys. The antibodies bind to Blys
XX   and so may be used to detect and quantitate the presence of Blys in
XX   biological samples and may be used in this way to diagnose disease
XX   associated with aberrant expression of Blys. They may also be
XX   administered to treat diseases associated with aberrant Blys expression
XX   and activity such as cancer, immune, and autoimmune disorders and
XX   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX   the antibodies and fragments of the antibodies described in the method of
XX   the invention
XX
SQ   Sequence 249 AA;
Query Match      59.4%; Score 800.5; DB 5; length 249;
Best Local Similarity 64.3%; Pred. No. 2.5e-46;
Matches 164; Conservative 27; Mismatches 55; Indels 9; Gaps 4;
OY      1 QVTLKESGPTLVKPIOTLTITCTFSGFSRLRTGEGVGVWRQPPGKALEWLLAIYWDDKR 60
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      1 QVQLQQWAGLGLKPEETLSLTCAVYGGSF--SGYYWSWIRQPPGKLEWIGELINHSGETN 58

```

Mon May 17 11:03:35 2004

us-10-072-301-23.rag

**Page 10**

[illegible]

Search completed: May 13, 2004, 15:00:58  
Job time : 53.0738 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:53:42 ; Search time 13.8782 Seconds  
(without alignments)  
941.146 Million cell updates/sec

Title: US-10-072-301-23

Perfect score: 1348

Sequence: 1 QVTLKESGPTLVKPTQTTLT.....CQSDYLPITFGGTXVDIK 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
  - 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
  - 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
  - 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
  - 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
  - 6: /cgn2\_6/ptodata/2/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	764	56.7	248	2	US-08-887-352B-22
2	764	56.7	248	3	US-09-109-207C-22
3	764	56.7	248	3	US-09-296-005-22
4	764	56.7	248	4	US-09-920-171-22
5	762	56.5	244	4	US-08-918-148-77
6	762	56.5	248	2	US-08-887-352B-23
7	762	56.5	248	3	US-09-109-207C-23
8	762	56.5	248	3	US-09-296-005-23
9	762	56.5	248	4	US-09-920-171-23
10	746.5	55.4	245	4	US-08-918-148-76
11	742	55.0	359	4	US-09-646-028-16
12	742	55.0	361	4	US-09-646-028-13
13	736	54.6	264	3	US-08-564-164A-4
14	734.5	54.5	240	1	US-08-488-113B-148
15	734.5	54.5	240	1	US-08-477-484B-148
16	734.5	54.5	240	2	US-08-646-360-148
17	734.5	54.5	240	3	US-08-839-765-148
18	734.5	54.5	240	3	US-09-136-389-148
19	734.5	54.5	240	4	US-09-610-838-148
20	734.5	54.5	240	4	US-09-711-485-148
21	730.5	54.2	245	4	US-08-918-148-78
22	720.5	53.4	235	2	US-08-190-199A-61
23	714.5	53.0	245	4	US-08-918-148-75
24	711	52.7	269	3	US-08-646-265A-109
25	708.5	52.6	263	2	US-08-752-844-66
26	708.5	52.6	263	4	US-09-293-533-66
27	707	52.4	301	2	US-08-661-052-14

28	707	52.4	301	3	US-09-188-082-14	Sequence 14, Appl
29	707	52.4	301	4	US-09-364-088-14	Sequence 14, Appl
30	707	52.4	301	4	US-09-102-716-14	Sequence 14, Appl
31	707	52.4	553	2	US-08-661-052-16	Sequence 16, Appl
32	707	52.4	553	3	US-09-188-082-16	Sequence 16, Appl
33	707	52.4	553	4	US-09-364-088-16	Sequence 16, Appl
34	707	52.4	553	4	US-09-102-716-16	Sequence 16, Appl
35	701.5	52.0	249	2	US-08-797-689-18	Sequence 18, Appl
36	701.5	52.0	249	4	US-09-984-186-18	Sequence 18, Appl
37	697.5	51.7	482	4	US-09-509-031-16	Sequence 16, Appl
38	685.5	50.9	277	2	US-08-256-790-2	Sequence 2, Appl
39	681.5	50.6	282	2	US-08-860-174A-10	Sequence 10, Appl
40	680.5	50.5	284	3	US-08-564-164A-2	Sequence 2, Appl
41	675	50.1	273	2	US-08-403-853-18	Sequence 18, Appl
42	672	49.9	243	1	US-07-958-140-2	Sequence 2, Appl
43	672	49.9	243	5	PCT-US93-09166-2	Sequence 2, Appl
44	664	49.3	240	4	US-10-092-246-36	Sequence 36, Appl
45	661	49.0	637	1	US-08-235-838-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-08-887-352B-22  
; Sequence 22, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 248 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-08-887-352B-22

Query Match 56.7%; Score 764; DB 2; Length 248;  
Best local Similarity 60.7%; Pred. No. 1.4e-53;  
Matches 156; Conservative 30; Mismatches 57; Indels 14; Gaps 4;

QY 1 QVTLKESGPTLVKPTQTTLTCTFSGLRTGEGVGVWRQPPGKALEWLAITYWDDDKR 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSI-TSGYSWNWIRQAPGKLEWVASITYDGSTN 59  
QY 61 YSPSLKRLTITKDTSKQVLTWNPADATATYCTHEQYYVDTSGQYYFDWGGGT 120  
DB 60 YNPSTYGRITTSRDSKNTFYQMNSLRAEDTAVYYCARGSHYFG---HWHFAVWGQGT 115

```

QY      121 LVTVSSGGGSGGGSGGGSGGGSGNIQTQSPSSLASVGDRTMTCRASQDI-----R 176
      ||||| | ||||| ||||| :|||:|||||:|||||:|||||:|||||:
Db      116 LVTVS-----SEGGSGEGGSEGGSDIQLTQSPSSLASVGDRTITCRASKPVDESD 170
      ||||| | ||||| ||||| :|||:|||||:|||||:|||||:|||||:
QY      177 KNINMYQOKPGKAPKVLIDASDLETGIPSRFSGSGSGTDFILITISLQPEDIATYCCQ 236
      ||||| | ||||| ||||| :|||:|||||:|||||:|||||:|||||:
Db      171 SYINMYQOKPGKAPKLLIYASYSLESGVPSRFSGSGSGTDFLTITISLQPEDFATYCCQ 230
      ||||| | ||||| ||||| :|||:|||||:|||||:|||||:|||||:
QY      237 SDYLPPLTFGGGTGVKDIK 253
      | | | | | ||||| :|||
Db      231 SHEDPYTFGGGTKEIK 247
      | | | | | ||||| :|||

```

```

RESULT 2
US-09-109-207C-22
: Sequence 22, Application US/09109207C
: Patent No. 6172213
: GENERAL INFORMATION:
: APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
: TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
: FILE REFERENCE: P1123R1
: CURRENT APPLICATION NUMBER: US/09/109,207C
: CURRENT FILING DATE: 1998-06-30
: PRIOR APPLICATION NUMBER: US 60/051,554
: PRIOR FILING DATE: 1997-07-03
: NUMBER OF SEQ ID NOS: 44
: SEQ ID NO 22
: LENGTH: 248
: TYPE: PRT
: ORGANISM: Artificial
: FEATURE:
: NAME/KEY: Artificial
: LOCATION: 1-248
: OTHER INFORMATION: sfv sequence derived from MAB11
US-09-109-207C-22

```

Query Match	56.7%;	Score 764;	DB 3;	Length 248;
Best Local Similarity	60.7%;	Pred. No. 1.4e-53;		
Matches 156;	Conservative 30;	Mismatches 57;	Indels 14;	Gaps 4;
QY	1	QVTLKESGPTLVKPTQTLLTCTFSGPSLRTTGEVGVWVRQPPKALEWLALTYWDDKR	60	
Dp	1	EVQLVESGGGLVQPGGSLRLSCAVSYSI-TSGYSMNWIRQAPKGLEWVASITYDGS	59	
QY	61	YSPSLKSRLLITKDTSKKQVLTMTNVDPADTATYYCTHEQYYDTSQPYFDWQGT	120	
Dp	60	YNPSYKGRITISRDSKNTFYLMNSLRAEDTAVVYCARGSHYFG---HMHFAVWGQGT	115	
QY	121	LVTYSSGGGGGGGGGGGGGSGNSNIQVTSPPSSISASVGDRTVMTCRASQDI----	176	
Dp	116	LVTYS-----SEGGGSEGGSEGGSDIQLTQSPSSISASVGDRTVITCRASKPVDGEGD	170	
QY	177	KNLNTMYQQKPGKAPKVLIVDASDLETGIPSRFSGSGSGTDFILTISSLQPEDIATYYCQ	236	
Dp	171	SYLNTYQQKPGKAPKLLIYAASYLESVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ	230	
QY	237	SDYLPLTFGGGKVDIK	253	
Dp	231	SHEDPYTFGGGTKEIK	247	

```

RESULT 3
US-09-296-005-22
; Sequence 22, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352

```

```

: EARLIER FILING DATE: 1997-07-02
: NUMBER OF SEQ ID NOS: 26
: SEQ ID NO 22
: LENGTH: 248
: TYPE: prt
: ORGANISM: Artificial
: FEATURE:
: NAME/KEY: Artificial
: LOCATION: 1-248
: OTHER INFORMATION: sfv sequence derived from MAR11
US-09-296-005-22

```

Query Match	56.7%	Score 764	DB 3	Length 248
Best Local Similarity	60.7%	Pred. No. 1.4e-53		
Matches 156	Conservative 30	Mismatches 57	Indels 14	Gaps 4
QY	1 QVTLKESGPTLVKPTQTLLTCTFSGFSLRTTGEVGVWVROPFGKALEMLALTYWDDKR	60		
Db	1 EVQLVESGGGLVQPGGSLRLSCAVSGYSI-TSGYSMMWIRQAPGKLEWVASITYDGSIN	59		
QY	61 YPSPLKSRLLTITKDTSKQVLLTMTNVDPADTATYYCTHEQYYYDTSGQPYFFDFWGQGT	120		
Db	60 YNPSVKGRITISRDSKNFTFYLOMNSLRADETAVYYCARGSHYFG---HWHFAYWGQGT	115		
QY	121 LVTVSSGGGSGGGSGGGSGGGSGGSGNIVQTQSPSSLSASVGDRTVMTCRASQDI-----R	176		
Db	116 LVTVS-----SEGGSGGGSGGGSGGGSDIQLTQSPSSLSASVGDRTVITCRASKVDGEGD	170		
QY	177 KNLNMYQQKPGKAPKVLIDASDLETGIPSRFSGSGSGTDFILTITSSLPREDIATYYCQQ	236		
Db	171 SYLNMYQQKPGKAPKLLIYAASYLESGVPSRFSGSGSGTDFLLTITSSLPREDIATYYCQQ	230		
QY	237 SDYLPPLTFGGGTAKVDIK	253		
Db	231 SHEDPYTFGGGTAKVEIK	247		

```

RESULT 4
US-09-920-171-22
; Sequence 22, Application US/09920171
; Patent No. 6682735
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-1GE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 22
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sfv sequence derived from MARI1
US-09-920-171-22

```

```

Query Match          56.7%; Score 764; DB 4; Length 248;
Best Local Similarity 60.7%; Pred. No. 1.4e-53;
Matches 156; Conservative 30; Mismatches 57; Indels 14; Gaps 4;

QY      1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVGWVRQPFGKALEWLALTYMDDDKR 60
       :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1 EVQLVESGGGLVQPGSRLRSCAVGSYSI-TSGYSMNWIRQAPEGKLEWVASITYDGSTN 59

QY      61 YSPSLKSRLTTTKDTSKKQAVLTMNVDPADATAYYCTHEQYYDYDTSGOPYEDFWGQGT 120
       ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

Db 60 YNPSVKGRITISRDSKNTFYLMQNSLRADTAVYYCARGSHYFG---HMHFAVWGQGT 115  
QY 121 LVTVSSGGGGGGGGGGGGGGGNIQVTSPPSSLSASVGDRTVMTCRASQDI----R 176  
Db 116 LVTVS-----SEGGSEGGSEGGSDIQLTQSPSSLSASVGDRTVITCRASKPVDGEGD 170  
QY 177 KNLNMYQOKPGKAPKVLIDASDLETGIPSRFSGSGSGTDFILTISSLPEDIATYYCCQ 236  
Db 171 SYLNMWYQOKPGKAPKLLIYAASYLESVPSRFSGSGSGTDFILTISSLPEDFATYYCCQ 230  
QY 237 SDYLPFTFGGGTKVDIK 253  
Db 231 SHEDPYTFGGGTKEIK 247

RESULT 5  
US-08-918-148-77  
; Sequence 77, Application US/08918148A  
; Patent No. 6342220  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camellia  
; APPLICANT: W.  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Fendly, Brian M.  
; APPLICANT: Gurney, Austin L.  
; TITLE OF INVENTION: Agonist Antibodies  
; FILE REFERENCE: P0979  
; CURRENT APPLICATION NUMBER: US/08/918,148A  
; CURRENT FILING DATE: 1997-08-25  
; NUMBER OF SEQ ID NOS: 79  
; SEQ ID NO 77  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: artificial  
US-08-918-148-77

Query Match 56.5%; Score 762; DB 4; Length 244;  
Best Local Similarity 60.6%; Pred. No. 1.9e-53;  
Matches 154; Conservative 33; Mismatches 51; Indels 16; Gaps 4;  
QY 1 QVTLKESGPTLVKPTQTLTLCTFSGFSLRTTGEVGVWRQPPGKALEWLLAIYWD-DK 59  
Db 3 QVQLVQSGGGLVVRPGSLSLSCAVSGITLRT--YGMHWVRQAPGKLEWVAGISFDGRSE 60  
QY 60 RYSPSLKSRLLITKDTSKQVLTMTNVDPADTATYYCTHEQYYDTSQPPYFDFWGQG 119  
Db 61 YYADSVGRFTISRDSKNTLYLQMSLRADTAVYYCAR-----GAHYGFDIHWGL 112  
QY 120 TLVTVSSGGGGGGGGGGGGGNIQVTSPPSSLSASVGDRTVMTCRASQDIRKNL 179  
Db 113 TMVTVS-----SGGGGTGGGGGGGSDIQMTQSPSTLSASIGDRVITTCRASEGIYHWL 167  
QY 180 NMWYQOKPGKAPKVLIDASDLETGIPSRFSGSGSGTDFILTISSLPEDIATYYCCQSDY 239  
Db 168 AWYQOKPGKAPKLLIYKASSLSASGAPSRFSGSGTDFLTITISSLPDDFATYYCCQYSN 227  
QY 240 LPLTFGGGTKVDIK 253  
Db 228 YPLTFGGGTLEIK 241

RESULT 6  
US-08-887-352B-23  
; Sequence 23, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
; TITLE OF INVENTION: Improving Polypeptides  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way

CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,352B  
FILING DATE: 03-Jul-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P1123  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 248 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-887-352B-23

Query Match 56.5%; Score 762; DB 2; Length 248;  
Best Local Similarity 60.3%; Pred. No. 2e-53;  
Matches 155; Conservative 32; Mismatches 56; Indels 14; Gaps 4;  
QY 1 QVTLKESGPTLVKPTQTLTLCTFSGFSLRTTGEVGVWRQPPGKALEWLLAIYWD-DK 60  
Db 1 EVQLVESGGGLVQPGSLRLSGCAVSGYSI-TSGYSWMWIRQAPGKLEWVASIKYSGETK 59  
QY 61 YSPSLKSRLLITKDTSKQVLTMTNVDPADTATYYCTHEQYYDTSQPPYFDFWGQGT 120  
Db 60 YNPSVKGRITISRDSKNTFYLMQNSLRADTAVYYCARGSHYFG---HMHFAVWGQGT 115  
QY 121 LVTVSSGGGGGGGGGGGGGNIQVTSPPSSLSASVGDRTVMTCRASQDI----R 176  
Db 116 LVTVS-----SEGGSEGGSEGGSDIQLTQSPSSLSASVGDRTVITCRASKPVDGEGD 170  
QY 177 KNLNMYQOKPGKAPKVLIDASDLETGIPSRFSGSGSGTDFILTISSLPEDIATYYCCQ 236  
Db 171 SYLNMWYQOKPGKAPKLLIYAASYLESVPSRFSGSGSGTDFLTITISSLPEDFATYYCCQ 230  
QY 237 SDYLPFTFGGGTKVDIK 253  
Db 231 SHEDPYTFGGGTKEIK 247

RESULT 7  
US-09-109-207C-23  
; Sequence 23, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; CURRENT FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 23  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Artificial  
; LOCATION: 1-248  
; OTHER INFORMATION: sfv sequence derived from MARI1







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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,164A
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR94/00714
; FILING DATE: 15-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93/07241
; FILING DATE: 16-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin F.
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: ST93030-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3816
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-564-164A-4
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Query Match          54.6%; Score 736; DB 3; Length 264;
Best Local Similarity 57.7%; Pred. No. 2.5e-51;
Matches 146; Conservative 32; Mismatches 61; Indels 14; Gaps 3;
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QY      1 QVTLKESGPTLVKPTQTLLTCTFSGFSLRTGEGVWVRQPPGKALEWLAITYWDDDKR 60
Db      11 QVQLQESGPGIGQPAQISITCTVSGFSL--SSYGVHWVRQSPGKLEWLVGIWRGGGTD 68
QY      61 YSPSLKSLRLITTKDTSKKQVLTMTNVPADATATYCTHEQYYDTSQQPYFDWGGGT 120
Db      69 YNAAFMSRLISITKDNSKSVFVKLSLQPDPTAMYYCAKR-----GGPGYFDVWGGGT 121
QY      121 LVTVSSGGGSGGGSGGGSGGGSNIQVTSPPSLASASVGDRTVMTCRASQDIRKNTN 180
Db      122 TVTVS-----SGGGSGGGSGGGSGGSDIELTQSPASLSASVGETVTMTCRASENITYSNLA 176
QY      181 WYQOKPGKAPKVLIDASDLETGIPSRFSGSGGTDIFLITSSLOPEDIAITYCCQSDYL 240
Db      177 WYQOKQKSPQLLVYAATKPGNVPSRFSGSGGTQFSLKINSLOPEDLGNYICLHFYGT 236
QY      241 PLTFGGGTKVDIK 253
Db      237 PYRFGGGTKLETK 249
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## RESULT 14

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; Sequence 148, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION DATA:
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-113B-148
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Query Match          54.5%; Score 734.5; DB 1; Length 240;
Best Local Similarity 57.9%; Pred. No. 2.9e-51;
Matches 147; Conservative 31; Mismatches 61; Indels 15; Gaps 4;
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Db      1 EIQLVQSGGGLVKGPGSVRISCAASYTF--TNYGMNVVRQAPGKLEWVGWINTHTGEP 58
QY      60 RYSPSLKSLRLITTKDTSKKQVLTMTNVPADATATYCTHEQYYDTSQQPYFDWGGG 119
Db      59 TYADSFGRFTFSLDSDSKNTAYLQINSIRAEDTAVYFCTR-----GYDWYFDVWGGG 111
QY      120 TLVTSSGGGSGGGSGGGSGGGSNIQVTSPPSLASASVGDRTVMTCRASQDIRKNTL 179
Db      112 TVTVS-----SGGGSGGGSGGGSGGSDIQVTSPPSLASASVGDRTVITCRASQDINSYL 166
QY      180 NMYQOKPGKAPKVLIDASDLETGIPSRFSGSGGTDIFLITSSLOPEDIAITYCCQSDY 239
Db      167 SWFQOKPGKAPKTLIYRANRLSGVPSRFSGSGGTDYTLTSSLOYEDFGITYCCQSDY 226
QY      240 LPLTFGGGTKVDIK 253
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## RESULT 15

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; Sequence 148, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 15:07:07 ; Search time 37.4587 Seconds  
(without alignments)  
1879.405 Million cell updates/sec

Title: US-10-072-301-23  
Perfect score: 1348  
Sequence: 1 QVTLKESGPTLVKPTQTTLT.....CQQSDYLPITFGGKVDIK 253

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145568 segs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
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15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1348	100.0	253	14	US-10-072-301-23 Sequence 23, Appl
2	1348	100.0	253	14	US-10-072-301-31 Sequence 31, Appl
3	1348	100.0	253	14	US-10-071-866-23 Sequence 23, Appl
4	1348	100.0	253	14	US-10-071-866-31 Sequence 31, Appl
5	1348	100.0	253	15	US-10-360-828-23 Sequence 23, Appl
6	1348	100.0	253	15	US-10-360-828-31 Sequence 31, Appl
7	821.5	60.9	286	12	US-10-406-830-8 Sequence 8, Appl1
8	811.5	60.2	251	10	US-09-880-748-1049 Sequence 1049, Ap
9	811.5	60.2	251	12	US-10-293-418-1049 Sequence 1049, Ap
10	803	59.6	248	10	US-09-880-748-1360 Sequence 1360, Ap
11	803	59.6	248	12	US-10-293-418-1360 Sequence 1360, Ap
12	801.5	59.5	255	10	US-09-880-748-1603 Sequence 1603, Ap
13	801.5	59.5	255	12	US-10-293-418-1603 Sequence 1603, Ap
14	800.5	59.4	249	10	US-09-880-748-1321 Sequence 1321, Ap
15	800.5	59.4	249	12	US-10-293-418-1321 Sequence 1321, Ap

16	794	58.9	253	14	US-10-072-301-17	Sequence 17, Appl
17	794	58.9	253	14	US-10-072-301-25	Sequence 25, Appl
18	794	58.9	253	14	US-10-071-866-17	Sequence 17, Appl
19	794	58.9	253	14	US-10-071-866-25	Sequence 25, Appl
20	794	58.9	253	15	US-10-360-828-17	Sequence 17, Appl
21	794	58.9	253	15	US-10-360-828-25	Sequence 25, Appl
22	789	58.5	248	10	US-09-880-748-1876	Sequence 1876, Ap
23	789	58.5	248	12	US-10-293-418-1876	Sequence 1876, Ap
24	787	58.4	248	10	US-09-880-748-1421	Sequence 1421, Ap
25	787	58.4	248	12	US-10-293-418-1421	Sequence 1421, Ap
26	781.5	58.0	243	10	US-09-880-748-1935	Sequence 1935, Ap
27	781.5	58.0	243	12	US-10-293-418-1935	Sequence 1935, Ap
28	781.5	58.0	249	10	US-09-880-748-1188	Sequence 1188, Ap
29	781.5	58.0	249	12	US-10-293-418-1188	Sequence 1188, Ap
30	777	57.6	250	10	US-09-880-748-1174	Sequence 1174, Ap
31	777	57.6	250	12	US-10-293-418-1174	Sequence 1174, Ap
32	777	57.6	287	12	US-10-406-830-5	Sequence 5, Appl1
33	769	57.0	266	12	US-10-257-864A-108	Sequence 108, Appl
34	769	57.0	291	12	US-10-406-830-10	Sequence 10, Appl
35	765	56.8	250	15	US-10-423-847-12	Sequence 12, Appl
36	764.5	56.7	333	14	US-10-059-261-61	Sequence 61, Appl
37	764	56.7	248	9	US-09-920-171-22	Sequence 22, Appl
38	764	56.7	248	14	US-10-113-996-22	Sequence 22, Appl
39	762	56.5	248	9	US-09-920-171-23	Sequence 23, Appl
40	762	56.5	248	10	US-09-880-748-1004	Sequence 1004, Ap
41	762	56.5	248	12	US-10-293-418-1004	Sequence 1004, Ap
42	762	56.5	248	14	US-10-113-996-23	Sequence 23, Appl
43	761	56.5	240	9	US-09-192-854-2	Sequence 2, Appl1
44	761	56.5	240	9	US-09-968-561A-2	Sequence 2, Appl1
45	761	56.5	240	10	US-09-968-744A-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1  
US-10-072-301-23  
; Sequence 23, Application US/10072301  
; Publication No. US20030152913A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF  
; FILE REFERENCE: 25636-718  
; CURRENT APPLICATION NUMBER: US/10/072,301  
; CURRENT FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.24  
US-10-072-301-23

Query Match	Best Local Similarity	Score	100.0%;	Pred. No. 2e-87;	DB 14;	Length 253;	Matches 253;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	QVTLKESGPTLVKPTQTTLTCTFSGFSRLTGBGVWTRQPPGKALEWLAIIYWD	DKR	60							
Db	1	QVTLKESGPTLVKPTQTTLTCTFSGFSRLTGBGVWTRQPPGKALEWLAIIYWD	DKR	60							
QY	61	YSPSLKSRLLTTTKDTSKQVLLMTNVPADTATYYCTHEQYYVDTSGQPYFDFWG	CGT	120							
Db	61	YSPSLKSRLLTTTKDTSKQVLLMTNVPADTATYYCTHEQYYVDTSGQPYFDFWG	CGT	120							
QY	121	LVTWSSGGGSGGGSGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRK	NLN	180							
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OY      181 WYQOKPGKAPKVLIDASDLETGIPSRFSGSGSGTDFILTISSLOPEDIAITYCCQSDYL 240
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Db      181 WYQOKPGKAPKVLIDASDLETGIPSRFSGSGSGTDFILTISSLOPEDIAITYCCQSDYL 240
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OY      241 PLTFGGGTAKVDIK 253
      |||||||
Db      241 PLTFGGGTAKVDIK 253
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## RESULT 2

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US-10-072-301-31
; Sequence 31, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 31
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24 Variant
US-10-072-301-31
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Query Match
Best Local Similarity 100.0%; Score 1348; DB 14; Length 253;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 QVTLKESGPTLVKPTQTTLTCTFSGFSRLRTTGEVGVWVROPFGKALEWLALITYWDDDKR 60
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OY      61 YSPSLKSRLTITKDTSKQVLLMTNVPADATATYYCTHEQYYVDTSGQPYFDFWGGGT 120
      |||||||
Db      61 YSPSLKSRLTITKDTSKQVLLMTNVPADATATYYCTHEQYYVDTSGQPYFDFWGGGT 120
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OY      121 LVTVSSGGGSGGGGSGGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKNLN 180
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Db      121 LVTVSSGGGSGGGGSGGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKNLN 180
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Db      241 PLTFGGGTAKVDIK 253
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## RESULT 3

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US-10-071-866-23
; Sequence 23, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST F
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
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; SEQ ID NO 23
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24
US-10-071-866-23
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Query Match
Best Local Similarity 100.0%; Score 1348; DB 14; Length 253;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 QVTLKESGPTLVKPTQTTLTCTFSGFSRLRTTGEVGVWVROPFGKALEWLALITYWDDDKR 60
      |||||||
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      |||||||
Db      61 YSPSLKSRLTITKDTSKQVLLMTNVPADATATYYCTHEQYYVDTSGQPYFDFWGGGT 120
      |||||||
OY      121 LVTVSSGGGSGGGGSGGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKNLN 180
      |||||||
Db      121 LVTVSSGGGSGGGGSGGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKNLN 180
      |||||||
OY      181 WYQOKPGKAPKVLIDASDLETGIPSRFSGSGSGTDFILTISSLOPEDIAITYCCQSDYL 240
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Db      181 WYQOKPGKAPKVLIDASDLETGIPSRFSGSGSGTDFILTISSLOPEDIAITYCCQSDYL 240
      |||||||
OY      241 PLTFGGGTAKVDIK 253
      |||||||
Db      241 PLTFGGGTAKVDIK 253
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## RESULT 4

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US-10-071-866-31
; Sequence 31, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST P
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 31
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24 Variant
US-10-071-866-31
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Query Match
Best Local Similarity 100.0%; Score 1348; DB 14; Length 253;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 QVTLKESGPTLVKPTQTTLTCTFSGFSRLRTTGEVGVWVROPFGKALEWLALITYWDDDKR 60
      |||||||
Db      1 QVTLKESGPTLVKPTQTTLTCTFSGFSRLRTTGEVGVWVROPFGKALEWLALITYWDDDKR 60
      |||||||
OY      61 YSPSLKSRLTITKDTSKQVLLMTNVPADATATYYCTHEQYYVDTSGQPYFDFWGGGT 120
      |||||||
Db      61 YSPSLKSRLTITKDTSKQVLLMTNVPADATATYYCTHEQYYVDTSGQPYFDFWGGGT 120
      |||||||
OY      121 LVTVSSGGGSGGGGSGGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKNLN 180
      |||||||
Db      121 LVTVSSGGGSGGGGSGGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKNLN 180
      |||||||
OY      181 WYQOKPGKAPKVLIDASDLETGIPSRFSGSGSGTDFILTISSLOPEDIAITYCCQSDYL 240
      |||||||
```

[illegible]

## RESULT 5

```

US-10-360-828-23
; Sequence 23, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24
US-10-360-828-23

```

Query Match	100.0%;	Score 1348;	DB 15;	Length 253;
Best Local Similarity	100.0%;	Pred. No. 2e-87;		
Matches 253; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	QVTLKESGPTLVKPTQTLLTCTFSGFSLRTTGEGVGWVRQPPGKALEWIALIYWDDDKR	60
Db	1	QVTLKESGPTLVKPTQTLLTCTFSGFSLRTTGEGVGWVRQPPGKALEWIALIYWDDDKR	60
QY	61	YSPSLKSRLLTITKDTSKKQVVLMTNVPADATATYYCTHEQYYYPDTSQBPYFDFWGGGT	120
Db	61	YSPSLKSRLLTITKDTSKKQVVLMTNVPADATATYYCTHEQYYYPDTSQBPYFDFWGGGT	120
QY	121	LVTVSSGGGGSGGGSGGGSGGGSNIQVTQSPSSLASAVGDRVMTTCRASQDIRKNLN	180
Db	121	LVTVSSGGGGSGGGSGGGSGGGSNIQVTQSPSSLASAVGDRVMTTCRASQDIRKNLN	180
QY	181	WYQOKPGKAPKVL IYDASDLETGIPSRFSGSGSGTDFILTISLQPEDIATYYCQOQSDYL	240
Db	181	WYQOKPGKAPKVL IYDASDLETGIPSRFSGSGSGTDFILTISLQPEDIATYYCQOQSDYL	240
QY	241	PLTFGGGKVDIK 253	
Db	241	PLTFGGGKVDIK 253	

## RESULT 6

```

US-10-360-828-31
: Sequence 31, Application US/10360828
: Publication No. US20030206909A1
: GENERAL INFORMATION:
: APPLICANT: Hua, Shaobing
: APPLICANT: Pauling, Michelle H.
: APPLICANT: Zhu, Li
: TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
: FILE REFERENCE: 25636-727
: CURRENT APPLICATION NUMBER: US/10/360,828
: CURRENT FILING DATE: 2003-02-07

```

```

; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24 Variant
US-10-360-828-31

```

Query Match	100.0%;	Score 1348;	DB 15;	Length 253;
Best Local Similarity	100.0%;	Pred. No. 2e-87;		
Matches 253; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY	I QVTLKESGPTLVKPQTOTLILCTFSGFSRLRTTGEVGWVRQPPGKALEWIALIYWDDDKR	60
Dp	1 QVTLKESGPTLVKPQTOTLILCTFSGFSRLRTTGEVGWVRQPPGKALEWIALIYWDDDKR	60
OY	61 YSPSLKSRLTITKTDSKKQVVLMTNVDPADTATYYCTHEQYYYDTSGGOPYFDFFWGQGT	120
Dp	61 YSPSLKSRLTITKTDSKKQVVLMTNVDPADTATYYCTHEQYYYDTSGGOPYFDFFWGQGT	120
OY	121 LVTVSSGGGGSGGGSGGGGSNIQVTQSPSSLASAVGDRTVMTGRASODIRKNLN	180
Dp	121 LVTVSSGGGGSGGGSGGGGSNIQVTQSPSSLASAVGDRTVMTGRASODIRKNLN	180
OY	181 WYQQPKGAPKVL IYDASDLETGI PSRFSGSGS GTFILTIISLQPEBIATYYCCQOSDYL	240
Dp	181 WYQQPKGAPKVL IYDASDLETGI PSRFSGSGS GTFILTIISLQPEBIATYYCCQOSDYL	240

QY	241	PLTFGGG	KVDIK	253
Db	241	PLTFGGG	KVDIK	253

## RESULT 7

```

; Sequence 8, Application US/10406830
; Publication No. US20040071696A1
;
; GENERAL INFORMATION:
;
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
;
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 407T-000410US
; CURRENT APPLICATION NUMBER: US/10/406,830
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
;
; SEQ ID NO 8
;
; LENGTH: 286
;
; TYPE: PRT
;
; ORGANISM: Artificial
;
; FEATURE:
;
; OTHER INFORMATION: Synthetic antibody.
;
US-10-406-830-8

```

```

Query Match      60.9%; Score 821.5; DB 12; Length 286;
Best Local Similarity 66.1%; Pred. NO. 2.7e-50;
Matches 168; Conservative 28; Mismatches 43; Indels 15; Gaps 6;

QY      1 QVTLKESGPTLVKPTQTLLTCTPSGFSLRTTGEVGVWRQPGKALEWLLALTYWDDKR 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```



[illegible]

```

RESULT 8
US-09-880-748-1049
; Sequence 1049, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that immunospecifically bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1049
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1049

```

Query Match	60.2%;	Score 811.5;	DB 10;	Length 251;
Best Local Similarity	63.0%;	Pred. No. 1.2e-49;		
Matches 160;	Conservative 31;	Mismatches 58;	Indels 5;	Gaps 3;
QY	1	QVTLKESGPTLVKPTQTLLTLLTCTFSGFSLRTTGEVGWVROPPGKALEWALITYMDDDKR	60	
Dp	1	QLQLQESGPGLVKPSSETLSLTCTVSGGFISSRTSYMGWIRQPPGKPEWIGNIYYTGKTY	60	
QY	61	YSPSLKSRLLITKDTSKQVLTMTNVDPADTATYYCTHEQYYVDTSGQPYFDFWGGST	120	
Dp	61	YSPSLKSRVLTISVDTSKNQLSLKLNSTADTAVVYCARAGVDLLT-GYPFYFDSMGKT	119	
QY	121	LVTYSSGGGGSGGGSGGGSGGGGSNIQVTSPPSLASVGDRTMTCRASQDIRKNLN	180	
Dp	120	LVTYSSGGGGSGGGSGGGSGGGGS---ALEIVLTQSPATLSLSPGERATLSCRASQSVSSYLA	176	
QY	181	WYQOKPGKAPKVLITYDASDLETGIPSRFSGSGSGTDFILLTSSLOPEDIATYYCQQSDYL	240	
Dp	177	WYQOKPGQAPRLLIYDASNRTATGIPARFSGSGSGTDFILLTSSLEPEDFAVYYCQQRSNW	236	
QY	241	P-LTFGGGTGVNDIK	253	
Dp	237	PFLTFGGGTKEIK	250	

## RESULT 9

```

US-10-293-418-1049
; Sequence 1049, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1049
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1049

```

Query Match	60.2%	Score 811.5	DB 12	Length 251
Best Local Similarity	63.0%	Pred. No. 1.2e-49		
Matches 160	Conservative 31	Mismatches 58	Indels 5	Gaps 3
QY	1 QVLTKESGPTLVKPTQTLLTCTCFSGFSLRTTGEVGVWTRQPPGKALEMLAIYWDDDKR	60		
Db	1 QLOQESGPGLVKPSSETLSLTCTVSGGFISSRISYMGWIRQPPGKPEWIGNIYTGKTY	60		
QY	61 YSPSLKRLTITKDTSKQVLLMTNVPADTATYYCTHEQYYYDTSQPPYFDFWGQGT	120		
Db	61 YSPSLKSRVTISVDTSKNQSLKLNSTADTAIVYYCARAGYDLLT-GYFFYFDSWGKGT	119		
QY	121 LVTVSSGGGGSGGGSGGGSGGGSNIQVTSPPSLASVGDRTVMTCRASODIRKULN	180		
Db	120 LVTVSSGGGGSGGGSGGGSGGGS--ALEIVLTQSPATLLSLSPGERATLSCASQSVSSYLA	176		
QY	181 WYQOKPGKAPKVLIVDASDLETGIPSRFSGSGSGTDFILTISSLOPEDIATYYCQQSDYL	240		
Db	177 WYQOKPGQAPRLLIYDASNRTATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNW	236		
QY	241 P-LTFGGGTKVDIK	253		
Db	237 PFLTFGGGTKVEIK	250		

RESULT 10  
US-09-880-748-1360  
; Sequence 1360, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PFS23  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16

## RESULT 9



;; PRIOR APPLICATION NUMBER: 60/277,379  
;; PRIOR FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/293,499  
;; PRIOR FILING DATE: 2001-05-25  
;; NUMBER OF SEQ ID NOS: 3239  
;; SOFTWARE: Patentln Ver. 2.0  
;; SEQ ID NO 1360  
;; LENGTH: 248  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-880-748-1360

Query Match 59.6%; Score 803; DB 10; Length 248;  
Best Local Similarity 63.2%; Pred. No. 4.6e-49;  
Matches 160; Conservative 32; Mismatches 55; Indels 6; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTTLTCTFSGFSRLRTGEGVGVWRQPPGKALEWLALIWDDDKR 60  
Db 1 QVQLQESGPGLVKPSSETLSLCTVSGGSIRS--YYMSWIRQSPGRGLEWIGHIYHSGSTD 58  
QY 61 YSPSLKSRLLTTKDTSKQVVLMTNVDPADTATYYCTHEQYYVDTSGQPYFDFWGQGT 120  
Db 59 YNPSLSRVRTMSIDTSKNQFSLNLTSTADTAIVYYCARDHYDLTGSYLQAFDVMGQGT 118  
QY 121 LVTVSSGGGSGGGSGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKNLN 180  
Db 119 LVTVSSGGGSGGGSGGGSGGGS--ALDIQLTQSPSSLSASVGDRTVITCRASQSIGRYLN 175  
QY 181 WYQKPKGAPKVLIDYASDLETGIPSRFSGSGSGTDFILTTISSLPEDIATYYCQOSDYL 240  
Db 176 WYQKPKGRAPRLIFVTSSLHSDVPSRFSGSGSGTDFSLTISNLQPEDFATYYCQOS-YT 234  
QY 241 PLTFGGGTGVNDIK 253  
Db 235 DPTFGGQTRLEIK 247

RESULT 11  
US-10-293-418-1360

;; Sequence 1360, Application US/10293418  
;; Publication No. US20030223996A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ruben et al.  
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
;; FILE REFERENCE: PF523P2  
;; CURRENT APPLICATION NUMBER: US/10/293,418  
;; PRIOR FILING DATE: 2002-11-27  
;; PRIOR APPLICATION NUMBER: 60/331,469  
;; PRIOR FILING DATE: 2001-11-16  
;; PRIOR APPLICATION NUMBER: 60/340,817  
;; PRIOR FILING DATE: 2001-12-19  
;; PRIOR APPLICATION NUMBER: 09/880,748  
;; PRIOR FILING DATE: 2001-06-15  
;; PRIOR APPLICATION NUMBER: 60/293,499  
;; PRIOR FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: 60/277,379  
;; PRIOR FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/276,248  
;; PRIOR FILING DATE: 2001-03-16  
;; PRIOR APPLICATION NUMBER: 60/240,816  
;; PRIOR FILING DATE: 2000-10-17  
;; PRIOR APPLICATION NUMBER: 60/212,210  
;; PRIOR FILING DATE: 2000-06-16  
;; NUMBER OF SEQ ID NOS: 3247  
;; SEQ ID NO 1360  
;; LENGTH: 248  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-293-418-1360

Query Match 59.6%; Score 803; DB 12; Length 248;  
Best Local Similarity 63.2%; Pred. No. 4.6e-49;  
Matches 160; Conservative 32; Mismatches 55; Indels 6; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTTLTCTFSGFSRLRTGEGVGVWRQPPGKALEWLALIWDDDKR 60  
Db 1 QVQLQESGPGLVKPSSETLSLCTVSGGSIRS--YYMSWIRQSPGRGLEWIGHIYHSGSTD 58  
QY 61 YSPSLKSRLLTTKDTSKQVVLMTNVDPADTATYYCTHEQYYVDTSGQPYFDFWGQGT 120  
Db 59 YNPSLSRVRTMSIDTSKNQFSLNLTSTADTAIVYYCARDHYDLTGSYLQAFDVMGQGT 118  
QY 121 LVTVSSGGGSGGGSGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKNLN 180  
Db 119 LVTVSSGGGSGGGSGGGSGGGS--ALDIQLTQSPSSLSASVGDRTVITCRASQSIGRYLN 175  
QY 181 WYQKPKGAPKVLIDYASDLETGIPSRFSGSGSGTDFILTTISSLPEDIATYYCQOSDYL 240  
Db 176 WYQKPKGRAPRLIFVTSSLHSDVPSRFSGSGSGTDFSLTISNLQPEDFATYYCQOS-YT 234  
QY 241 PLTFGGGTGVNDIK 253  
Db 235 DPTFGGQTRLEIK 247

RESULT 12

US-09-880-748-1603  
;; Sequence 1603, Application US/09880748  
;; Publication No. US20030059937A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ruben et al.  
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
;; FILE REFERENCE: PF523  
;; CURRENT APPLICATION NUMBER: US/09/880,748  
;; PRIOR FILING DATE: 2001-06-15  
;; PRIOR APPLICATION NUMBER: 60/212,210  
;; PRIOR FILING DATE: 2000-06-15  
;; PRIOR APPLICATION NUMBER: 60/240,816  
;; PRIOR FILING DATE: 2000-10-17  
;; PRIOR APPLICATION NUMBER: 60/276,248  
;; PRIOR FILING DATE: 2001-03-16  
;; PRIOR APPLICATION NUMBER: 60/277,379  
;; PRIOR FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/293,499  
;; PRIOR FILING DATE: 2001-05-25  
;; NUMBER OF SEQ ID NOS: 3239  
;; SOFTWARE: Patentln Ver. 2.0  
;; SEQ ID NO 1603  
;; LENGTH: 255  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-880-748-1603

Query Match 59.5%; Score 801.5; DB 10; Length 255;  
Best Local Similarity 62.0%; Pred. No. 6.1e-49;  
Matches 163; Conservative 27; Mismatches 54; Indels 19; Gaps 6;

QY 1 QVTLKESGPTLVKPTQTTLTCTFSGFSRLRTGEGVGVWRQPPGKALEWLALIWDDDKR 56  
Db 1 QVQLQESGPGLVKPSQTLSLCAISGDSVGSNGAAMWIRQSPGRGLEWIGRTYRSQWY 60  
QY 57 DDKRYSPSLKSRLLTTKDTSKQVVLMTNVDPADTATYYCTHEQYYVDTSGQPYFDFWGQGT 112  
Db 61 SD--YGASVRSRITINADTSKNQFSLQNSVTPEDTAVYYCARDHSDVLTG--YSSGG 116  
QY 113 --PDEFWGQGLVTVSSGGGSGGGSGGGSGGGSNIQVTPSSLSASVGDRTVMTCR 170  
Db 117 GMDVWGRGTLTVTS-----SGGGSGGGSGGGSGGGSDIQMTQSPSTLSASIGDRVITTCR 171  
QY 171 ASQDIRKNLNMWYQKPKGAPKVLIDYASDLETGIPSRFSGSGSGTDFILTTISSLPEDIA 230  
Db 172 ASEGIVHWLAWYQKPKGAPKVLIIYKASSLASGAPSRFSGSGSGTDFILTTISSLPDDFA 231  
QY 231 TTYCQOSDYLPLTFGGGTGVNDIK 253  
Db 232 TTYCQOYSNYPPLTFGGGTGVNDIK 254

## RESULT 13

```
US-10-293-418-1603
; Sequence 1603, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1603
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1603
```

```
Query Match          59.5%; Score 801.5; DB 12; Length 255,
Best Local Similarity 62.0%; Pred. No. 6.1e-49;
Matches 163; Conservative 27; Mismatches 54; Indels 19; Gaps 6;
```

```
QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVWVRQPPGKALEMLLIY---WD 56
   ||::|||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 QVQLQSGSGPGLVKPSQTLISLCAISGDSVSGAAMNIRQSPRGLEWLGRTYRSQWY 60

QY 57 DDKRYSPLSKRLTITKDTSKQVLTMTNVPADTATYCTHEQYYD-TSGQPY--- 112
   ||::|||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 61 SD--YGASVSRITINADTSKNQFSLQLNSVTPEDTAVYYCARSGRYDILTG--YSSGG 116

QY 113 --FDFWGQGITLVSSGGGGSGGGGGSGGSGNSIQVTQSPSSLSASVGDRTVMTCR 170
   ||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 117 GGMVWGRTLVTVS-----SGGGSGGGGGSGGSDIQMTQSPSTLSASIGDRVITTCR 171

QY 171 ASQDIRKLNMYQQKPKAPKVLIVDASDLETGIPSRFSGSGSGTDFILTTISSLPEDIA 230
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 172 ASEGIVHWLAWYQQKPKAPKLLIKASSLSASGAPSRFSGSGSGTDFLTITSSLPDDFA 231

QY 231 TYYCQQSDDVLPPLTFGGGTKVDIK 253
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 232 TYYCQQYSNYPPLTFGGGTKLEIK 254
```

## RESULT 14

```
US-09-880-748-1321
; Sequence 1321, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
```

```
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1321
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1321
```

```
Query Match          59.4%; Score 800.5; DB 10; Length 249;
Best Local Similarity 64.3%; Pred. No. 7e-49;
Matches 164; Conservative 27; Mismatches 55; Indels 9; Gaps 4;
```

```
QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVWVRQPPGKALEMLLIYWD DDKR 60
   ||::|||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 QVQLQWAGALLKPSSETLSLTCVYGGSF--SGYWSWIRQPPGKLEWIGEINHSSTN 58

QY 61 YSPSLKSRLLTITKDTSKQVLTMTNVPADTATYCTHEQYYD-TSGQPY-YFDWQ 118
   ||::|||:|||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 59 YNPSLSKRVTVISVDTSKNQFSLKLSVTAADTAVYYCARGPRIYYDILTGIRYWFDPWGR 118

QY 119 GTLVTVSSGGGGSGGGGGSGGSGGSGNSIQVTQSPSSLSASVGDRTVMTCRASQDIRKN 178
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 119 GTLVTVS-----SGGGSGGGGGSGGSDIVMTQSPSTLSASVGDRTVITTCRASQGISW 173

QY 179 LNWYQQKPKAPKVLIVDASDLETGIPSRFSGSGSGTDFILTTISSLPEDIAATYCCQSD 238
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 174 LNWYQQKPKRAPKVLIVKASTLESQVPSRFSGSGSGTDFLTITSSLPEDFATYCCQGSY 233
```

```
QY 239 YLPLTFGGGTKVDIK 253
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 234 STPWTFGGGTKLEIK 248
```

## RESULT 15

```
US-10-293-418-1321
; Sequence 1321, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1321
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1321
```



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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 14:50:27 ; Search time 11.4218 Seconds  
(without alignments)  
2130.694 Million cell updates/sec

Title: US-10-072-301-23

Perfect score: 1348  
Sequence: 1 QVTLKESGPTLVKPTQTTLT.....CQSDYLPITFGGGRKVDIK 253

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	611	45.3	268	2	A56446	Ig heavy chain V r
2	578.5	42.9	249	2	S41374	single chain Fv an
3	551	40.9	124	2	A49002	Ig heavy chain V r
4	538.5	39.9	138	2	S31513	Ig heavy chain - h
5	534.5	39.7	374	2	S69339	Ig heavy chain V r
6	533.5	39.6	233	2	UC5322	p53 specific singl
7	487	36.1	119	2	S18555	Ig heavy chain V r
8	485.5	36.0	125	1	MHHUMC	Ig heavy chain V-I
9	474.5	35.2	121	1	G1HUME	Ig heavy chain V-I
10	470.5	34.9	118	2	S18556	Ig heavy chain V r
11	469.5	34.8	121	2	A36005	Ig heavy chain V r
12	468	34.7	108	1	K1HURY	Ig kappa chain V-I
13	468	34.7	129	2	S52789	Ig kappa chain V r
14	462	34.3	110	2	S44118	Ig kappa chain V-J
15	456	33.8	108	1	K1HUAU	Ig kappa chain V-I
16	456	33.8	108	2	B49047	Ig kappa chain V r
17	456	33.8	125	2	S40349	Ig kappa chain V-J
18	449	33.3	107	2	S36264	Ig lambda chain V
19	448	33.2	108	1	K1HUSW	Ig kappa chain V-I
20	447	33.2	107	2	S36269	Ig lambda chain V
21	445	33.0	122	2	S11740	Ig heavy chain pre
22	445	33.0	123	2	S40331	Ig kappa chain - h
23	443	32.9	108	2	S19674	Ig kappa chain V r
24	443	32.9	129	2	S52793	Ig kappa chain V r
25	442	32.8	108	1	K1HUGG	Ig kappa chain V-I
26	442	32.8	124	2	S40348	Ig kappa chain V-J
27	441	32.7	125	2	S40316	Ig kappa chain - h
28	441	32.7	127	2	S40367	Ig kappa chain V-J
29	440	32.6	107	2	S36262	Ig lambda chain V

30	439	32.6	129	2	S40317	Ig kappa chain - h
31	437	32.4	139	2	S40365	Ig kappa chain - h
32	435	32.3	108	1	K1HURE	Ig kappa chain V-I
33	435	32.3	108	1	K1HUSC	Ig kappa chain V-I
34	435	32.3	120	1	G1HUCO	Ig heavy chain V-I
35	434	32.2	108	2	I39154	Ig kappa chain (BR
36	432	32.0	109	2	S31981	Ig kappa chain - h
37	431	32.0	105	2	S36266	Ig lambda chain V
38	431	32.0	129	2	S52792	Ig kappa chain V r
39	430	31.9	117	2	S46376	Ig kappa chain V-J
40	429	31.8	125	2	S40350	Ig kappa chain - h
41	429	31.8	143	2	PT0174	Ig heavy chain pre
42	428	31.8	109	2	S31998	Ig kappa chain - h
43	427	31.7	108	2	S36279	Ig lambda chain V
44	427	31.7	117	2	S43528	Ig kappa chain V r
45	427	31.7	117	2	S42263	Ig kappa chain V r

ALIGNMENTS

RESULT 1

A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Jan-1996 #sequence\_rev1sion 19-Jan-1996 #text\_change 16-Aug-1996  
C:Accession: A56446  
R:Tang, P.M.; Foitz, L.A.; Mahoney, W.C.; Schueler, P.A.  
J. Biol. Chem. 270, 7829-7835, 1995  
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident:  
A:Reference number: A56446; MUID:95229583; PMID:7713873  
A:Accession: A56446  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-268 <TAN>  
A:Cross-references: GB:U20617  
C:Keywords: heterotetramer; immunoglobulin

Query Match 45.3%; Score 611; DB 2; Length 268;

Best Local Similarity 49.6%; Pred. No. 1.3e-34;  
Matches 126; Conservative 42; Mismatches 70; Indels 16; Gaps 6;

Qy	1	QVTLKESGPTLVKPTQTTLTCTPSGFSRLTGEVGWVRQPGKALEWLALIV-WDDDK 59
Db	3	QVKLQESGAEVLVPGASVKLSCTTSGFNKDT--YMAWVKQRPBGLEWIGRIAPANGIT 60
Qy	60	RYSPLKSRLLTITKDTSKQVVLWTNVPADATATYCTHEQYYDTSGOPYFDFWGG 119
Db	61	KYDPRKQKATIAADTSSNTAYQLSLTSEDTAVYYCAS---YVLR---YENYWGQ 113
Qy	120	TLVTWSSGGGSGGGSGGGSGGGSNIQVTPSPSLASVGDRTVMTCRASQDIRKTL 179
Db	114	TTVTWS-----SGGGSGGGSGGGSDIELTQSPAIMSASLGEKVTMSCRASSV-NFI 167
Qy	180	NWYQKPKGKAPKVLIDASDLTEGIPSRFGSGSGGTDFILITISSLPEDIATYYCQGS 239
Db	168	YMYQKSDASPKLWVYTTSHLPFGVPARFGSGSGGNSYSLTSSMEGEDATYYCQGF 227
Qy	240	LPLTFGGGTRKVDIK 253
Db	228	SPFTFGSGTKLEIK 241

RESULT 2

S41374  
single chain Fv antibody - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_rev1sion 06-Jan-1995 #text\_change 06-Jan-1995  
C:Accession: S41374  
R:Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.  
submitted to the EMBL Data Library, January 1994  
A:Description: Construction and functional characterization of a single chain Fv antiboc  
A:Reference number: S41374

A/Accession: S41374  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-249 <ART>  
A/Cross-references: EMBL:Z29480

Query Match 42.9%; Score 578.5; DB 2; Length 249;  
Best Local Similarity 44.8%; Pred. No. 1.9e-32;  
Matches 116; Conservative 50; Mismatches 74; Indels 19; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVGVWRQPPGKALEWLAITYWDDDK 59  
Db 1 QVQLQDSGAEIVRPGASVYKLSCTASGFNFK--DDYIHVWKQRPKKGLEWIAPIASGVN 58  
QY 60 YSPSLKSRLLTITKDTSKQVVLMTNVPADPATYCTHEQYYYDTSQGPYYFDWGGG 119  
Db 59 KYVPRFQDKATITADTSSNTAVLLSLTSEDTAVYYCARRDTLYTSLG-----YWGQG 112  
QY 120 TLVTVSSGGSGGGSGGGSGGGSGGSGNIQVTSPPSSLSASVGDVMTCTRASQDIRKN- 178  
Db 113 STVTVS-----SRGGSGGGSGGGSGGGSDIELTQSPPSVVIPEGSVSISCRSSKSLYSD 167  
QY 179 ----LMYQOKPGKAPKVLIDASDLETGIPSRFSGSGSGTDFILTISLQPEDIAITYC 234  
Db 168 GDSYLFWFLLQRPQGSFQLLIYRMSNLASGVDPDRFSGSGSGTSTFTLRISRVEAEDVGVYYC 227  
QY 235 QQSDYLPITFGGGTKVDIK 253  
Db 228 MQHREYPLTFGAGTKLEIK 246

RESULT 3  
A49002

Ig heavy chain V region, rheumatoid factor RF antibody - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999  
C/Accession: A49002  
R/Stuber, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, H.W.J.; Gaskin, F.  
Arthritis Rheum. 35, 900-904, 1992  
A/Title: A rheumatoid factor from a normal individual encoded by VH2 and V kappa II gene  
A/Reference number: A49002; MUID:92352481; PMID:1322670  
A/Accession: A49002  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-124 <STU>  
A/Cross-references: GB:M90808; NID:G185515; PIDN:AAA52989.1; PID:G567176  
A/Experimental source: EBV-transformed lymphoblastoid cell line SSH23  
A/Note: sequence extracted from NCBI backbone (NCBIN:110261, NCBIPI:110262)  
C/Superfamily: immunoglobulin V region, immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-99/Domain: immunoglobulin homology <IMM>

Query Match 40.9%; Score 551; DB 2; Length 124;  
Best Local Similarity 81.7%; Pred. No. 6.9e-31;  
Matches 103; Conservative 10; Mismatches 11; Indels 2; Gaps 1;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVGVWRQPPGKALEWLAITYWDDDKR 60  
Db 1 QITLKESGPTLVKPTQTLLTCTFSGFSRLSTSGVGVWRQPPGKALEWLAITYWDDRR 60  
QY 61 YSPSLKSRLLTITKDTSKQVVLMTNVPADPATYCTHEQYYYDTSQGPYYFDWGGG 120  
Db 61 YSPSLKSRLLTITKDTSKQVVLMTNVPADPATYCTHEQYYYDTSQGPYYFDWGGG 120  
QY 121 LVTVSS 126  
Db 119 LVTVSS 124

RESULT 4  
S31513  
Ig heavy chain - human  
C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C/Accession: S31513  
R/Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A/Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
A/Reference number: S31509  
A/Accession: S31513  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-138 <CHA>  
A/Cross-references: EMBL:X69861; NID:G33084; PIDN:CAA49495.1; PID:G33085  
C/Superfamily: immunoglobulin V region, immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/30-114/Domain: immunoglobulin homology <IMM>

Query Match 39.9%; Score 538.5; DB 2; Length 138;  
Best Local Similarity 80.8%; Pred. No. 5.4e-30;  
Matches 101; Conservative 7; Mismatches 14; Indels 3; Gaps 1;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVGVWRQPPGKALEWLAITYWDDDKR 60  
Db 16 QITLKESGPTLVKPTQTLLTCTFSGFSRLSTSGVGVWRQPPGKALEWLAITYWDDDKR 75  
QY 61 YSPSLKSRLLTITKDTSKQVVLMTNVPADPATYCTHEQYYYDTSQGPYYFDWGGG 120  
Db 76 YSPSLKSRLLTITKDTSKQVVLMTNVPADPATYCTHEQYYYDTSQGPYYFDWGGG 132  
QY 121 LVTVSS 125  
Db 133 LVTVSS 137

RESULT 5  
S69339

Ig heavy chain V region precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C/Accession: S69339; S72664  
R/Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A/Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A/Reference number: S69339; MUID:95262687; PMID:7744049  
A/Accession: S69339  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-374 <KHA>  
A/Cross-references: EMBL:X81695  
R/Khamlichi, A.A.  
submitted to the EMBL Data Library, September 1994  
A/Reference number: S72664  
A/Accession: S72664  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-140,'C',142-374 <KH2>  
A/Cross-references: EMBL:X81695  
C/Superfamily: immunoglobulin C region, immunoglobulin homology

Query Match 39.7%; Score 534.5; DB 2; Length 374;  
Best Local Similarity 81.0%; Pred. No. 2.8e-29;  
Matches 102; Conservative 8; Mismatches 13; Indels 3; Gaps 1;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVGVWRQPPGKALEWLAITYWDDDKR 60  
Db 20 QITLKESGPTLVKPTQTLLTCTFSGFSLSKSGVGVWRQPPGQALEWLAITYWDDDKR 79  
QY 61 YSPSLKSRLLTITKDTSKQVVLMTNVPADPATYCTHEQYYYDTSQGPYYFDWGGG 120  
Db 80 YSPSLKSRLLTITKDTSKQVVLMTNVPADPATYCTHEQYYYDTSQGPYYFDWGGG 136  
QY 121 LVTVSS 126  
Db 137 LVTVSS 142

## RESULT 6

JC5322

p53 specific single-chain antibody Pab421 - human

C:Species: Homo sapiens (man)

C:Date: 15-May-1997 #sequence\_revision 15-May-1997 #text\_change 18-Jul-1997

C:Accession: JC5322

R:Jannot, C.B.; Hynea, N.E.

Biochem. Biophys. Res. Commun. 230, 242-246, 1997

A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.

A:Reference number: JC5322; MUID:97168950; PMID:9016757

A:Accession: JC5322

A:Molecule type: mRNA

A:Residues: 1-233 &lt;JAN&gt;

A:Experimental source: hybridoma cell

C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 39.6%; Score 533.5; DB 2; Length 233;

Best Local Similarity 45.5%; Pred. No. 2e-29;

Matches 116; Conservative 46; Mismatches 64; Indels 29; Gaps 8;

QY 5 KESGPTLVKPTQTTLTCTFSGFSLRTGEGVGVWRQPPGKALEWLAII---YWDDDKRY 61

Db 1 QESGAEIVRSASVKSCTTSGFNI--NDYYMHVWKRPEQGLEWIGRIDPENGADDMTR 58

QY 62 SPSLKRLTITKDTSKQVLTMTNVDPADTATYCTHEQYYVDTSGQPYFDWFGQGT 121

Db 59 SSGVKA--TMTADTSSNTAYLQLSSLTSEDVAVYC-----NAG---MDYWGQGT 104

QY 122 VTVSSGGCGSGGGSGGGSGGSGSNIQVTPSSLSASVGDRTWTCRASQDIRKN--- 178

Db 105 VTVS-----SGGGSGGRASGGSDIELTQSPASLAVSLGQRAFISCRASKSVSTSGYS 159

QY 179 -LNVYQOKPKAPKVLIVDASDLEETGPSRFSSGSGTDFTLTSSLPEDIATYCCQS 237

Db 160 YMHVNOQKPGQPPRLILYLVSNLESGVPAFSGSGGTDFTLNHPVEEDATYCCQHI 219

QY 238 DYLPITFGGGTKVDI 252

Db 220 RELTRS-EGGTKEI 233

## RESULT 7

S18555

Ig heavy chain V region precursor (VII-5) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence\_revision 06-Jun-1997 #text\_change 21-Jul-2000

C:Accession: S18555

R:Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H

EMBO J. 10, 3641-3645, 1991

A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl

A:Reference number: S18551; MUID:92037524; PMID:1935893

A:Accession: S18555

A:Molecule type: DNA

A:Residues: 1-119 &lt;SHI&gt;

A:Cross-references: EMBL:X62111, NID:G37839, PIDN:CAA44021.1; PID:G3980125

C:Genetics:

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted &lt;SIG&gt;

F:20-119/Product: Ig heavy chain V region (VII-5) #status predicted &lt;MAT&gt;

F:34-118/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 36.1%; Score 487; DB 2; Length 119;

Best Local Similarity 89.9%; Pred. No. 1.5e-26;

Matches 89; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 QVTLKESGPTLVKPTQTTLTCTFSGFSLRTGEGVGVWRQPPGKALEWLAIIYWDDDKR 60

Db 20 QITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGWVIRQPPGKALEWLAIIYWDDDKR 79

QY 61 YSPSLKRLTITKDTSKQVLTMTNVDPADTATYCTH 99

Db 80 YSPSLKRLTITKDTSKQVLTMTNVDPVDTATYCAH 118

## RESULT 8

MEHUMC

Ig heavy chain V-II region (MCE) - human

C:Species: Homo sapiens (man)

C:Date: 14-Nov-1983 #sequence\_revision 22-Nov-1983 #text\_change 02-Sep-1997

C:Accession: A02092

R:Gerber-Jenson, B.; Kazin, A.; Kehoe, J.M.; Scheffel, C.; Erickson, B.W.; Litman, G.W.

J. Immunol. 126, 1212-1216, 1981

A:Title: Molecular basis for the temperature-dependent insolubility of cryoglobulins. X

A:Reference number: A02092; MUID:8118242; PMID:6780622

A:Accession: A02092

A:Molecule type: protein

A:Residues: 1-125 &lt;GER&gt;

A:Note: this chain was derived from a monoclonal IgM cryoimmunoglobulin

C:Genetics:

A:Gene: GDB:IGHV@

A:Cross-references: GDB:128528; OMIM:147070

A:Map position: 14q32.33-14q32.33

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid

F:15-99/Domain: immunoglobulin homology &lt;IMM&gt;

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 36.0%; Score 485.5; DB 1; Length 125;

Best Local Similarity 73.8%; Pred. No. 1.9e-26;

Matches 93; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY 1 QVTLKESGPTLVKPTQTTLTCTFSGFSLRTGEGVGVWRQPPGKALEWLAIIYWDDDKR 60

Db 1 QITLKESGPTLVKPTETTLTCTFSGFSLSTSGVGWVIRQPPGKALEWLAIIYWDDDKR 60

QY 61 YSPSLKRLTITKDTSKQVLTMTNVDPADTATYCTHEQYYVDTSGQPYFDWFGQGT 120

Db 61 YSPSLKRLTITKDTSRNQVLTITNMDPVDSGTFFCAHRPPWRFT-GNLGFDXWQGT 119

QY 121 LVTVSS 126

Db 120 LVTVSS 125

## RESULT 9

GIHUME

Ig heavy chain V-II region (He) - human

C:Species: Homo sapiens (man)

C:Date: 07-May-1981 #sequence\_revision 07-May-1981 #text\_change 24-Nov-1999

C:Accession: A02093

R:Cunningham, B.A.; Pflumm, M.N.; Rutishauser, U.; Edelman, G.M.

Proc. Natl. Acad. Sci. U.S.A. 64, 997-1003, 1969

A:Title: Subgroups of amino acid sequences in the variable regions of immunoglobulin hea

A:Reference number: A02093; MUID:70114712; PMID:5264153

A:Accession: A02093

A:Molecule type: protein

A:Residues: 1-121 &lt;GUN&gt;

C:Comment: This gamma-1 chain was isolated from a myeloma protein.

C:Genetics:

A:Gene: GDB:IGHV@

A:Cross-references: GDB:128528; OMIM:147070

A:Map position: 14q32.33-14q32.33

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: blocked amino end; heterotetramer; immunoglobulin

F:15-100/Domain: immunoglobulin homology &lt;IMM&gt;

F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu

Query Match 35.2%; Score 474.5; DB 1; Length 121;

Best Local Similarity 71.7%; Pred. No. 1e-25;

Matches 91; Conservative 10; Mismatches 19; Indels 7; Gaps 2;

QY 1 QVTLKESGPTLVKPTQTTLTCTFSGFSLRTGEGVGVWRQPPGKALEWLA-LIYWDDDK 59



Db 1 QVTLKENGPTLVKPTETLLTCTLSGLSLTDDGVAVGWIRQGPGRALFWLAWLTYWDDK 60  
QY 60 RYSPSLKSRLTITKDTSKQVVLTMNVDPADTATYYCTHEQYYDTSQGPYPDFWGGQ 119  
Db 61 RYSPSLKSRLTITKDTSKQVVLTMNVDPADTATYYCTHEQYYDTSQGPYPDFWGGQ 119  
QY 120 TLVTSS 126  
Db 115 TKVAVSS 121

RESULT 10  
S18556  
Ig heavy chain V region precursor (VH-5b) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 06-Jun-1997 #text\_change 23-Jul-1999  
C/Accession: S18556  
R/Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H  
EMBO J. 10, 3641-3645, 1991  
A/Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: c1  
A/Reference number: S18551; MUID:92037524; PMID:1935893  
A/Accession: S18556  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-118 <SHI>  
A/Cross-references: EMBL:X62108; NID:g37840; PIDN:CAA44018.1; PID:g37841  
C/Genetics:  
A/Introns: 16/1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/1-19/Domain: signal sequence #status predicted <SIG>  
F/20-118/Product: Ig heavy chain V region (VH-5b) #status predicted <MAT>  
F/34-116/Domain: immunoglobulin homology <IMM>

Query Match 34.9%; Score 470.5; DB 2; Length 118;  
Best Local Similarity 88.9%; Pred. No. 1.9e-25;  
Matches 88; Conservative 4; Mismatches 6; Indels 1; Gaps 1;  
QY 1 QVTLKESGPTLVKPTQTLTCTFSGFSRLTGEVGVWRQPPGKALEWLALTYWDDDKR 60  
Db 20 QVTLKESGPTLVKPTQTLTCTFSGFSRLTGEVGVWRQPPGKALEWLALTYWDDDKR 78  
QY 61 YSPSLKSRLTITKDTSKQVVLTMNVDPADTATYYCTH 99  
Db 79 YSPSLKSRLTITKDTSKQVVLTMNVDPADTATYYCAH 117

RESULT 11  
A36005  
Ig heavy chain V region (M60) - human  
C/Species: Homo sapiens (man)  
C/Date: 21-Dec-1990 #sequence\_revision 13-Sep-1991 #text\_change 16-Dec-1998  
C/Accession: A36005  
R/Schroeder Jr., H.W.; Wang, J.Y.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene  
A/Reference number: A36005; MUID:90349571; PMID:2117273  
A/Accession: A36005  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-121 <SCH>  
A/Cross-references: GB:M34027  
C/Genetics:  
A/Gene: GDB:IGHG; IGHDX1  
A/Cross-references: GDB:118731; OMIM:146910  
A/Map position: 14q32.33-14q32.33  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-99/Domain: immunoglobulin homology <IMM>

Query Match 34.8%; Score 469.5; DB 2; Length 121;  
Best Local Similarity 72.2%; Pred. No. 2.3e-25;  
Matches 91; Conservative 10; Mismatches 20; Indels 5; Gaps 1;

QY 1 QVTLKESGPTLVKPTQTLTCTFSGFSRLTGEVGVWRQPPGKALEWLALTYWDDDKR 60  
Db 1 EVTLRSGPALVKPTQTLTCTLYGFSLSSTGMCVSWIRQPPGKALEWLALTYWDDDKR 60  
QY 61 YSPSLKSRLTITKDTSKQVVLTMNVDPADTATYYCTHEQYYDTSQGPYPDFWGGQ 120  
Db 61 YSTSLKRLTITKDTSKQVVLTMNVDPADTATYYCARINNWGE-----YFDLWGRGT 115  
QY 121 LVTSS 126  
Db 116 LVTSS 121

RESULT 12  
K1HURY  
Ig kappa chain V-I region (Roy) - human (tentative sequence)  
C/Species: Homo sapiens (man)  
C/Date: 24-Apr-1984 #sequence\_revision 02-Jul-1998 #text\_change 31-Mar-2000  
C/Accession: A91638; B94417; A01874; S02575  
R/Hiltschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 348, 1077-1080, 1967  
A/Title: Die chemische Struktur von zwei Bence-Jones-Proteinen (Roy und Cum.) vom kappa  
A/Reference number: A91638; MUID:68362076; PMID:5595110  
A/Accession: A91638  
A/Molecule type: protein  
A/Residues: 1-38, 'GPX', 42-108 <HIL>  
A/Note: the sequence of the C region, which has the Inv (1,2) marker, is also given  
R/Hiltschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponsingl, H.; Steinmetz-Kayne,  
in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74,  
A/Reference number: A94417  
A/Contents: revisions to residues 39 and 41  
A/Accession: B94417  
A/Molecule type: protein  
A/Residues: 39/41 <HIL>  
R/Steiner, V.; Chang, J.Y.  
FEBS Lett. 222, 6-10, 1987  
A/Title: Chemical modification of the carboxyl groups of protein substrates enhances th  
A/Reference number: S02572; MUID:88005152; PMID:3115831  
A/Contents: annotation  
C/Comment: This is a Bence Jones protein.  
C/Genetics:  
A/Gene: GDB:IGKV1  
A/Cross-references: GDB:136264  
A/Map position: 2p12-2p12  
C/Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds; in some cases, such as Iga and Igm, the subunits associate into 1a  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/16-90/Domain: immunoglobulin homology <IMM>  
F/23-88/Disulfide bonds: #status predicted

Query Match 34.7%; Score 468; DB 1; Length 108;  
Best Local Similarity 84.1%; Pred. No. 2.6e-25;  
Matches 90; Conservative 7; Mismatches 10; Indels 0; Gaps 0;  
QY 147 NIOVTQSPSSLSASVGDRTVMTCRASQDIRKLNWYQQRKAPKVLTYDASDLETGIPS 206  
Db 1 DIOVTQSPSSLSASVGDRTVMTTCASQDISIFLNWYQQRKAPKVLTYDASKLEAGVPS 60  
QY 207 RFSGSGSGTDFITLTISSLPEDATYYCCQSDYLPFTFGGKTKVDIK 253  
Db 61 RFSGSGSGTDFITLTISSLPEDATYYCCQSDYLPFTFGGKTKVDIK 107

RESULT 13  
S52789  
Ig kappa chain V region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C/Accession: S52789  
R/Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret,  
submitted to the EMBL Data Library, March 1995



A;Description: Light chain V region gene usage restriction and peculiarities in myeloma  
A;Reference number: S52789  
A;Accession: S52789  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-129 <ROC>  
A;Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match	34.7%	Score 468;	DB 2;	Length 129;
Best Local Similarity	81.1%;	Pred. No. 3.1e-25;		
Matches	90;	Conservative	9;	Mismatches 12;
			Indels	0;
			Gaps	0;

```
Qy      143 GGGSNIQVTSPLSASVGDRVTMTCSRQDIRKLNLMWQQKPGKAPKRLIYDASDET 202
          |   :|:|||||||:|||||   |||||:|:|:|   |
Db      19  GARCDIQMTPSSLSASVGDRVITTCOASQDISNYLNMWQQKPGKAPKRLITHAASSLET 78
```

Qy	203	GIPSRFSGSGSTDFILTTISSLOPEDLATYCCQSDYLPLTFGGGTRVDIK	253
	:	:	:
Db	79	GVPSRFSGSGSTDFSTLISSLOPEDLATYCCQYDNLPLTFGGGTRVEIK	129

RESULT 14  
S4418  
Ig kappa chain V-J region - human  
C:Species: Homo sapiens (man)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C:Accession: S4418  
R: Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable  
A:Reference number: S44105  
A:Accession: S4418  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-110 <HAW>  
A:Cross-references: EMBL:Z31395; NID:g472972; PIDN:CAA83270.1; PID:g940529  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

[illegible]

RESULT 15  
KIHUAV  
Ig kappa chain V-I region (Au) - human  
C:Species: Homo sapiens (man)  
C:Date: 24-Apr-1984 #sequence\_revision 02-Jul-1998 #text\_change 21-Jan-2000  
C:Accession: A91653; A01862; S02573  
R:Schiechl, H.; Hilschmann, N.  
Hoppe-Seyley's Z. Physiol. Chem. 353, 345-370, 1972  
A:Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Subt  
A:Reference number: A91653; MUID:72189444; PMID:5028201  
A:Accession: A91653  
A:Molecule type: protein  
A:Residues: 1-108 <SCH>  
A>Note: the C region of this chain has the Inv (3) marker  
R:Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Stei  
Biophys. Struct. Mech. 1, 139-146, 1975  
A:Title: The structure determination of the variable portion of the Bence-Jones protein

A;Reference number: A90729; MUID:77022433; PMID:1234024  
A;Contents: annotation; X-ray crystallography  
A;Note: the structure of the V region was determined by molecular replacement methods ut  
R;Steiner, V.; Chang, J.Y.  
FEBS Lett. 222, 6-10, 1987  
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances thr  
A;Reference number: S02572; MUID:88005152; PMID:3115831  
A;Contents: annotation  
C;Comment: This is a Bence Jones protein.  
C;Genetics:  
A;Gene: GDB:IGKV1  
A;Cross-references: GDB:136264  
A;Map position: 2p12-2p12  
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kay  
hain disulfide bonds; in some cases, such as Iga and Igm, the subunits associate into 1f  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>  
F;23-88/Disulfide bonds: #status predicted

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Query Match      33.8%; Score 456; DB 1; Length 108;  
Best Local Similarity 81.3%; Pred. No. 1.7e-24;  
Matches      87; Conservative    9; Mismatches   11; Indels     0; Gaps       0;
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OY      147 NIQTQSPSSLASVGDVRTMTCRASQDIRKNLNMWQQKPGAKPVLITYDASDLRTGPS 206  
         :  
Db         1 DIQMTPSSLSASVGDRVITTCQASODISDYLNMYQQKPKAPKLIIYDASNLESVS 60

OY      207 RFGSGSGETFILTSLQPEDIATYYCCQS DYLP LTFGGGKTVDIK 253  
         :  
Db         61-RFSGGGS GAHFTFI TISSLOPEDIA TYCC Q YDI LP WT FG GGT KEI K 107

Search completed: May 13, 2004, 15:08:43  
Job time : 12.4218 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:01 ; Search time 7.1233 Seconds  
(without alignments)  
1849.388 Million cell updates/sec

Title: US-10-072-301-23

Perfect score: 1348

Sequence: 1 QVTLKESGPTLVKPTQTTLT.....CQGS DYLP LTFGGGTKVDIK 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	485.5	36.0	125	1	HV2D_HUMAN P01817 homo sapien
2	474.5	35.2	121	1	HV2E_HUMAN P01818 homo sapien
3	468	34.7	108	1	KV1P_HUMAN P01608 homo sapien
4	468	34.7	108	1	KV1Y_HUMAN P80362 homo sapien
5	456	33.8	108	1	KV1B_HUMAN P01594 homo sapien
6	448	33.2	108	1	KV1Q_HUMAN P01609 homo sapien
7	442	32.8	108	1	KV1A_HUMAN P01593 homo sapien
8	435	32.3	108	1	KV1O_HUMAN P01607 homo sapien
9	435	32.3	108	1	KV1S_HUMAN P01611 homo sapien
10	435	32.3	120	1	HV2B_HUMAN P01815 homo sapien
11	425	31.5	108	1	KV1C_HUMAN P01595 homo sapien
12	425	31.5	108	1	KV1H_HUMAN P01600 homo sapien
13	423	31.4	108	1	KV1E_HUMAN P01597 homo sapien
14	423	31.4	108	1	KV1V_HUMAN P04430 homo sapien
15	423	31.4	129	1	KV1W_HUMAN P04431 homo sapien
16	418	31.0	108	1	KV1G_HUMAN P01599 homo sapien
17	418	31.0	108	1	KV1M_HUMAN P01605 homo sapien
18	415	30.8	108	1	KV1R_HUMAN P01610 homo sapien
19	413	30.6	108	1	KV1K_HUMAN P01603 homo sapien
20	411	30.5	147	1	HV2H_HUMAN P04438 homo sapien
21	408.5	30.3	107	1	KV1D_HUMAN P01596 homo sapien
22	408.5	30.3	109	1	KV1T_HUMAN P01612 homo sapien
23	406	30.1	129	1	KV1X_HUMAN P04432 homo sapien
24	405	30.0	108	1	KV5S_MOUSE P01652 mus musculu
25	404	30.0	108	1	KV1L_HUMAN P01604 homo sapien
26	403	29.9	108	1	KV1N_HUMAN P01606 homo sapien
27	402.5	29.9	119	1	HV2C_HUMAN P01816 homo sapien
28	401	29.7	108	1	KV5Q_MOUSE P01650 mus musculu
29	401	29.7	108	1	KV5T_MOUSE P01653 mus musculu
30	397	29.5	108	1	KV1F_HUMAN P01598 homo sapien
31	391	29.0	108	1	KV5R_MOUSE P01651 mus musculu
32	389	28.9	126	1	HV2A_HUMAN P01814 homo sapien
33	388	28.8	108	1	KV5O_MOUSE P01648 mus musculu

34	387	28.7	108	1	KV5L_MOUSE	P01645 mus musculu
35	387	28.7	117	1	KV1J_HUMAN	P01602 homo sapien
36	386	28.6	108	1	KV5K_MOUSE	P01644 mus musculu
37	386	28.6	108	1	KV5M_MOUSE	P01646 mus musculu
38	385	28.6	108	1	KV5N_MOUSE	P01647 mus musculu
39	382	28.3	112	1	KV1U_HUMAN	P01613 homo sapien
40	381	28.3	108	1	KV5P_MOUSE	P01649 mus musculu
41	378	28.0	108	1	KV5J_MOUSE	P01643 mus musculu
42	373.5	27.7	144	1	HV43_MOUSE	P01619 mus musculu
43	372	27.6	117	1	KV1I_HUMAN	P01601 homo sapien
44	367	27.2	128	1	KV5E_MOUSE	P01637 mus musculu
45	363.5	27.0	133	1	KV4B_HUMAN	P06313 homo sapien

ALIGNMENTS

RESULT 1

HV2D\_HUMAN  
ID HV2D\_HUMAN STANDARD; PRT; 125 AA.  
AC P01817;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-II region MCE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81118242; PubMed=6780622;  
RA Gerber-Jenson B., Kazin A., Kehoe J.M., Scheffel C., Erickson B.W.,  
RA litman G.W.;  
RT "Molecular basis for the temperature-dependent insolubility of  
RT cryoglobulins. X. The amino acid sequence of the heavy chain variable  
RT region of MCE."  
RL J. Immunol. 126:1212-1216(1981).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM  
CC CRYOIMMUNOGLOBULIN.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; A02092; MHMNC.  
DR HSSP; P01825; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.  
FT DOMAIN 1 113 IG-LIKE.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT NON\_TER 125 125  
SQ SEQUENCE 125 AA; 13783 MW; 7A1ADF4C40F47BB5 CRC64;

Query Match 36.0%; Score 485.5; DB 1; Length 125;  
Best local Similarity 73.8%; Pred. No. 1.4e-31;  
Matches 93; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY	1	QVTLKESGPTLVKPTQTTLTCTFGSGLRTTGEVGVWVRQPPGKALEWLAIIYWD	DKR	60
DB	1	QITLKESGPTLVKPTETLTCTFGSGLSTSGVGWIRQRPGLALEWLAFINWDD	DNR	60
QY	61	YSPSLKRLITKDTSKQVLTMTNVPADATATYCTHEQYYVDTSGQPYFDFW	GQT	120
DB	61	YSPSLKRLITGTXTSRNQVLTITNMDPVDSGTYFCAHRRPWRFT-GNLGG	FDXWGQT	119
QY	121	LVTVSS	126	
DB	120	LVTVSS	125	

RESULT 2

```
RT HV2E_HUMAN STANDARD; PRT; 121 AA.
ID HV2E_HUMAN
AC P01818;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region HE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70114712; PubMed=5264153;
RA Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.;
RT "Subgroups of amino acid sequences in the variable regions of
RT immunoglobulin heavy chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 64:997-1003(1969).
CC -1- MISCELLANEOUS: THIS GAMMA-1 CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02093; GIHUE.
DR HSSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Pyrrrolidone carboxylic acid.
KW DOMAIN 1 120 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13483 MW; 88A5082C273753B4 CRC64;
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Query Match:

Best Local Similarity 35.2%; Score 474.5; DB 1; Length 121;  
Matches 91; Conservative 71.7%; Pred. No. 1e-30;  
Mismatches 10; Indels 19; Gaps 7; Gaps 2;

```
OY 1 QVTLKESGPTLVKPTQLTLCTFSGLRTGEGVGVNRQPPGKALEWLA-LIYWDGK 59
Db 1 QVTLKENGPTLVKPTETTLCTTSLGSLTGDGAVAVGIRQGPRALEWLA-LIYWDGK 60
OY 60 RYSPSLKSLRLTTTKDTSKQVVLTMNVDPADATATYCTHEQYYDTSQOPYFDFGQG 119
Db 61 RFSPSLKSLRLTVTRDTSKQVVLTMNVDPADATATYCTHEQYYDTSQOPYFDFGQG 114
OY 120 TLVTVSS 126
Db 115 TKVAVSS 121
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RESULT 3

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ID KVI1P_HUMAN STANDARD; PRT; 108 AA.
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
```

RESULT 4

```
RT Cum.).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Fonslingl H.,
RA Steimetz-Kayne M., Suter L., Watanabe S.,
RL (in) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RL New York (1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91638; KIHURY.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACDE5A313DF3A CRC64;
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Query Match:

Best Local Similarity 34.7%; Score 468; DB 1; Length 108;  
Matches 90; Conservative 84.1%; Pred. No. 2.8e-30;  
Mismatches 7; Indels 10; Gaps 0;

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OY 147 NIQVTSPLSLASVGDVMTGRASQDIRKLNLYQKPGKAPKVLTPASDLETGIPS 206
Db 1 DIQVTSPLSLASVGDVMTGRASQDIRKLNLYQKPGKAPKVLTPASDLETGIPS 206
OY 207 RFSGSGSGNDFILTISSLPEDIAATYCCQSDYLPFTGGTKVDIK 253
Db 61 RFSGSGSGDFTFTISSLPEDIAATYCCQSDYLPFTGGTKVDIK 107
```

RESULT 4

```
ID KVI1P_HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7993911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eultz M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
RT structural origin of altered domain interactions in immunoglobulin
RT light-chain dimers.";
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;
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RT "Characterization and preliminary crystallographic data on the VL-  
RT related fragment of the human ki Bence Jones protein Wat.";  
CC J. Mol. Biol. 147:185-193(1981).  
DR -1- MISCELLANEOUS: This is a Bence-Jones protein.  
DR PDB; 1WTL; 01-NOV-94.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT CONFLICT 30 31 TN -> SD (IN REF. 2).  
FT STRAND 4 7  
FT STRAND 10 13  
FT TURN 15 16  
FT STRAND 19 25  
FT TURN 30 31  
FT STRAND 33 38  
FT TURN 40 41  
FT STRAND 45 49  
FT TURN 50 52  
FT STRAND 53 54  
FT TURN 56 57  
FT TURN 60 61  
FT STRAND 62 67  
FT TURN 68 69  
FT STRAND 70 75  
FT STRAND 80 82  
FT HELIX 84 90  
FT STRAND 98 98  
FT STRAND 102 106  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;  
Query Match 34.7%; Score 468; DB 1; Length 108;  
Best Local Similarity 84.1%; Pred. No. 2.8e-30;  
Matches 90; Conservative 8; Mismatches 9; Indels 0; Gaps 0;  
QY 147 NIQVTSPPSSLSASVGDRTVMTCRASQDIRKNLNMWYQOKPGKAPKVLIDASDLETGIPS 206  
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQDITNVNWFQQRPGQAPKVLITYGASILETGVP 60  
QY 207 RFSGGSGTDFILTISSLOPEDIAITYCCQSDYLPLTFGGGTVKVDIK 253  
DB 61 RFSGGSGTDFITFTISSLQPEDIAITYCCQYDYLPLTFGGGTVKVDIK 107  
RESULT 5  
KV1B\_HUMAN STANDARD; PRT; 108 AA.  
ID KV1B\_HUMAN  
AC P01594;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig kappa chain V-I region AU.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=72189444; PubMed=5028201;

RA Schiechl H., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
RT protein Au).";  
RN Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).  
RP X-RAY CRYSTALLOGRAPHY.  
RX MEDLINE=77022433; PubMed=1234024;  
RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,  
RA Schwager P., Steigemann W., Schramm H.J.;  
RT "The structure determination of the variable portion of the  
RT Bence-Jones protein Au.";  
RL Biophys. Struct. Mech. 1:139-146(1975).  
CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY  
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V  
CC REGION OF THE KAPPA CHAIN REI.  
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR; A91653; KIHUAV.  
DR PDB; 1JVS; 30-JAN-02.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; PF00047; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11939 MW; E8011187BE6F6FB9 CRC64;  
Query Match 33.8%; Score 456; DB 1; Length 108;  
Best Local Similarity 81.3%; Pred. No. 2.5e-29;  
Matches 87; Conservative 9; Mismatches 11; Indels 0; Gaps 0;  
QY 147 NIQVTSPPSSLSASVGDRTVMTCRASQDIRKNLNMWYQOKPGKAPKVLIDASDLETGIPS 206  
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQDISDYLNMWYQOKPGKAPKVLIDASNLESGVPS 60  
QY 207 RFSGGSGTDFILTISSLOPEDIAITYCCQSDYLPLTFGGGTVKVDIK 253  
DB 61 RFSGGSGAHFTFTISSLQPEDIAITYCCQYDYLPLTFGGGTVKVEIK 107  
RESULT 6  
KV1Q\_HUMAN STANDARD; PRT; 108 AA.  
ID KV1Q\_HUMAN  
AC P01609;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Scw.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75059271; PubMed=4435756;  
RA Eulitz M., Hilschmann N.;  
RT "The primary structure of a human immunoglobulin L-chain of  
RT kappa-type (Bence-Jones protein Scw.), II: The chymotryptic peptides  
RT and the complete amino acid sequence.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).

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CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC PIR; A01875; KIHUSW.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 25 49
FT DOMAIN 35 49
SQ SEQUENCE 108 AA; 11764 MW; 32CECDDDE9644414 CRC64;

Query Match
Best Local Similarity 33.2%; Score 448; DB 1; Length 108;
Matches 84; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 147 NIQTQSPSSLSASVGDRTVMTCRASQDIRKMLNMYQQKPKAPKVLIDASDLETGIPS 206
Db 1 DIQMTQSPSSLSASVGDRTVITTCQASQDIRKMLNMYDQKPKAPRLIYGASTLETGIPS 60
QY 207 RFSGSGSGTDFILTISSLPEDIAITYCCQSDYLPLTFGGGTKVDIK 253
Db 61 RFSGSGSGTDFITLTISTLPEDIGNYYCCQYDNPITFGGTRVENK 107

RESULT 7
KV10_HUMAN
ID KV10_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region AG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC PIR; A01861; KIHUAG.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 25 49
FT DOMAIN 35 49
SQ SEQUENCE 108 AA; 11764 MW; 32CECDDDE9644414 CRC64;
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FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match
Best Local Similarity 32.8%; Score 442; DB 1; Length 108;
Matches 85; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 147 NIQTQSPSSLSASVGDRTVMTCRASQDIRKMLNMYQQKPKAPKVLIDASDLETGIPS 206
Db 1 DIQMTQSPSSLSASVGDRTVITTCQASQDIRKMLNMYDQKPKAPKVLIDASDLETGIPS 60
QY 207 RFSGSGSGTDFILTISSLPEDIAITYCCQSDYLPLTFGGGTKVDIK 253
Db 61 RFSGSGSGTDFITLTISTLPEDIAITYCCQYDNPITFGGTRVENK 107

RESULT 8
KV10_HUMAN
ID KV10_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region Rel.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=7603968; PubMed=1182131;
RA Epp O., Lattman E.B., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC PIR; A91653; KIHURE.
DR PDB; IREI; 17-FEB-84.
DR PDB; IAR2; 12-NOV-97.
DR PDB; 1BMW; 29-DEC-99.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;
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OY 121 LVTVSS 126  
Db 115 PVTVSS 120

## RESULT 11

KVIC\_HUMAN  
ID KVIC\_HUMAN STANDARD; PRT; 108 AA.  
AC P01595;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE 1g kappa chain V-I region B1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=73029807; PubMed=4563064;  
RA Braun M., Leibold W., Barnikol H.U., Hilschmann N.;  
RT "Principle of antibody structure. The primary structure of a  
RT monoclonal kappa I-type immunoglobulin L-chain (Bence Jones protein  
RT B1). 3. The complete amino acid sequence and the genetic  
RT significance of the variability principles for the mechanism of  
RT antibody formation."  
RL Hoppe-Seyler's Z. Physiol. Chem. 353:1284-1306(1972).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
DR PIR; A01863; K1HUBI.  
DR HSSP; P01607; IREI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 3 35 49 FRAMEWORK-2.  
FT DOMAIN 4 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 5 57 88 FRAMEWORK-3.  
FT DOMAIN 6 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 7 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 12026 MW; 7A83983986A431E7 CRC64;

## Query Match

Best Local Similarity 31.5%; Score 425; DB 1; Length 108;  
Matches 82; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

OY 147 NIQVTSPLSASVGDRTVMTCRASQDIRKNLNMWYQOKPGKAPKVLIVDASDLETGIPS 206  
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQDIRNSLIWYQOKPGKAPKFLIYDAENLEIGVPS 60  
OY 207 RFGSGSGTDFILITSSLOPEDIAITYCQSDYLPLTFGGGTRVDIK 253  
Db 61 RFRGSGSGTDFALISISLQPEDFATYYCQYVNLPTFGGQTKLEIK 107

## RESULT 12

KV1H\_HUMAN  
ID KV1H\_HUMAN STANDARD; PRT; 108 AA.  
AC P01600;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE 1g kappa chain V-I region Hau.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71032830; PubMed=4097974;  
RA Watanabe S., Hilschmann N.;  
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-  
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within  
RT subgroups."  
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
DR PIR; A01868; K1HUBU.  
DR HSSP; P80362; IWTU.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 2 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 3 35 49 FRAMEWORK-2.  
FT DOMAIN 4 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 5 57 88 FRAMEWORK-3.  
FT DOMAIN 6 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

## Query Match

Best Local Similarity 31.5%; Score 425; DB 1; Length 108;  
Matches 82; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

OY 147 NIQVTSPLSASVGDRTVMTCRASQDIRKNLNMWYQOKPGKAPKVLIVDASDLETGIPS 206  
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQDIRNSLIWYQOKPGKAPKVLIVDASDLETGIPS 60  
OY 207 RFGSGSGTDFILITSSLOPEDIAITYCQSDYLPLTFGGGTRVDIK 253  
Db 61 RFGSGSGTDFILITSSLOPEDFATYYCQYVNLPTFGGQTKLEIK 107

## RESULT 13

KV1E\_HUMAN  
ID KV1E\_HUMAN STANDARD; PRT; 108 AA.  
AC P01597;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE 1g kappa chain V-I region DEE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=72053133; PubMed=5124396;  
RA Milstein C.P., Deverson E.V.;  
RT "The amino acid sequence of a human kappa light chain."  
RT Biochem. J. 123:945-958(1971).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC PIR; A01865; K1HUBD.  
DR HSSP; P01607; IREI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.



DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;  
  
Query Match  
Best Local Similarity 31.4%; Score 423; DB 1; Length 108;  
Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;  
  
QY 147 NIQVTSPLSASVGDRTVMTCRASQDIRKNLNMWYQOKPGKAPKYLIDASDLETGIPS 206  
Db 1 BIZMTQSPSSLSASVGDRTVITTCRAGOSVNVKYLNMWYQOKPGKAPKYLIFAASSLKSGVPS 60  
  
QY 207 RFGSGSGTDFILTISSLOPEDIAITYCCQSDYLPPLTFGGGTRVDI 252  
Db 61 RFGSGSGTDFILTISSLOPEDIAITYCCQSYTTPYTFGGGTRVEM 106

RESULT 14  
KV1V HUMAN  
ID KV1V\_HUMAN STANDARD; PRT; 108 AA.  
AC P04430;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region BAN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=86174817; PubMed=3083240;  
RA Dwulet F.E., O'Connor T.P., Benson M.D.;  
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";  
RL Mol. Immunol. 23:73-78(1986).  
DR PIR; A01878; KIHUBN.  
DR HSSP; P80362; 1WTL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Amyloid.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;  
  
Query Match  
Best Local Similarity 31.4%; Score 423; DB 1; Length 108;  
Matches 81; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 147 NIQVTSPLSASVGDRTVMTCRASQDIRKNLNMWYQOKPGKAPKYLIDASDLETGIPS 206  
Db 1 DIQLTQSPSSLSASVGDRTVITTCRASQSVNVVAMFQOKPGKAPKSLIYDASTLQSGVPS 60  
  
QY 207 RFGSGSGTDFILTISSLOPEDIAITYCCQSDYLPPLTFGGGTRVDI 253  
Db 61 NFGSGSGTDFILTISSLOPEDIAITYCCQNSYPTTFGGGTRVQIK 107  
  
RESULT 15  
KV1W HUMAN  
ID KV1W\_HUMAN STANDARD; PRT; 129 AA.  
AC P04431;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Walker precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85014148; PubMed=6091049;  
RA Klobeck H.G., Combratio G., Zachau H.G.;  
RT "Immunoglobulin genes of the kappa light chain type from two human  
lymphoid cell lines are closely related."  
RL Nucleic Acids Res. 12:6995-7006(1984).  
CC  
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CC  
DR EMBL; X00965; CAA25477.1; ALT\_TERM.  
DR PIR; A01883; KIHUWK.  
DR HSSP; P01607; 1REI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1. 22  
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.  
FT DOMAIN 23 45 FRAMEWORK-1.  
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 57 71 FRAMEWORK-2.  
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 79 110 FRAMEWORK-3.  
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 120 129 FRAMEWORK-4.  
FT DISULFID 45 110 BY SIMILARITY.  
FT NON\_TER 129 129  
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;  
  
Query Match  
Best Local Similarity 31.4%; Score 423; DB 1; Length 129;  
Matches 83; Conservative 11; Mismatches 17; Indels 0; Gaps 0;  
  
QY 143 GGSNIQVTSPLSASVGDRTVMTCRASQDIRKNLNMWYQOKPGKAPKYLIDASDLET 202  
Db 19 GARCDIQMTQSPSSLSASVGDRTVITTCRASQISINYNLMWYQOKPGKAPKLLIYAASSLQS 78  
  
QY 203 GIPSRFSGSGTDFILTISSLOPEDIAITYCCQSDYLPPLTFGGGTRVDI 253  
Db 1:||||| 11:||||| 17:||||| 0:||||| 0:|||||

Db 79 GVTSRFSGSGTDFTLTISLQPEDSATYCCQOSYSTLITFGQGTREIK 129

Search completed: May 13, 2004, 15:02:05  
Job time : 8.1233 secs



Db 40 QVKLQSGGGGLVKPGSLKLSAASGSDF--SRVMSWVRQAPGKLEWIGELINPDSSTI 97  
QY 60 RYSPSLKSRLLITKDTSKQVLTMTNVPADTATYYCTHEQYYDTSQGPYYFDWGGG 119  
Db 98 NYTPSLKDKFIISRDNAKNTLYLMSKVRSEDTALYYCARASYGHSA-----YMGQG 150  
QY 120 TLVTVSSGGGGSGGGSGGGSGGGSNIQVTPSSLSASVGDRTMTCRASQDIRKNL 179  
Db 151 TTVTVS-----SGGGSGGGGGGGGGSDIELTQSPASLSASVGETVTLTCRASGNHNYL 205  
QY 180 NWYQOKPKAPKVLIDASDLETGIPSRFSGSGSGTDFILTISSLOPEDIAATYYCQSDY 239  
Db 206 AMYQOKQKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYCQHFWT 265  
QY 240 LPLTFGGGTKVDIK 253  
Db 266 TPYTFGGGTKEIK 279

RESULT 2  
Q921A6 PRELIMINARY; PRT; 241 AA.  
ID Q921A6  
AC Q921A6;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Anti-CEA 79 single chain Fv fragment (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98170165; Pubmed=9509426;  
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,  
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;  
RT "Cloning and characterization of cDNAs encoding VH and VL of a  
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and  
RT generation of a single-chain Fv molecule (scfv).";  
RL Mol. Cells 7:816-819(1997).  
DR EMBL; U88067; AAB48044.1; -  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
FT NON TER 1  
FT NON TER 1  
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 48.4%; Score 652; DB 11; Length 241;  
Best Local Similarity 51.2%; Pred. No. 3.6e-48;  
Matches 132; Conservative 41; Mismatches 61; Indels 24; Gaps 7;  
QY 1 QVTLKESGPTLVKPTQTTLTCTFSGFSRLRTGEGVWVRQPPGKALEWLIY-WDDDK 59  
Db 1 QVKLQSGSELVRPGASVKLSCKASGYTFT--YMHVWVRQHGQGLEWIGNIVPGSIT 58  
QY 60 RYSPSLKSRLLITKDTSKQVLTMTNVPADTATYYCTHEQYYDTSQGPYYFDWGGG 119  
Db 59 TYADDFRGRFAFSLETASTAYLIQINNKNEDTATYFCARKDLL-----RYFDYMGQG 111  
QY 120 TLVTVSSGGGGSGGGSGGGSGGGSNIQVTPSSLSASVGDRTMTCRASQDIRKNL 179  
Db 112 TTVTVS-----SGGGSGGGGGGGGGSDIELTQSPASLSASVGETVTLTCRASGNHNYL 205  
QY 180 NWYQOKPKAPK----VLIDASDLETGIPSRFSGSGSGTDFILTISSLOPEDIAATYYCQ 235  
Db 167 AMYQOKPKGPRSAHTLHY----IQGPISRFSGSGSGRDYSPFISINLEPEDIAATYYCL 222  
QY 236 QSDYLPITFGGTTKVDIK 253  
Db 223 HYDNLH-TFGGTTKLEIK 239

RESULT 3  
Q7QM2 PRELIMINARY; PRT; 243 AA.  
ID Q7QM2  
AC Q7QM2;  
DT 01-OCT-2003 (Tremblrel. 25, Created)  
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Scfv 6H8 protein (Fragment).  
GN SCFV 6H8.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Balb/C;  
RA Peter J.C., Birekhar P., Billiald P., Wallukat G.;  
RT "scfv single chain antibody variable fragment as inverse agonist for  
RT the beta-2 adrenergic receptor.";  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ574851; CAB00495.1; -  
FT NON TER 1  
FT NON TER 1  
SQ SEQUENCE 243 AA; 25976 MW; BEFF64D2DCFAF76 CRC64;

Query Match 46.1%; Score 621; DB 11; Length 243;  
Best Local Similarity 50.8%; Pred. No. 1.7e-45;  
Matches 129; Conservative 40; Mismatches 67; Indels 18; Gaps 6;  
QY 1 QVTLKESGPTLVKPTQTTLTCTFSGFSRLRTGEGVWVRQPPGKALEWLIY-WDDDK 59  
Db 1 QVKLQSGSELVRPGASVKLSCKASGYTFT--YMHVWVRQHGQGLEWIGNIVPGSIT 58  
QY 60 RYSPSLKSRLLITKDTSKQVLTMTNVPADTATYYCTHEQYYDTSQGPYYFDWGGG 119  
Db 59 NYDEKFKNKGLITVDTSSSTAYMHLSLASEDSAVYYCAR-----GGRG--LDVWGAG 109  
QY 120 TLVTVSSGGGGSGGGSGGGSGGGSNIQVTPSSLSASVGDRTMTCRASQDIRKNL 179  
Db 110 TTVTVS-----SGGGSGGGGGGGGGSDIQMTQSSSFVSLGDRVTITCKASEDIYNRL 164  
QY 180 NWYQOKPKAPKVLIDASDLETGIPSRFSGSGSGTDFILTISSLOPEDIAATYYCQSDY 239  
Db 165 AMYQOKPGNAPRLISGATSLTGTVPSPRFSGSGSKDYTLSTSLQTEVDATYYCQY-W 223  
QY 240 LPLTFGGGTKVDIK 253  
Db 224 STRTFGGGTKEIK 237

RESULT 4  
Q9UL96 PRELIMINARY; PRT; 121 AA.  
ID Q9UL96  
AC Q9UL96;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; Pubmed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035018; AAD56254.1; -.



DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 121  
SQ SEQUENCE 121 AA; 13695 MW; D582D450596BDD35 CRC64;

Query Match 40.8%; Score 549.5; DB 4; Length 121;  
Best Local Similarity 82.5%; Pred. No. 1e-39;  
Matches 104; Conservative 6; Mismatches 11; Indels 5; Gaps 1;

Qy 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVGVWRQPPGKALEWLALTYWDDDKR 60  
Db 1 QITLKESGPTLVKPTQTLLTCTFSGFSRLTSGMDVGWIRQPPGKALEWLALTYWDDDKR 60  
Qy 61 YSPSLKSRLLTTKDTSKKQVVLMTNVDPADTATYCTHEQYYYDTSGQPYFDFWGGGT 120  
Db 61 YSPSLKSRLLTTKDTSKKQVVDLTMTFMDPMDTATYYCAHRK-----SGDGYFDFWGGGT 115  
Qy 121 LVTVSS 126  
Db 116 LVTVSS 121

RESULT 5

Q925S1 PRELIMINARY; PRT; 218 AA.  
AC Q925S1;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE MRP5 (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX PubMed=11819679;  
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X., Su C.;  
RA "Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after irradiation in mice.";  
RL World J. Gastroenterol. 6:709-717(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Cui D., Zeng G., Yan X., Li X., Su C.;  
RT "Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same strain.";  
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
DR EMBL; AF240168; AAK43733.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 218  
FT NON\_TER 218  
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 36.8%; Score 496.5; DB 11; Length 218;  
Best Local Similarity 44.8%; Pred. No. 7.8e-35;  
Matches 103; Conservative 42; Mismatches 66; Indels 19; Gaps 6;

Qy 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVGVWRQPPGKALEWLALTYWDDDKR 59  
Db 3 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVGVWRQPPGKALEWLALTYWDDDKR 60

Qy 60 RYSPSLKSRLLTTKDTSKKQVVLMTNVDPADTATYCTHEQYYYDTSGQPYFDFWGGG 119  
Db 61 KYAEERKGRFAFSLTASVAYLIQISNLKNEDTATYFCM--RWDYDGG-----FAYWGGG 113  
Qy 120 TLVTYSSGGGGSGGGSGGGSGGGSGGNIQVTSPPSLASVGDRTMTCRASQDIR--- 176  
Db 114 TTVTVS-----SGGGSGGGSGGGSGGSDIVLTQSPASLAVSLGQRATISCRASESVDNIG 168  
Qy 177 -KNLWYQOKPGKAPKVLIDASDLETGIPSRFSGSGSGTDFILTISSLQ 225  
Db 169 ISFNMWFQOKPGOPPKLLIYAASKOGSGVPAGLLASGSGTDFSLNIYPM 218

RESULT 6

Q811U5 PRELIMINARY; PRT; 118 AA.  
ID Q811U5  
AC Q811U5;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Anti-human Fc gamma receptor III 368 gamma heavy chain variable region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Bruenke J., Valerius T., Repp R., Fey G.H.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY173025; AAO18227.1; -.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00409; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
DR Receptor.  
KM Receptor.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 118 AA; 12979 MW; F57BB0703742E99 CRC64;

Query Match 33.4%; Score 450; DB 11; Length 118;  
Best Local Similarity 66.7%; Pred. No. 3.6e-31;  
Matches 84; Conservative 17; Mismatches 17; Indels 8; Gaps 1;

Qy 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVGVWRQPPGKALEWLALTYWDDDKR 60  
Db 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVGVWRQPPGKALEWLALTYWDDDKR 60  
Qy 61 YSPSLKSRLLTTKDTSKKQVVLMTNVDPADTATYCTHEQYYYDTSGQPYFDFWGGGT 120  
Db 61 YNPALKSRLLTTKDTSSNQVFLKIASVDTADTATYYCAQT-----NPWFAYWGGGT 112  
Qy 121 LVTVSS 126  
Db 113 LVTVSA 118

RESULT 7

Q96SA9 PRELIMINARY; PRT; 107 AA.  
ID Q96SA9  
AC Q96SA9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98375893; PubMed=9712075;  
RA Adderson E.B., Shikhan A.R., Ward K.E., Cunningham M.W.;  
RT "Molecular analysis of polyclonal antibodies from  
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin  
RL antibody V region genes.";  
DR J. Immunol. 161:2020-2031(1998).  
DR EMBL; U96396; AAB68785.1; -.  
DR PIR; B49047; B49047.  
DR PIR; S34083; S34083.  
DR PIR; S34086; S34086.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 33.3%; Score 448.5; DB 4; Length 107;  
Best Local Similarity 82.2%; Pred. No. 4.3e-31;  
Matches 88; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

OY 147 NIQVQSPSSLSASVGDRTMTTCRASQDIRKNLNMWYQOKPGKAPKVLIDASDLETGIPS 206  
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQSSISYLNWYQOKPGKAPKVLIDASDLETGIPS 60  
OY 207 RFSGSGSGTDFILITISLQPEDIAATYCCQSDYLPLTFGGGTRVDIK 253  
Db 61 RFSGSGSGTDFILITISLQPEDFATYCCQS-YSTLTFGGGTRKVEIK 106

RESULT 8  
O9UL77 PRELIMINARY; PRT; 108 AA.  
AC O9UL77;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035037; AAD56273.1; -.  
DR PIR; B49047; B49047.  
DR PIR; S34083; S34083.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 31.8%; Score 429; DB 4; Length 108;  
Best Local Similarity 78.5%; Pred. No. 2.1e-29;  
Matches 84; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

OY 147 NIQVQSPSSLSASVGDRTMTTCRASQDIRKNLNMWYQOKPGKAPKVLIDASDLETGIPS 206  
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQSSISYLNWYQOKPGKAPKVLIDASDLETGIPS 60  
OY 207 RFSGSGSGTDFILITISLQPEDIAATYCCQSDYLPLTFGGGTRVDIK 253  
Db 61 RFSGSGSGTDFILITISLQPEDFATYCCQSYSTSWTFGGGTRKVEIK 107

RESULT 9  
O9UL81 PRELIMINARY; PRT; 107 AA.  
AC O9UL81;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035037; AAD56269.1; -.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 31.5%; Score 424.5; DB 4; Length 107;  
Best Local Similarity 78.5%; Pred. No. 5e-29;  
Matches 84; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

OY 147 NIQVQSPSSLSASVGDRTMTTCRASQDIRKNLNMWYQOKPGKAPKVLIDASDLETGIPS 206  
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQSSISYLNWYQOKPGKAPKVLIDASDLETGIPS 60  
OY 207 RFSGSGSGTDFILITISLQPEDIAATYCCQSDYLPLTFGGGTRVDIK 253  
Db 61 RFSGSGSGTDFILITISLQPEDFATYCCQS-YSALTFGGTRVDIK 106

RESULT 10  
O96PF6 PRELIMINARY; PRT; 116 AA.  
AC O96PF6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Kappa 1 light chain variable region (Fragment).  
DE SDNK1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21361171; PubMed=11468171;  
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;  
RT "The tropism of organ involvement in primary systemic amyloidosis;





Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC013496; AAH13496.1; -  
 DR InterPro; IPR007110; Ig\_Like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig\_2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 28.9%; Score 390; DB 11; Length 233;  
 Best Local Similarity 67.6%; Pred. No. 1.3e-25;  
 Matches 75; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 143 GGSNNIOVTPSSLSASVGDRTMTCTCRASQDIRKLNLMWYQKPGKAPKVLIDASDIET 202  
 DB 16 GSRCDIOMTQTSSLSASLGDRVTISCSGSGIGIANYLNWYQKPGKAPKVLIDASDIET 202  
 QY 203 GIPSRFSGSGGTDFILTISSLOPEDIAITYCCQSDYLPITFGGKTKVDIK 253  
 DB 76 GVPSRFSGSGGTDFILTISSLOPEDIAITYCCQSDYLPITFGGKTKVDIK 126

RESULT 14

ID Q72473 PRELIMINARY; PRT; 234 AA.  
 AC Q72473;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueidl T.B., Toshikiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,  
 RA Borsak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Matra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Strausberg R.,  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC056256; AAH56256.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 28.7%; Score 387; DB 4; Length 234;  
 Best Local Similarity 69.4%; Pred. No. 2.3e-25;

Matches 77; Conservative 10; Mismatches 24; Indels 0; Gaps 0;  
 QY 143 GGSNNIOVTPSSLSASVGDRTMTCTCRASQDIRKLNLMWYQKPGKAPKVLIDASDIET 202  
 DB 17 GARCAIRMTQSPSSFSASTGDRVTITCRASQSIGSYLAWYQKPGKAPQLIYAASLQS 76  
 QY 203 GIPSRFSGSGGTDFILTISSLOPEDIAITYCCQSDYLPITFGGKTKVDIK 253  
 DB 77 GVPSRFSGSGGTDFILTISSLOPEDIAITYCCQSDYLPITFGGKTKVDIK 127

RESULT 15

ID O43234 PRELIMINARY; PRT; 97 AA.  
 AC O43234;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Rheumatoid factor RF-ET13 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Borretzen M., Natvig J.B., Thompson K.M.,  
 RT "Heterogeneous RF structures between and within healthy individuals are  
 not related to HLA DRB1\*0401."  
 RL Mol. Immunol. 0:0-0(1997).  
 DR EMBL; AF035802; AAB88534.1; -  
 DR HSSP; P01789; 1MCP.  
 DR InterPro; IPR007110; Ig\_Like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 97  
 SQ SEQUENCE 97 AA; 10748 MW; DDC0BF47B9A812D CRC64;

Query Match 28.5%; Score 384; DB 4; Length 97;  
 Best Local Similarity 76.8%; Pred. No. 1.4e-25;  
 Matches 73; Conservative 8; Mismatches 14; Indels 0; Gaps 0;  
 QY 3 TLKESGPTLVKPTQTTLCTFSGFSLRTTGGVGVWRQPGKALEWLAIIYDDDKRYS 62  
 DB 1 TLKESGPTLVKPTQTTLCTFSGFSLSNRRMGVSWIRQPGKALEWLAIIYDDDKRYS 60  
 QY 63 PSLSRLTITKDTSKQVVLMTNVDPAATATYYC 97  
 DB 61 TSLKSLTITKDTSKQVVLMTNVDPAATATYYC 95

Search completed: May 13, 2004, 15:06:58  
 Job time : 35.0199 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:48:56 ; Search time 52.0738 Seconds  
(without alignments)  
1372.754 Million cell updates/sec

Title: US-10-072-301-25

Perfect score: 1351  
Sequence: 1 QVTLKESGPTLVKPTQTTLT.....CQAWDTSTAVFGTGTKLTVL 253

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	788.5	58.4	245	4	AAB67620	Aab67620 Human leu
2	783	58.0	250	5	ABP45537	Abp45537 Human Bly
3	779.5	57.7	247	5	ABP45640	Abp45640 Human Bly
4	771.5	57.1	249	6	AAE36257	Aae36257 TRAIL rec
5	756.5	56.0	245	4	AAB67621	Aab67621 Human leu
6	753.5	55.8	245	4	AAB67622	Aab67622 Human leu
7	753	55.7	237	6	ABR62332	Abrr62332 Anti-EBV
8	752.5	55.7	245	4	AAB67623	Aab67623 Human leu
9	752.5	55.7	280	4	AAE02186	Aae02186 PAM2 sing
10	751.5	55.6	245	4	AAB67619	Aab67619 Human leu
11	747	55.3	254	5	ABP45955	Abp45955 Human Bly
12	742	54.9	250	5	ABP45469	Abp45469 Human Bly
13	736	54.5	256	5	ABP45596	Abp45596 Human Bly
14	734.5	54.4	251	5	ABP44979	Abp44979 Human Bly
15	733	54.3	252	5	ABP45318	Abp45318 Human Bly
16	732.5	54.2	245	4	AAB67617	Aab67617 Human leu
17	731	54.1	254	5	ABP44833	Abp44833 Human Bly
18	730	54.0	252	6	ABJ19827	Abj19827 Human VEG
19	729.5	54.0	245	4	AAB67618	Aab67618 Human leu
20	728.5	53.9	247	5	ABP45007	Abp45007 Human Bly
21	723.5	53.6	251	5	ABP45305	Abp45305 Human Bly
22	723.5	53.6	253	5	ABP45608	Abp45608 Human Bly
23	722.5	53.5	251	5	ABP44941	Abp44941 Human Bly
24	721.5	53.4	255	5	ABP44830	Abp44830 Human Bly
25	721	53.4	248	5	ABP45984	Abp45984 Human Bly

26	719.5	53.3	249	5	ABP45714	Abp45714 Human Bly
27	718.5	53.2	249	5	ABP45713	Abp45713 Human Bly
28	718.5	53.2	251	5	ABP45527	Abp45527 Human Bly
29	718	53.1	244	5	ABP45831	Abp45831 Human Bly
30	717	53.1	244	2	AAy06718	Aay06718 Antibody
31	717	53.1	266	5	ABG97835	Abg97835 Single ch
32	717	53.1	266	5	ABG35336	Abg35336 Thrombopo
33	716.5	53.0	253	5	ABP45491	Abp45491 Human Bly
34	716	53.0	254	5	ABP45648	Abp45648 Human Bly
35	715.5	53.0	249	5	ABP45104	Abp45104 Human Bly
36	715.5	53.0	249	5	ABP45991	Abp45991 Human Bly
37	715.5	53.0	251	5	ABP44971	Abp44971 Human Bly
38	715	52.9	234	6	ABR62333	Abrr62333 Anti-EBV
39	714.5	52.9	247	5	ABP45459	Abp45459 Human Bly
40	714.5	52.9	247	5	ABP45195	Abp45195 Human Bly
41	714.5	52.9	253	5	ABP44927	Abp44927 Human Bly
42	712.5	52.7	247	5	ABP45311	Abp45311 Human Bly
43	711	52.6	250	5	ABP44982	Abp44982 Human Bly
44	710.5	52.6	249	5	ABP44946	Abp44946 Human Bly
45	710	52.6	246	3	AAy15126	Aay15126 Anti-muri

ALIGNMENTS

RESULT 1	
AAB67620	
ID AAB67620	standard; protein; 245 AA.
XX	
AC AAB67620;	
XX	
DT 29-MAY-2001	(first entry)
XX	
DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_4.	
XX	
KW Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;	
XX	
OS miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.	
XX	
OS Homo sapiens.	
XX	
PN WO200114558-A1.	
XX	
PD 01-MAR-2001.	
XX	
PF 28-AUG-2000; 2000WO-EP008388.	
XX	
PR 26-AUG-1999; 99EP-00116691.	
XX	
PA (MORP-) MORPHOSYS AG.	
XX	
PI Kretzschmar T, Tesar M, Marget M, Kroenke M;	
XX	
DR WPI; 2001-218451/22.	
XX	
PT Novel isolated human immunoglobulin or functional immunoglobulin fragment	
PT	specific for human leukocyte antigen Cw6, useful for treatment of humans
PT	and for human leukocyte antigen phenotyping.
XX	
PS Claim 3; Fig 1; 23pp; English.	
XX	
CC AAB67617-23 represent single chain antibody (scFv) fragments which are	
CC	specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived
CC	from a synthetic human combinatorial antibody library based on molecular
CC	consensus frameworks and CDRs randomised with trinucleotides. The
CC	specification describes a human immunoglobulin fragments specific for HLA
CC	-Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of
CC	natural killer cell silencing as well as miscarriages. HLA-Cw6
CC	demonstrates a disequilibrium in some recurrent abortions. Psoriasis may
CC	also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are
CC	useful for the preparation of a pharmaceutical for the treatment of
CC	humans. They are also useful for HLA phenotyping
XX	
SQ	Sequence 245 AA;

Query Match 58.4%; Score 788.5; DB 4; Length 245;  
Best Local Similarity 62.4%; Pred. No. 2.9e-45;  
Matches 159; Conservative 30; Mismatches 53; Indels 13; Gaps 4;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLASINMNDKC 60  
DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSSYAMS--WYQAPEGKLEWVASISGSGST 58  
QY 61 -YSPSLKSRLLTTKDTPKNOVLAMSNMADPATATYSCALDMPHDSGPQSFSDASDVWGP 119  
DB 59 YYADSVKGRFTISRDNKNTLYQMNSLRADTAIVYCA-----RYSFSPVDWVGQ 109  
QY 120 GTMTVSSGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYA 179  
DB 110 GTLVTVSSAGGGSGGGSGGGSGGGSDIELTQPPSVAPGQTARISCSGDALGDKYA 169  
QY 180 CWYQOKRGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAWDT 239  
DB 170 SWYQOKRGPQAPVLVIYDDSDRPSGIPERFSGNSGNTATLTISGTQAEDEADYYCQSYDN 229  
QY 240 -STAVFGTGTKLTVL 253  
DB 230 FDSFVFGGGLTVL 244

RESULT 2  
ABP45537  
ID ABP45537 standard; protein; 250 AA.  
XX ABP45537;  
AC 19-AUG-2002 (first entry)  
DT 19-AUG-2002 (first entry)  
XX

DE Human Blys binding scFv SEQ ID 1548.  
XX  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX Homo sapiens.  
OS  
XX  
XX WO200202641-A1.  
PN  
XX 10-JAN-2002.  
PD  
XX 15-JUN-2001; 2001WO-US019110.  
PF  
XX 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
PI WPI; 2002-114799/15.  
XX  
XX WPI; 2002-114799/15.  
DR  
XX  
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.  
XX  
XX Claim 1; Page 2250-2251; 3148pp; English.  
XX  
XX This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have

CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 250 AA;

Query Match 58.0%; Score 783; DB 5; Length 250;  
Best Local Similarity 63.5%; Pred. No. 6.8e-45;  
Matches 162; Conservative 29; Mismatches 56; Indels 8; Gaps 4;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLASINMNDKC 60  
DB 1 QVQLQESGPGLVKPSSETISLTCAVSGYIS--SGYWGVMIRQPPGKLEWIGSIYHSGSTY 59  
QY 61 YSPSLKSRLLTTKDTPKNOVLAMSNMADPATATYSCALDMPHDSGPQSFSDASDVWGP 120  
DB 60 YNPSLKSRVTISVDTSKNQPSLKLSSVTADTAIVYCA--RVHYDILLTGYLWAFDIWGG 117  
QY 121 TMVTVSSGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 180  
DB 118 TMVTVSSGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 180  
QY 181 WYQOKRGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAWDT 240  
DB 175 WYQOKRGPQAPVLVIYGNKNNRPSGIPDRFSSGSSGNTATLTISGTQAEDEADYYCNSRDS 234  
QY 241 --TAVFGTGTKLTVL 253  
DB 235 GNHVFVGGGTQLTVL 249

RESULT 3  
ABP45640  
ID ABP45640 standard; protein; 247 AA.  
XX ABP45640;  
AC 19-AUG-2002 (first entry)  
DT 19-AUG-2002 (first entry)  
XX

DE Human Blys binding scFv SEQ ID 1651.  
XX  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX Homo sapiens.  
OS  
XX  
XX WO200202641-A1.  
PN  
XX 10-JAN-2002.  
PD  
XX 15-JUN-2001; 2001WO-US019110.  
PF  
XX 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX  
DR WPI; 2002-114799/15.  
XX  
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.  
XX  
PS Claim 1; Page 2373-2374; 3148bp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 247 AA;  
  
Query Match 57.7%; Score 779.5; DB 5; Length 247;  
Best Local Similarity 60.5%; Pred. No. 1.2e-44;  
Matches 161; Conservative 28; Mismatches 44; Indels 33; Gaps 5;  
  
QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSGVSVMIRQPPGKALEMLASINWDDKC 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSNYSIS-SGYWGMIRQPPGKLEWIGSIYSGSTY 59  
  
QY 61 YSPSLKSRLLITTKDTPKNQVFLAMSNMPPADTATYSCA-----LDMPPHDSGPQ 109  
Db 60 YNPSLKSRLTISVDTSKNQFSLKLSSTVTAADTAVYYCARFRYDILTGYYYDM----- 111  
  
QY 110 SFDASDVWPGTMTVTVSSGGGGSGGGSGGGSSYEIMQLPSVSPGQTASITC 169  
Db 112 -----DVMGRGLTVTVSSGGGGSGGGSGGGSS-----ELTQDPNAVVALGQTVRITC 160  
  
QY 170 SGNLGDKYACWYQOKKPGRSPVLVITYGDNKRPSGIPERFSGSNSGNTATLTISGTQAMDE 229  
Db 161 QGDSLRSYASWYQOKPGQAPVLVITYGKNRPSGIPDRFSGSSSGNTASLTITGAQAEDE 220  
  
QY 230 ADYYCQAMDT--TAVFGTGKLTVL 253  
Db 221 ADYYCNSRDSGNHVVFGGKLTVL 246  
  
RESULT 4  
AAE36257  
ID AAE36257 standard; protein; 249 AA.  
XX  
AC AAE36257;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE TRAIL receptor protein binding scFv protein, T1006F07.  
XX  
KW TRAIL receptor; TR4; cancer; Kaposi's sarcoma; cerebellar degeneration;  
KW hyperproliferative disorder; neurodegenerative disorder; immune disorder;  
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
KW retinitis pigmentosa; Huntington's disease; Hashimoto's thyroiditis;  
KW rheumatoid arthritis; multiple sclerosis; Sjogren's syndrome; asthma;  
KW biliary cirrhosis; Behcet's disease; Crohn's disease; allergic disorder;  
KW glomerulonephritis; immune deficiency syndrome; myasthenia gravis;

KW polymyositis; inflammatory disorder; rheumatoid arthritis; septic shock;  
KW infectious disease; acquired immunodeficiency syndrome; viral infection;  
KW AIDS; proliferative disorder; myelodysplastic syndrome; aplastic anaemia;  
KW ischaemic injury; myocardial infarction; reperfusion injury; cachexia;  
KW anorexia; stroke; cardiovascular disorder; peripheral artery disease;  
KW limb ischaemia; arrhythmia; congestive heart failure; neovascularisation;  
KW ocular disorder; wound healing; angiogenesis; transplantation.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Domain 1. .125  
FT /note= "VH domain"  
FT Region 26. .35  
FT /note= "VH domain complementarity determining region 1  
FT (CDR1)"  
FT Region 50. .66  
FT /note= "VH domain complementarity determining region 2  
FT (CDR2)"  
FT Region 99. .114  
FT /note= "VH domain complementarity determining region 3  
FT (CDR3)"  
FT Domain 142. .249  
FT /note= "VL domain"  
FT Region 164. .174  
FT /note= "VL domain complementarity determining region 1  
FT (CDR1)"  
FT Region 190. .196  
FT /note= "VL domain complementarity determining region 2  
FT (CDR2)"  
FT Region 229. .238  
FT /note= "VL domain complementarity determining region 3  
FT (CDR3)"  
XX  
PN WO200297033-A2.  
XX  
PD 05-DEC-2002.  
XX  
PF 07-MAY-2002; 2002WO-US014268.  
XX  
PR 25-MAY-2001; 2001US-0293473P.  
PR 04-JUN-2001; 2001US-0294981P.  
PR 02-AUG-2001; 2001US-0309176P.  
PR 21-SEP-2001; 2001US-0323807P.  
PR 09-OCT-2001; 2001US-0327364P.  
PR 07-NOV-2001; 2001US-0331044P.  
PR 14-NOV-2001; 2001US-0331310P.  
PR 20-DEC-2001; 2001US-0341237P.  
PR 05-APR-2002; 2002US-0369860P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Salcedo T, Ruben SM, Rosen CA, Albert VR, Dobson CL, Vaughan TJ;  
XX  
DR WPI; 2003-140454/13.  
DR N-PSDB; AAD54858.  
XX  
PT Novel antibody useful for treating cancers and other hyperproliferative  
PT disorders, immunospecifically binds to TRAIL receptor and comprises  
PT variable heavy or light chain complementarity determining regions.  
XX  
PS Claim 1; Page 294-295; 301pp; English.  
XX  
CC The present invention relates to novel antibodies that immunospecifically  
CC bind to TRAIL receptor (TR4). Sequences of the invention are useful for  
CC treating, preventing or ameliorating cancer (e.g. colon, breast, uterine,  
CC pancreatic, lung, gastrointestinal or central nervous system cancer e.g.  
CC medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in  
CC human. They are useful for detecting expression of TR4 polypeptide and  
CC detecting, diagnosing, prognosing or monitoring cancers and other hyper-  
CC proliferative disorders. Antibodies of the invention are useful for  
CC treating, preventing or ameliorating neurodegenerative disorders (e.g.  
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,



CC retinitis pigmentosa, cerebellar degeneration and Huntington's disease),  
CC immune disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis),  
CC Sjogren's syndrome, biliary cirrhosis, Behcet's disease, Crohn's disease,  
CC polymyositis, immune-related glomerulonephritis, myasthenia gravis,  
CC Hashimoto's thyroiditis and immune deficiency syndrome), inflammatory  
CC disorders (e.g. asthma, allergic disorders and rheumatoid arthritis),  
CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS),  
CC herpes viral infections and other viral infections) and proliferative  
CC disorders. They are also useful for treating myelodysplastic syndromes  
CC (e.g. aplastic anaemia), ischaemic injury (such as that caused by stroke,  
CC myocardial infarction and reperfusion injury), septic shock, cachexia,  
CC anaemia and toxin-induced liver diseases (such as alcohol). They are  
CC also useful for treating cardiovascular disorders including peripheral  
CC artery diseases such as limb ischaemia, arrhythmia, congestive heart  
CC failure and cardiovascular tuberculosis, diseases or disorders associated  
CC with neovascularisation and ocular disorders, for wound healing, for  
CC promoting angiogenesis and as adjuvants to enhance immune responsiveness  
CC to specific antigen e.g. viral antigen. They are also useful in the  
CC preparation or recovery from surgery, trauma, radiation therapy and  
CC transplantation. The present sequence is T1006F07 single chain Fv (scFv)  
CC antibody that immunospecifically bind to TR4 protein. This sequence is  
CC used in the invention  
SQ Sequence 249 AA;

Query Match 57.1%; Score 771.5; DB 6; Length 249;  
Best Local Similarity 62.4%; Pred. No. 4e-44;  
Matches 159; Conservative 28; Mismatches 59; Indels 9; Gaps 5;  
QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVGWIRQPPGKALEWLASINWDDKC 60  
Db 1 EVQLLESQGGIVQPGGSLRLSCAASGFTFSSYAMS--WVRQAPGKGLEWVASISGGSGT 58  
QY 61 -YSPSLKSRLLITTKDTPKNOVVLAMSNMDDPADTATYSCALDMPRHDSGQSFDAADVMGP 119  
Db 59 YYADSVKGRFTISRDNKNTLYIQMNSLRRAEDTAVVYCARPESFQQWGHYSY-GMDVMGQ 117  
QY 120 GTMTVTSVSGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASTITCSGDNLGDKYA 179  
Db 118 GTMTVTSVSGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQAARTITCSGDKLGDKYA 173  
QY 180 CMYQOKPGRSPVLVIYGDNRKPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAMD 239  
Db 174 SMYQORPGQSPVLVIYQDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCCLANDS 233  
QY 240 STA-VFGTGTKLTVL 253  
Db 234 SADWVFGGKTIVL 248

RESULT 5  
AAB67621  
ID AAB67621 standard; protein; 245 AA.  
XX  
AC AAB67621;  
XX  
DT 29-MAY-2001 (first entry)  
XX  
DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6\_5.  
XX  
KW Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;  
XX  
XX miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.  
OS Homo sapiens.  
XX  
PN W0200114558-A1.  
XX  
PD 01-MAR-2001.  
XX  
PF 28-AUG-2000; 2000WO-EP008388.  
XX  
PR 26-AUG-1999; 99EP-00116691.  
XX

PA (MORP-) MORPHOSYS AG.  
XX  
PI Kretzschmar T, Tesar M, Marget M, Kroenke M;  
XX  
DR WPI; 2001-218451/22.  
XX  
PT Novel isolated human immunoglobulin or functional immunoglobulin fragment  
PT specific for human leukocyte antigen Cw6, useful for treatment of humans  
XX  
XX and for human leukocyte antigen phenotyping.  
PS Claim 3; Fig 1; 23pp; English.  
XX  
CC AAB67617-23 represent single chain antibody (scFv) fragments which are  
CC specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived  
CC from a synthetic human combinatorial antibody library based on molecular  
CC consensus frameworks and CDRs randomised with trinucleotides. The  
CC -Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of  
CC natural killer cell silencing as well as miscarriages. HLA-Cw6  
CC demonstrates a disequilibrium in some recurrent abortions. Psoriasis may  
CC also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are  
CC useful for the preparation of a pharmaceutical for the treatment of  
CC humans. They are also useful for HLA phenotyping  
XX  
SQ Sequence 245 AA;

Query Match 56.0%; Score 756.5; DB 4; Length 245;  
Best Local Similarity 60.2%; Pred. No. 4e-43;  
Matches 154; Conservative 32; Mismatches 55; Indels 15; Gaps 5;  
QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVGWIRQPPGKALEWLASINWDDK 59  
Db 1 EVQLVQSGAEVKKRPGESLKISCKSGYSFTS--YWIQWVRQMPGKGLEWVGIRYPGDSDT 58  
QY 60 CYSPLKSRLLITTKDTPKNOVVLAMSNMDDPADTATYSCALDMPRHDSGQSFDAADVMG 118  
Db 59 RYSPSPFGQVTTISADKSIISTAYLQWSSLSKASDTAMYCA-----RSWDYPFDIWG 108  
QY 119 PGTMVTSVSGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASTITCSGDNLGDKY 178  
Db 109 OGTLVTSVSSAGGGSGGGSGGGSGGGSDIELTQPPSVSVAPGQIARISCSGDALGDKY 168  
QY 179 ACWYQOKPGRSPVLVIYGDNRKPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAMD 238  
Db 169 ASWYQOKPQGAAPVLVIYDDSDRPSGIPERFSGNSGNTATLTISGTQAEADYYCQSYD 228  
QY 239 T-STAVFGTGTKLTVL 253  
Db 229 DHDRIVFGGKTIVL 244

RESULT 6  
AAB67622  
ID AAB67622 standard; protein; 245 AA.  
XX  
AC AAB67622;  
XX  
DT 29-MAY-2001 (first entry)  
XX  
DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6\_6.  
XX  
KW Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;  
XX  
XX miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.  
OS Homo sapiens.  
XX  
PN W0200114558-A1.  
XX  
PD 01-MAR-2001.  
XX  
PF 28-AUG-2000; 2000WO-EP008388.  
XX  
PR 26-AUG-1999; 99EP-00116691.  
XX





Matches 154; Conservative 25; Mismatches 51; Indels 30; Gaps 5;  
QY 1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSSTSGSVGWIRPPGKALEWLASI----- 53  
Db 1 QVQLVQSGSELKPKGSSSVKVSCKASGCTFSSYAIS--WVRQAPGQGLEWMGIIPIFGTA 58  
QY 54 NWNDKCYSPSLKSRLLTITKDTPKNQVVLAMSNMADPADTATYSCALDMPHDSGPQSFDA 113  
Db 59 N-----YAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCA-----RGRDG 102  
QY 114 SDVWPGMTVTVSSGGGGSGGGGGGGSSSYELMQLPSVSVSPGQTASITCSGDN 173  
Db 103 MDVWQGQSTLVTVSSGGGGSGGGGGGGSGGSGPQ-----LTQPPSVSVPGQTASITCSGDE 157  
QY 174 LGDKRYACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYY 233  
Db 158 LGNRYAYWYQOKPGQSPVLVIYQDRKRPSGIPERFSGNSGNTATLTISGTQAMDEADYY 217  
QY 234 QQAMDTSTAVFGTGTKLTVL 253  
Db 218 QQAMASGTGVFGTGTKLTVL 237

RESULT 8  
AAB67623

ID AAB67623 standard; protein; 245 AA.  
AC AAB67623;  
XX  
DT 29-MAY-2001 (first entry)  
XX  
DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6\_7.  
XX  
KW Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;  
XX miscearriage; abortion; psoriasis; antibody; HLA phenotyping; ss.  
OS Homo sapiens.  
XX  
PN WO200114558-A1.  
XX  
PD 01-MAR-2001.  
XX  
PF 28-AUG-2000; 2000MO-EP008388.  
XX  
PR 26-AUG-1999; 99EP-00116691.  
XX  
PA (MORP-) MORPHOSYS AG.  
XX  
PI Kretzschmar T, Tesar M, Marget M, Kroenke M;  
XX WPI; 2001-218451/22.  
XX  
PT Novel isolated human immunoglobulin or functional immunoglobulin fragment  
PT specific for human leukocyte antigen Cw6, useful for treatment of humans  
PT and for human leukocyte antigen phenotyping.  
XX  
PS Claim 3; Fig 1; 23pp; English.  
XX  
CC AAB67617-23 represent single chain antibody (scFv) fragments which are  
CC specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived  
CC from a synthetic human combinatorial antibody library based on molecular  
CC consensus frameworks and CDRs randomised with trinucleotides. The  
CC specification describes a human immunoglobulin fragments specific for HLA  
CC -Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of  
CC natural killer cell silencing as well as miscearriages. HLA-Cw6  
CC demonstrates a disequilibrium in some recurrent abortions. Psoriasis may  
CC also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are  
CC useful for the preparation of a pharmaceutical for the treatment of  
CC humans. They are also useful for HLA phenotyping  
XX  
SQ Sequence 245 AA;

Query Match 55.7%; Score 752.5; DB 4; Length 245;

Best Local Similarity 60.0%; Pred. No. 7.4e-43;  
Matches 153; Conservative 31; Mismatches 58; Indels 13; Gaps 4;  
QY 1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSSTSGSVGWIRPPGKALEWLASINMD-DK 59  
Db 1 EQVLVQSGAEVAKKPGESLKISKCKSGYSFTS--YWGVRQMPFGKLEWMGIIPGSDT 58  
QY 60 CYSPSLKSRLLTITKDTPKNQVVLAMSNMADPADTATYSCALDMPHDSGPQSFDA SDVWGP 119  
Db 59 RYSPSFGQVITISADKISITAYLQWSSLIKASDTAMYYCARFVPPY-----MDNWQ 109  
QY 120 GTMTVTVSSGGGGSGGGGGGGGGSSSYELMQLPSVSVSPGQTASITCSGDN LGDKYA 179  
Db 110 GTLVTVSSAGGGSGGGGGGGGGGGGGSDIELTQPPSVSVA PGQTARISCSGDALGDKYA 169  
QY 180 CMYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAMD- 238  
Db 170 SMYQOKRQQA PVLVIYDSDRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQSYDX 229  
QY 239 TSTAVFGTGTKLTVL 253  
Db 230 FRDVVFGGCTKLTVL 244

RESULT 9  
AAE02186

ID AAE02186 standard; protein; 280 AA.  
AC AAE02186;  
XX  
DT 10-AUG-2001 (first entry)  
XX  
DE PAM2 single chain variable region (scFv) antibody.  
XX  
KW Pectin; PAM1 antibody; single chain variable region; scFv; food; jam;  
XX yogurt; gel; homogalacturonan; HG; plant cell wall.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..22  
FT /label= pelt\_leader\_sequence 23..138  
FT /label= Heavy\_chain\_fragment 139..154  
FT /label= Linker 155..275  
FT /label= Light\_chain\_fragment 265..275  
FT /label= Myc\_epitope 279..80  
FT /note= "Encoded by TAGACT"  
XX  
PN US6228599-B1.  
XX  
PD 08-MAY-2001.  
XX  
PF 26-FEB-1999; 99US-00260527.  
XX  
PR 24-DEC-1998; 98GB-00028700.  
XX  
PA (DANI-) DANISCO AS.  
XX  
PI Knox JP, Willats WGT, Mikkelsen JD;  
XX WPI; 2001-342672/36.  
XX N-PSDB; AAD06194.  
XX  
PT New PAM1 and PAM2 antibodies capable of binding de-esterified  
PT homogalacturonan, useful for identifying a pectin moiety, for quantifying  
PT the amount of pectin in a sample or for extracting pectin from a sample.  
XX  
PS Claim 2; Fig 4B; 21pp; English.

XX The invention relates to antibodies specific to pectin, such as PAM1 and  
CC PAM2 scFv (single chain variable region). These antibodies are derived  
CC from a naive phage display library known as the synthetic scFv library  
CC (#1). PAM1 and PAM2 antibodies are capable of binding to de-esterified  
CC and un-substituted homogalacturonan (HG), useful for identifying a pectin  
CC motif. PAM antibody is useful for identifying a pectin functional group  
CC and in assays to determine if a particular pectin composition has the  
CC pectin motif or can be used to prepare a food for human and animal  
CC consumption, such as jams, yogurts or gels. The PAM antibodies are  
CC further useful for quantifying the amount of pectin in a sample or for  
CC extracting pectin from a sample. PAM antibodies are also used to identify  
CC de-esterified homogalacturonan blocks in the primary cell walls of  
CC plants. The present sequence is PAM2 scFv antibody specific to pectin.  
CC Note: This sequence is stated as being the same as that shown as SEQ ID  
CC NO: 3 in the sequence listing of the specification, however the sequence  
CC has 2 extra residues at the C-terminal end  
XX  
SQ Sequence 280 AA;

Query Match 55.7%; Score 752.5; DB 4; Length 280;  
Best Local Similarity 60.4%; Pred. No. 8.4e-43;  
Matches 154; Conservative 31; Mismatches 51; Indels 19; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTSGSVSGWIRQPPGKALEWLASINWDDKC 60  
Db 23 QVQLQESGPGILVKPSDTLSLTCAVSGYSISSN-WWGIRQPPGKLEWIGYIYSGSTY 81  
QY 61 YSPSLKSRLLITKDTPKNQVVLAMSNMDPADTATYSCALDMPPHDSGPQSPDASDVWGP 120  
Db 82 YNPSLKSRVTMSVDTSKNQPSLKLSSVTAVDTAVYYCA-----RPHRYVD---WGQG 131  
QY 121 TMTVTVSSGGGSGGGSGGGSGGGSSYEIMQLPSVSVSPGQTASITCSGDNLGDKYAC 180  
Db 132 TLVTVSSRGGGSGGGSGGGSS-----ELTQDPAVSVAGQTVRITTCQGDLSRYAS 185  
QY 181 WYQOKPGRSPVLVIYGDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDT 240  
Db 186 WYQOKPGRQAPVLVIYGNKNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDS 245  
QY 241 --TAVFGTGTKLTVL 253  
Db 246 GNHVFEGGTKLTVL 260

RESULT 10

AAB67619  
ID AAB67619 standard; protein; 245 AA.

XX AAB67619;

DT 29-MAY-2001 (first entry)

XX Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6\_3.

KW Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;

KW miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.

OS Homo sapiens.

XX WO200114558-A1.

PD 01-MAR-2001.

PF 28-AUG-2000; 2000WO-EP008388.

PR 26-AUG-1999; 99EP-00116691.

PA (MORP-) MORPHOSYS AG.

PI Kretzschmar T, Tesar M, Marget M, Kroenke M;

DR WPI; 2001-218451/22.

XX Novel isolated human immunoglobulin or functional immunoglobulin fragment  
PT specific for human leukocyte antigen Cw6, useful for treatment of humans  
PT and for human leukocyte antigen phenotyping.  
XX  
PS Claim 3; Fig 1; 23pp; English.

XX AAB67617-23 represent single chain antibody (scFv) fragments which are  
CC specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived  
CC from a synthetic human combinatorial antibody library based on molecular  
CC consensus frameworks and CDRs randomised with trinucleotides. The  
CC specification describes a human immunoglobulin fragments specific for HLA  
CC -Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of  
CC natural killer cell silencing as well as miscarriages. HLA-Cw6  
CC demonstrates a disequilibrium in some recurrent abortions. Psoriasis may  
CC also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are  
CC useful for the preparation of a pharmaceutical for the treatment of  
CC humans. They are also useful for HLA phenotyping  
XX  
SQ Sequence 245 AA;

Query Match 55.6%; Score 751.5; DB 4; Length 245;  
Best Local Similarity 59.2%; Pred. No. 8.6e-43;  
Matches 151; Conservative 32; Mismatches 59; Indels 13; Gaps 4;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTSGSVSGWIRQPPGKALEWLASINWDDKC 60  
Db 1 QVQLVSGAEVKKPGASVKVCKASGYTFTS--YYMHWVRQAPGCGLEWMGINPNSGCT 58  
QY 61 -YSPSLKSRLLITKDTPKNQVVLAMSNMDPADTATYSCALDMPPHDSGPQSPDASDVWGP 119  
Db 59 NYAQKFGGRVTMTTRDTSISTAYMELSLRSEDTAVYYCARG-----SDFMDNWGQ 109  
QY 120 GTMTVTVSSGGGSGGGSGGGSGGGSSYEIMQLPSVSVSPGQTASITCSGDNLGDKYA 179  
Db 110 GTLVTVSSAGGSGGGSGGGSGGGSGGSDIELTQPPSVSVAPGQTARISCSGDALGDKYA 169  
QY 180 CWYQOKPGRSPVLVIYGDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAW-D 238  
Db 170 SWYQOKPGRQAPVLVIYDDSDRPSGIPERFSGSNSGNTATLTISGTQADEADYYCQSYDD 229  
QY 239 TSTAVFGTGTKLTVL 253  
Db 230 TDLIVFEGGTKLTVL 244

RESULT 11

ABP45955  
ID ABP45955 standard; protein; 254 AA.

XX ABP45955;

DT 19-AUG-2002 (first entry)

XX Human BlyS binding scFv SEQ ID 1966.

KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

KW tumour necrosis factor; B cell proliferation; B cell differentiation;

KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

XX WO200202641-A1.

PN 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.



PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
DR  
XX  
XX

Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
diagnosis and treatment of cancers and immune disorders.

Claim 1; Page 2746-2747; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to  
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 254 AA;

Query Match 55.3%; Score 747; DB 5; Length 254;  
Best Local Similarity 59.8%; Pred. No. 1.8e-42;  
Matches 155; Conservative 34; Mismatches 58; Indels 12; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVGWIRPPGKALEWLASINWDDKC 60  
Db 1 QVQLQESGPGIVERSGTSLTCAVSGASISSNNL-WSWVRQPPKGLWIGELIYHSGSTS 59  
QY 61 YSPSLKSRLLTITKDTPKNOVLAMSNMPPADATATYSCALDMPPHDSGPQS---FDASDV 116  
Db 60 YNPSLRGRVTISVDKSNQPSLKLTSVTADTDVYYCARDY--YDSSSYSSGDYYTMDV 117  
QY 117 WGPMTMTVSSGGGGSGGGSGGGSSSYELMQLPSVSVSPGQTASITCSGDNLGD 176  
Db 118 WGGGTTVTVSSGGGGSGGGSGGGSS---ALSYELTQPPSVSPGQTATITCSGALPK 174  
QY 177 KYACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQA 236  
Db 175 QNAYWYQOKPQAPVLIYRDSERRSGIPERFSGSSGTTATLTISGVQAEDEADYYCQS 234  
QY 237 WDTSTA--VFGTGTKLTVL 253  
Db 235 ADSTVSYYVFGGKTIVL 253

RESULT 12  
ABP45469  
ID ABP45469 standard; protein; 250 AA.  
XX  
AC ABP45469;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scfv SEQ ID 1480.  
XX  
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
tumour necrosis factor; B cell proliferation; B cell differentiation;

KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
XX WO200202641-A1.  
XX  
XX 10-JAN-2002.  
XX  
XX 15-JUN-2001; 2001WO-US019110.  
XX  
XX

PR 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
DR  
XX

Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
diagnosis and treatment of cancers and immune disorders.

Claim 1; Page 2169-2170; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to  
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 250 AA;

Query Match 54.9%; Score 742; DB 5; Length 250;  
Best Local Similarity 56.9%; Pred. No. 3.8e-42;  
Matches 152; Conservative 30; Mismatches 53; Indels 32; Gaps 6;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVGWIRPPGKALEWLASINWDDK 59  
Db 1 QVQLVQSGAEVKKPGASVKVCKTSGYFDNYGIT--WVRQAPGQGLEWMGWLISAYDGR 58  
QY 60 CYSPLKSRLLTITKDTPKNOVLAMSNMPPADATATYSCALDMPPHDSGPQSFASDV--- 116  
Db 59 NYAQKLGRVTMTTDTSTSTAYMELSLRPDDTAVYYCAR-----DSDILTN 106  
QY 117 -----WGPMTMTVSSGGGGSGGGSGGGSSSYELMQLPSVSVSPGQTASIT 168  
Db 107 YYLEYFQHWGKTLTVTVSSGGGGSGGGSGGGSS---AQSVLTQPPSVSPGQTASIT 162  
QY 169 CSGDNLGDKYACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMD 228  
Db 163 CSGHNLGDKYVSWYQOKPQGPVLIYQDTKRPISGIPERFSGNSGNTATLTISGTQAMD 222  
QY 229 EADYYCQAMD--TSTAVFGTGTKLTVL 253



Db 223 EADYSCQTWDGSTSSVFGGKLTVL 249

RESULT 13

ABP45596

ID ABP45596 standard; protein; 256 AA.

XX

AC ABP45596;

XX

DT 19-AUG-2002 (first entry)

XX

DE Human Blys binding scFv SEQ ID 1607.

XX

KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

KW tumour necrosis factor; B cell proliferation; B cell differentiation;

KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX

OS Homo sapiens.

XX

PN WO200202641-A1.

XX

PD 10-JAN-2002.

XX

PF 15-JUN-2001; 2001WO-US019110.

XX

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX

DR WPI; 2002-114799/15.

XX

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the

PT diagnosis and treatment of cancers and immune disorders.

XX

PS Claim 1; Page 2320-2321; 3148pp; English.

XX

CC This invention describes novel antibodies that immunospecifically bind to

CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the

CC tumour necrosis factor (TNF) super family and induces B cell

CC proliferation and differentiation. The antibodies of the invention have

CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to

CC inhibit the expression and activity of Blys. The antibodies bind to Blys

CC and so may be used to detect and quantitate the presence of Blys in

CC biological samples and may be used in this way to diagnose disease

CC associated with aberrant expression of Blys. They may also be

CC administered to treat diseases associated with aberrant Blys expression

CC and activity such as cancer, immune, and autoimmune disorders and

CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,

CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and

CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent

CC the antibodies and fragments of the antibodies described in the method of

CC the invention

XX

SQ Sequence 256 AA;

Query Match 54.5%; Score 736; DB 5; Length 256;

Best Local Similarity 58.5%; Pred. No. 9.8e-42;

Matches 152; Conservative 33; Mismatches 63; Indels 12; Gaps 5;

Qy 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSGVSVMGIRQPPGKALEWLASINWMDKC 60

Db 1 QVQLQESGSGLVKPSQTLSTCAVSGSGSISGYSWWSWIRQPPGKLEWIGYIYHSGSTY 60

Qy 61 YSPSLKSRLLTITKDTPKNOVVLAMSNMDPADTATYS-CA-LDMPPHD--SGPQSPDASDWM 117

Db 61 YNPSLKSRVTVISVDRSKNQFSLKLSSTVTAADTAVYYCARQKQRGVDILTGYQLGYAFDIW 120

Qy 118 GPGTMVTVSSGGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASITCSG--DNLG 175

Db 121 GRGTPVTVS-----SGGGSGGGGGSGGGSGSVLTQPPSVSAAPGQKVTISCSGSTSNIG 175

Qy 176 DKYACWYQOKPGRSPVLVIYGDNKRPGGIPERFSGSNSGNTATLTISGTQAMDEADYCCQ 235

Db 176 NNYSWYQOHGKAPKLMYDVSKRPGVPDRFSGSKSGNSASLISGLQSEDEADYCA 235

Qy 236 AMDTSTA--VFGTGKLTVL 253

Db 236 AMWDSLSEFLFGTGKLTVL 255

RESULT 14

ABP44979

ID ABP44979 standard; protein; 251 AA.

XX

AC ABP44979;

XX

DT 19-AUG-2002 (first entry)

XX

DE Human Blys binding scFv SEQ ID 990.

XX

KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

KW tumour necrosis factor; B cell proliferation; B cell differentiation;

KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX

OS Homo sapiens.

XX

PN WO200202641-A1.

XX

PD 10-JAN-2002.

XX

PF 15-JUN-2001; 2001WO-US019110.

XX

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX

DR WPI; 2002-114799/15.

XX

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the

PT diagnosis and treatment of cancers and immune disorders.

XX

PS Claim 1; Page 1583-1584; 3148pp; English.

XX

CC This invention describes novel antibodies that immunospecifically bind to

CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the

CC tumour necrosis factor (TNF) super family and induces B cell

CC proliferation and differentiation. The antibodies of the invention have

CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to

CC inhibit the expression and activity of Blys. The antibodies bind to Blys

CC and so may be used to detect and quantitate the presence of Blys in

CC biological samples and may be used in this way to diagnose disease

CC associated with aberrant expression of Blys. They may also be

CC administered to treat diseases associated with aberrant Blys expression

CC and activity such as cancer, immune, and autoimmune disorders and

CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 251 AA;

Query Match 54.4%; Score 734.5; DB 5; Length 251;  
Best Local Similarity 59.9%; Pred. No. 1.2e-41;  
Matches 154; Conservative 30; Mismatches 62; Indels 11; Gaps 4;

QY 1 QVTLKESGPTLVKPTQTTLTLCTLSGFSLSSTGVSVMIRQPPGKALEWLASINMNDKC 60  
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSYVMWIRQPPGKLEWIGSIYSGSTY 60  
QY 61 YSPSLKSRLLTITKDTPKNQVVLAMSNMADPATATYSCALDMPHDSGPGSFDASDVWGP 120  
DB 61 YNPSLKSRLTISVDTSKNQFSLKLSVTAADTAIVYCARFR--YDILTSYYGMDVWGRG 118  
QY 121 TMVTVSSGGGSGGGSGGGSGGGSSYLEMQLPSVSVSPGQTASITCSG--DNIGDK 177  
DB 119 TMVTVS-----SGGGSGGGSGGGSGGGSGSVLTQPASVSGSPQSITISCTGTSSDVGYN 173  
QY 178 YACWYQOKPGRSPVLYIGDNKRPSPGIPRFGSGNSGNTATLTISGTQAMDEADYVCOAM 237  
DB 174 YVSWYQOHPGKAPKLMIEGSKRPSGVNRFSGSKSGNTASLTISGLQAEDEADYVCSSTY 233  
QY 238 DT-STAVFGTGTKLTVL 253  
DB 234 TTRSTRVFGGCTKLTVL 250

RESULT 15  
ABP45318  
ID ABP45318 standard; protein; 252 AA.  
XX  
AC ABP45318;  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scFv SEQ ID 1329.  
XX  
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US019110.  
XX  
PR 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
PT Antibodies against B lymphocyte stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.

XX  
PS Claim 1; Page 1989-1990; 3148pp; English.  
XX

CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 252 AA;

Query Match 54.3%; Score 733; DB 5; Length 252;  
Best Local Similarity 58.0%; Pred. No. 1.5e-41;  
Matches 153; Conservative 31; Mismatches 56; Indels 24; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTTLTLCTLSGFSLSSTGVSVMIRQPPGKALEWLASINMNDKC 60  
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSYVMWIRQPPGKLEWIGSIYSGSTY 60  
QY 61 YSPSLKSRLLTITKDTPKNQVVLAMSNMADPATATYSCA-----LDMPHDSGPGSFD 113  
DB 61 YNPSLKSRLTISVDTSKNQFSLKLSVTAADTAIVYCARGDYDILTGYPFH-----A 112  
QY 114 SDVWGPSTVTVSSGGGSGGGSGGGSGGGSSYLEMQLPSVSVSPGQTASITCSGDN 173  
DB 113 FDIWKGKTLTVS-----SGGGSGGGSGGGSGGGSGSVLTQPASVSGSPQSITISCTGTS 167  
QY 174 L--GDKYACWYQOKPGRSPVLYIGDNKRPSPGIPRFGSGNSGNTATLTISGTQAMDEA 230  
DB 168 SAVGGYNYVSWYQOHPGKAPKLMIEGSKRPSGVNRFSGSKSGNTASLTISGLQAEDEA 227  
QY 231 DYVCOAWDT-STAVFGTGTKLTVL 253  
DB 228 DYVCSSTYTRSTRVFGGCTKLTVL 251

Search completed: May 13, 2004, 15:00:59  
Job time : 53.0738 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:53:42 ; Search time 13.8782 Seconds  
(without alignments)  
941.146 Million cell updates/sec

Title: US-10-072-301-25  
Perfect score: 1351  
Sequence: 1 QVTLKESGPTLVKPTQTTLT.....CQAWDTSTAVFGTGTKLTVL 253

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/iaa/PCtUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/2/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	771.5	57.1	249	4	US-10-039-785-53 Sequence 53, Appl
2	752.5	55.7	278	3	US-09-260-527-3 Sequence 3, Appl
3	717	53.1	244	4	US-08-918-148-79 Sequence 79, Appl
4	694	51.4	250	4	US-10-039-785-50 Sequence 50, Appl
5	692	51.2	309	4	US-09-079-029-9 Sequence 9, Appl
6	688.5	51.0	312	4	US-09-079-029-10 Sequence 10, Appl
7	684	50.6	244	4	US-10-039-785-44 Sequence 44, Appl
8	668.5	49.5	280	3	US-09-260-527-1 Sequence 1, Appl
9	630.5	46.7	310	4	US-09-079-029-11 Sequence 11, Appl
10	617.5	45.7	258	2	US-08-665-202-5 Sequence 5, Appl
11	617.5	45.7	258	4	US-09-315-574-5 Sequence 5, Appl
12	607.5	45.0	235	2	US-08-190-199A-61 Sequence 61, Appl
13	606.5	44.9	249	4	US-08-918-148-74 Sequence 74, Appl
14	592.5	43.9	263	2	US-08-752-844-66 Sequence 66, Appl
15	592.5	43.9	263	4	US-09-293-533-66 Sequence 66, Appl
16	587.5	43.5	281	4	US-09-025-769B-178 Sequence 178, App
17	584.5	43.3	334	4	US-09-646-028-53 Sequence 53, Appl
18	584.5	43.3	339	4	US-09-646-028-55 Sequence 55, Appl
19	584.5	43.3	348	4	US-09-646-028-51 Sequence 51, Appl
20	574.5	42.5	245	4	US-10-039-785-42 Sequence 42, Appl
21	565.5	41.9	245	4	US-10-039-785-47 Sequence 47, Appl
22	565	41.8	248	2	US-08-887-352B-23 Sequence 23, Appl
23	565	41.8	248	3	US-09-109-207C-23 Sequence 23, Appl
24	565	41.8	248	3	US-09-296-005-23 Sequence 23, Appl
25	565	41.8	248	4	US-09-920-171-23 Sequence 23, Appl
26	563	41.7	248	2	US-08-887-352B-22 Sequence 22, Appl
27	563	41.7	248	3	US-09-109-207C-22 Sequence 22, Appl

28	563	41.7	248	3	US-09-296-005-22	Sequence 22, Appl
29	563	41.7	248	4	US-09-920-171-22	Sequence 22, Appl
30	561	41.5	264	3	US-08-564-164A-4	Sequence 4, Appl
31	552.5	40.9	245	4	US-08-918-148-76	Sequence 76, Appl
32	552.5	40.9	245	4	US-10-039-785-46	Sequence 46, Appl
33	549.5	40.7	482	4	US-09-509-031-16	Sequence 16, Appl
34	549	40.6	255	4	US-09-553-498-8	Sequence 8, Appl
35	549	40.6	255	4	US-09-618-869-8	Sequence 8, Appl
36	547.5	40.5	245	4	US-10-039-785-49	Sequence 49, Appl
37	546.5	40.5	245	4	US-08-918-148-78	Sequence 78, Appl
38	546.5	40.5	284	3	US-08-564-164A-2	Sequence 2, Appl
39	542.5	40.2	245	4	US-10-039-785-51	Sequence 51, Appl
40	541.5	40.1	245	4	US-10-039-785-48	Sequence 48, Appl
41	541.5	40.1	249	2	US-08-797-689-18	Sequence 18, Appl
42	541.5	40.1	249	4	US-09-984-186-18	Sequence 18, Appl
43	541.5	40.1	282	2	US-08-860-174A-10	Sequence 10, Appl
44	538.5	39.9	245	4	US-10-039-785-45	Sequence 45, Appl
45	537.5	39.8	245	4	US-08-918-148-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1  
US-10-039-785-53  
Sequence 53, Application US/10039785  
Patent No. 6538938  
GENERAL INFORMATION:  
APPLICANT: Salcedo et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL  
FILE REFERENCE: PF550  
CURRENT APPLICATION NUMBER: US/10/039,785  
CURRENT FILING DATE: 2002-05-07  
PRIOR APPLICATION NUMBER: 60/369,860  
PRIOR FILING DATE: 2002-04-05  
PRIOR APPLICATION NUMBER: 60/341,237  
PRIOR FILING DATE: 2001-12-20  
PRIOR APPLICATION NUMBER: 60/331,310  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/331,044  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: 60/327,364  
PRIOR FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: 60/323,807  
PRIOR FILING DATE: 2001-09-21  
PRIOR APPLICATION NUMBER: 60/309,176  
PRIOR FILING DATE: 2001-08-02  
PRIOR APPLICATION NUMBER: 60/294,981  
PRIOR FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: 60/293,473  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 53  
LENGTH: 249  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: T1006F07 bcfv  
US-10-039-785-53

Query Match 57.1%; Score 771.5; DB 4; Length 249;  
Best local Similarity 62.4%; Pred. No. 1.1e-50;  
Matches 159; Conservative 28; Mismatches 59; Indels 9; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSGVSVGWIRQPPGKALEWLASINWNDKC 60  
DB 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMS--WVRQAPGKGLEWVSAISGSGST 58  
QY 61 -YSPSLKSLRLTITKDTPKNQVVLAMSNMDPADTATYSCALDMPRHDSGPQSFSDASDVWGP 119  
DB 59 YVADSVKGRFTISRDNKNTLYIQMNSLRADDTAVVYCARPSPFQQWGHYSY-GMDVWVGQ 117



```
QY      120 GTMTVSSGGGGSGGGSGGGSSVYELMQLPSVSVSPGQTASITCSGDNIGDKYA 179
      Db      118 GTMTVSSGGGGSGGGSGGGSSVYELMQLPSVSVSPGQTASITCSGDNIGDKYA 173
QY      180 CWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCOAWDT 239
      Db      174 SWYQORPGSPVLVIYQDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCLAWDS 233
QY      240 STA-VFSGTGTKLTVL 253
      Db      234 SADWVFSGGTXTVL 248
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## RESULT 2

```
US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikelsen, J.D.
; APPLICANT: Willats, W.G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DY0U19.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 278
; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected
; OTHER INFORMATION: from a naive phage display library known as the
; OTHER INFORMATION: Synthetic scFv library (#1) from the Centre for
; OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
US-09-260-527-3
```

## Query Match

Best Local Similarity 55.7%; Score 752.5; DB 3; Length 278;  
Matches 154; Conservative 31; Mismatches 51; Indels 19; Gaps 5;

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QY      1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLASINWMDKC 60
      Db      23 QVQLQESGPGLVKPSDITSLTCAVSGYSSISN-WMGWIRQPPKGLEWIGYIYSGSTY 81
QY      61 YSPSLKSRLLTITKDTPPNQVVLAMSNMPPADTATYSCALDMPHDSGQSFSDASDVWGP 120
      Db      82 YNPSLKSRTVMSVDTISKQFSLKLSVTAVDATVYYCA-----RHPRVYD---WGQG 131
QY      121 TMVTVSSGGGGSGGGSGGGSSYEIMQLPSVSVSPGQTASITCSGDNIGDKYAC 180
      Db      132 TLVTVSRGGGGSGGGSGGGSS-----ELTQDPAVSVALGQTVRITCGDLSRYYAS 185
QY      181 WYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCOAWDT 240
      Db      186 WYQOKPGQAPVLVIYKNNRPSGIDRFSSSSGNTASLTITGAQAEDEADYYCNSRDS 245
QY      241 --TAVFGTGTKLTVL 253
      Db      246 GNHVVFGGTGTKLTVL 260
```

## RESULT 3

```
US-08-918-148-79
; Sequence 79, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
```

```
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 79
; LENGTH: 244
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-79
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## Query Match

Best Local Similarity 53.1%; Score 717; DB 4; Length 244;  
Matches 152; Conservative 30; Mismatches 53; Indels 22; Gaps 5;

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QY      1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLASINWMDKC 60
      Db      3 QVQLQESGPGLVKPSSETLSLTCTVSGDSISYYWS--WIRQPPKGLEWIGYIYSGSTN 60
QY      61 YSPSLKSRLLTITKDTPPNQVVLAMSNMPPADTATYSCALDMPHDSGQSFSDASDVWGP 120
      Db      61 YNPSLKSRTVMSVDTISKQFSLKLSVTAVDATVYYCARGR-----YFDVWGRG 109
QY      121 TMVTVSSGGGGSGGGSGGGSSYEIMQLPSVSVSPGQTASITCSG---DNLGDK 177
      Db      110 TMVTVS-----SGGGSGGGSGGGSSYVLTPPSVSGSPQSITISCTGTSSDVGGYN 164
QY      178 YACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCOAW 237
      Db      165 YVSMYQOHPGKAPKLMITYEGSKRPSGVNRFSSKSGKNTASLTISGLQAEDEADYYCNSY 224
QY      238 DT-STAVFGTGTKLTVL 253
      Db      225 TTRSTRVFGGTGTKLTVL 241
```

## RESULT 4

US-10-039-785-50  
; Sequence 50, Application US/10039785  
; Patent No. 6538938

; GENERAL INFORMATION:  
; APPLICANT: Salcedo et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL  
; FILE REFERENCE: PF550

; CURRENT APPLICATION NUMBER: US/10/039,785  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: 60/369,860  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 60/341,237  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 60/331,310  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/331,044  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/327,364  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/323,807  
; PRIOR FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 60/309,176  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: 60/294,981  
; PRIOR FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: 60/293,473  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 50

; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:



OTHER INFORMATION: T1015A02 BCFV  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (250)  
OTHER INFORMATION: Xaa equals either Gly or Ser  
US-10-039-785-50

Query Match 51.4%; Score 694; DB 4; Length 250;  
Best Local Similarity 54.5%; Pred. No. 7.3e-45;  
Matches 140; Conservative 36; Mismatches 69; Indels 12; Gaps 4;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVGWIRQPPGKALEWLASINWMDKC 60  
DB 1 QVQLQESGPGLVKPSQTLSTLKCNSGSGSIGTDYYSWIRQPPGKLEWIGYIHSSTY 60  
QY 61 YSPSLKRLTITKDTPKNQVVLAMSNMADPATATYSCALDMPHDSGPQSFSDASDVWGP 120  
DB 61 YKPSLSRLTWSMDTSRNQSLKLTSTADTALYYCVREMANGD---HMSAFDLWGQ 116  
QY 121 TMTVYSSGGGGSGGGSGGGSSYELMQLPSVSVSPQQTASITCSG--DNLGDKY 178  
DB 117 TLVTVSSGGGGSGGGSGGGSS---AQAVLTQPSASGTPGQRTVIPCSSSNIGNT 172  
QY 179 ACWYQKPGRSPLVLYIGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYCCQAWD 238  
DB 173 VNWYQQLPGTAPKLLIYGNDRPSGVDFRFSGSKSGTSASLAITGLQSEDEADYCCAWD 232  
QY 239 TSTA--VEGTGKLTVL 253  
DB 233 DSLIGYVFGTGTQLTVL 249

## RESULT 5

US-09-079-029-9  
Sequence 9, Application US/09079029  
Patent No. 6342369  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilia W.  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Chuntharapai, Anan  
APPLICANT: Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,029  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-079-029-9

Query Match 51.2%; Score 692; DB 4; Length 309;  
Best Local Similarity 55.9%; Pred. No. 1.3e-44;  
Matches 143; Conservative 33; Mismatches 64; Indels 16; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVGWIRQPPGKALEWLASINWMDKC 60  
DB 40 EVQLVQSGGVERPFGSLRLSCAASGFTFDYGMSS--WVRQAPGKLEWVSGINWNGST 97  
QY 61 -YSPSLKRLTITKDTPKNQVVLAMSNMADPATATYSCALDMPHDSGPQSFSDASDVWGP 119  
DB 98 GYADSVKGRVTISRDNKNSLYLQMNSLRAEDTAVYYCAKIL-----GAGRGMVFDLWGK 152  
QY 120 GTMTVYSSGGGGSGGGSGGGSSYELMQLPSVSVSPQQTASITCSGDNLGDKYA 179  
DB 153 GTTVYSSGGGGSGGGSGGGSS-----ELTQDPAVSVAGQTVRITCOGDSLRSYA 206  
QY 180 CWYQKPGRSPLVLYIGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYCCQAWDT 239  
DB 207 SWYQKPGQAPLVLYIGKNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCCNSRDS 266  
QY 240 S--TAVFGTGTCLTVL 253  
DB 267 SGNHYVFGGKLTCLTVL 282

## RESULT 6

US-09-079-029-10  
Sequence 10, Application US/09079029  
Patent No. 6342369  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilia W.  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Chuntharapai, Anan  
APPLICANT: Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,029  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 312 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-079-029-10

Query Match 51.0%; Score 688.5; DB 4; Length 312;  
Best Local Similarity 56.9%; Pred. No. 2.4e-44;  
Matches 145; Conservative 31; Mismatches 66; Indels 13; Gaps 5;

QY 2 VTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVGWIRQPPGKALEWLASINWMDKC 60  
DB 41 VQLVESGGGLVQPGSLRLSCAASGFTFSYWMSS--WVRQAPGKLEWVANIKQDGSSEK 98

[illegible]

```

RESULT 7
US-10-039-785-44
; Sequence 44, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014A02 BCFV
US-10-039-785-44

```

	Query Match	Best Local Similarity	Score 684;	DB 4;	Length 244;
	Matches 143; Conservative 31; Mismatches 65; Indels 18; Gaps 5;	55.6%; Pred. No. 4e-44;			
QY	1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGSVSVGIROPPEKALEWLASINWNDDKC	60			
Dd	1 QVQLQESGPGLVKPSETILSLTCTIVSGSISIDYYWS--WVRQSPGKGLEWIGSIDYAGSTN	58			
QY	61 YSPSLKSRLTITKDTPKNQVLAMSNMNDPADATATYSCALDMDPHDSGPQSFDASDVWGPG	120			
Dd	59 YNPSSLKSRVTMTIDSKSKQFLPKIDSVTAADTAMYCA-----RQLGRISDYWGQG	109			
QY	121 TMWTVVSSGGGSGGGGSGGGGSSYELMQLPVSVPFGQTASITCSG--DNLGDKY	178			
Dd	110 TLTVTSSGGGSGGGGSGGGG---ALSIVLTQPPSASGTPGQRVTIISCAGSSSNIGCNT	166			

[illegible]

```

RESULT 8
US-09-260-527-1
; Sequence 1, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelson, J.D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOU19.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 280
; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
; OTHER INFORMATION: phage display library known as the Synthetic scFv
; OTHER INFORMATION: library (#1) from the Centre for Protein
; OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
US-09-260-527-1

```

	Query Match	49.5%;	Score 668.5;	DB 3;	Length 280;	
	Best Local Similarity	54.7%;	Pred. No. 6.8e-43;			
	Matches 141;	Conservative 31;	Mismatches 63;	Indels 23;	Gaps 5;	
QY	1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSTGSVSGMIRPPGKALEWLASINWDD--	58				
Dp	23 EVQLVESGGGLVKPGSRLRSCAASGFTFSNAMS--WVRQAPEGLEWVGRIKSKTDGG	80				
QY	59 -KCYSPLKSRLLTTKDTPKNQVLAMSNMDPADATYSCALDMPHDSGPQSPFADSVW	117				
Dp	81 TTDYAAPVKGRFTISRDSKNTLLYLQMNSLKTEDTAHYCA-----RKWRKALRW	130				
QY	118 GPGTMTVTSSSGGSGSGGGSGGGSSYLEMLPISVSVPQGQTASITCSGDNLGDK	177				
Dp	131 GGGTLVTVSRGGSGSGGGSGGGSS-----ELTGDPAVSVALGQTVRITCGQDSLRSY	184				
QY	178 YACWYQQKPKGRSPVLVIYGDNKRPSGIPERFGSGNSGNTALLTISGTQAMDEADYYCQAW	237				
Dp	185 YASWYQQKPKGAPFLVIYGNRRPSPGIPIPRFSGSSSGNTASLTITGAQAEDEADYYCNSR	244				
QY	238 DTS--TAVFGTGTKLTVL	253				
Dp	245 DSSGNHVVFEGGKITLVL	262				

RESULT 9  
 US-09-079-029-11  
 ; Sequence 11, Application US/09079029  
 ; Patent No. 6342369  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Adams, Camilla W.  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Chunarapatt, Anan  
 ; APPLICANT: Kim, Kyung J.  
 ; TITLE OF INVENTION: Apo-2 Receptor  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way



```
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/315,574
/ FILING DATE: 20-MAY-99
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/000,238
/ FILING DATE: 14-JUN-1995
/ APPLICATION DATA:
/ APPLICATION NUMBER: US 60/000,250
/ FILING DATE: 15-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/665,202
/ FILING DATE: 13-JUN-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hunter, Tom
/ REGISTRATION NUMBER: 38,498
/ REFERENCE/DOCKET NUMBER: 02307E-061411
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 258 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-315-574-5

Query Match
Best Local Similarity 45.7%; Score 617.5; DB 4; Length 258;
Matches 132; Conservative 39; Mismatches 68; Indels 29; Gaps 8;

QY 1 QVTLKESGPTLVKPTQTTLTCTTSGFSLSTSGSVGVGWRQPPGKALEWLASINWMD-DK 59
DB 1 QVQLQSGAELKKPGESLTKISCKSGSYSTSYWIA--WVRQMPGKGLEWMLIYPGDSDT 58
QY 60 CYSPLKSRLLITKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSG-----PQ 109
DB 59 KYSPSPFGQVTLISVDKSVSTAYLQWSSLSKPSDSAYFCA----RHQVGYCSSSNCAKWE 114
QY 110 SFDASDVWPGTMTVTVSSGGGSGGGGSGGGGSSYELMQLPSVSVSPGQTASITC 169
DB 115 YFGH---WGQGTLVTVS-----SGGGSGGGGSGGGGSGSVLTQPPSVSAAPGQKVTISC 166
QY 170 SG--DNLGDKYACWYQOKGRSPVLVIYGDNRKPSGIPERFSGSNGTATLTISGTQAM 227
DB 167 SGSSSNIGNNYSWYQQLPGTAPKLLIYGHTRPAGVPDRFSGSGSGTSASIASISGRSE 226
QY 228 DEADYYCQAMDSTA--VFGTGKLTVL 253
DB 227 DEADYYCAAWDDSLSGWVFGGKLTVL 254

RESULT 12
US-08-190-199A-61
/ Sequence 61, Application US/08190199A
/ Patent No. 5830663
/ GENERAL INFORMATION:
/ APPLICANT: EMBLETON, Michael J.
/ APPLICANT: GOROCHOV, Guy
/ APPLICANT: JONES, Peter T.
/ APPLICANT: WINTER, Gregory P.
/ TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS
/ NUMBER OF SEQUENCES: 70
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
/ STREET: 1100 New York Avenue, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005-3918
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
```

```
/
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Microsoft Word
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/190,199A
/ FILING DATE: 13-JUL-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/GB92/01483
/ FILING DATE: 10-AUG-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9212419.7
/ FILING DATE: 11-JUN-1992
/ APPLICATION DATA:
/ APPLICATION NUMBER: GB 9117352.6
/ FILING DATE: 10-AUG-1991
/ INFORMATION FOR SEQ ID NO: 61:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 235 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-190-199A-61

Query Match
Best Local Similarity 45.0%; Score 607.5; DB 2; Length 235;
Matches 128; Conservative 31; Mismatches 71; Indels 21; Gaps 5;
```

```
QY 1 QVTLKESGPTLVKPTQTTLTCTTSGFSLSTSGSVGVGWRQPPGKALEWLASINWMDKC 60
DB 1 QVQLKESGPTLVKPSQSLSTCTTSGFSLSTSYGVH--WVRQPPGKGLEWLVAGGSTN 58
QY 61 YSPSLKSRLLITKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGPQSFASDVWGP 120
DB 59 YNSALMSRLSISKDNSKSVFLKMSLQTDITAMYYCARDGAY-----WGQG 106
QY 121 TMTVSSGGGSGGGGSGGGGSGGGGSSYELMQLPSV--SVSPGQTASITSGDNLGDKYA 179
DB 107 TLVTVS-----AGGGSGGGGSGGGGSGVLTQSPALMSASPGQKVTMTCSASS--SVSYM 160
QY 180 CWYQOKGRSPVLVIYGDNRKPSGIPERFSGSNGTATLTISGTQAMDEADYYCQAMD 239
DB 161 HWYQOKSGTSPKRWITPYSKLASGVPARFSGSGSATSYSLTSSMEADATYYCCQWSS 220
QY 240 STAVFGTGTKL 250
DB 221 NPLTFGAGTKL 231
```

```
RESULT 13
US-08-918-148-74
/ Sequence 74, Application US/08918148A
/ Patent No. 6342220
/ GENERAL INFORMATION:
/ APPLICANT: Adams, Camellia
/ APPLICANT: W.
/ APPLICANT: Carter, Paul J.
/ APPLICANT: Fendly, Brian M.
/ APPLICANT: Gurney, Austin L.
/ TITLE OF INVENTION: Agonist Antibodies
/ FILE REFERENCE: P0979
/ CURRENT APPLICATION NUMBER: US/08/918,148A
/ CURRENT FILING DATE: 1997-08-25
/ NUMBER OF SEQ ID NOS: 79
/ SEQ ID NO 74
/ LENGTH: 249
/ TYPE: PRT
/ ORGANISM: artificial
/ US-08-918-148-74
```

```
Query Match
Best Local Similarity 44.9%; Score 606.5; DB 4; Length 249;
Matches 128; Conservative 41; Mismatches 70; Indels 19; Gaps 6;
```



```

QY      1 QVTLKESGPTLVKPTQTLTLTCTLSGSLSTSGVSVGMIRQPPGKALEWTLASI-NWNDK 59
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      3 QVQLQESGGEMKKPPGESLTKISCKGYISFATSW--IGWVRQMPGRGLEWMAIMYPGNSDT 60

QY      60 CYSPLSKRLTITKDTPKQVVLAMSNMDPADTATYSCALDMPPHDSGPQSFEDASDVWGP 119
      ::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      61 RHNPSEFDQVLTMSADTSINTAYLQWSLSKASDTAMYCA-----RAGVAGAFDLWGK 113

QY      120 GTMTVTVSSGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASITCSGNL---GD 176
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      114 GTMTVTS-----SGGGSGGGSGGGSGGSSQSVLTQPASVSGSPGQSITISCTGTS SGVGY 168

QY      177 KYACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQA 236
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      169 NYVSWYQQHPRKAPKALLIYGNNSNRPSPGVPDRFSASKSGNTASLTISGLQAEDEADYFCST 228

QY      237 W-DTSTAVFGTGKLTVL 253
      :||| ||||| |||||
Db      229 YAPPGIIMFGGKLTVL 246

```

RESULT 14  
US-08-752

```

; Sequence 66, Application US/08752844
; Patent No. 5935821
;
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
;
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
;
; TELEX: 706141
;
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-752-844-66

```

	Query Match	43.9%;	Score 592.5;	DB 2;	Length 263;
	Best Local Similarity	51.7%;	Pred. No. 3.1e-37;		
	Matches	134;	Conservative 30;	Mismatches 72;	Indels 23; Gaps 7;
Qy	1 QVTLKESGPTLVKPQTLLTLCISGFSLSTSGVSVGWIRQPGEALFWLASINWNDDKC	60			
	:       :	:	:	:	: :
Db	20 QVOVKESGPFLVPSPQSLSITCTIVSDFSLLTYGV--WIROPDGLEWLGAIWGDGT	76			

```

QY      61  YSPSLKSRLLTITKOTPEKNQVILAMSNMDPADTATYSCALDMPPHDSGQSPDASDVWGP 113
      : |||::||| :|||::||| :|||::||| :|||::||| :|||::||| :|||::|||
Db      77  NYHSALISRLSISKDNSKQVFLKLSLQTDTDATYCA-----KLGNYDALDYWGQ 128

QY      120 GTMVTVSSGGGGSGGGSGGGSSYELMQLP-SVSVPGQTASITCSGD-----N 173
      ||||| ||||| ||||| ||||| :|||::||| :|||::||| :|||::||| :|||::|||
Db      129 GTSVTVS-----SGGGSGGGSGGGSGDVLMTQTPLSPVSLGDQASISCRSSQSVHS 183

QY      174 IGDKXACWYQOKPGRSPVLVTYGNDKRPSGIPERFSGNSGNTATLTISGQAMDEADYY 233
      ||: |||||::||| :|||::||| :|||::||| :|||::||| :|||::||| :|||::|||
Db      184 NGWTYLLEWYLQKPGQSPNLLIFYFVSNRFSGVPDRFSGSGSTDFLTKISRVEAEDLVYY 243

QY      234 QQAMDSTAVFGTGTCLTV 252
      ||||| ||||| :|||::||| :|||::||| :|||::||| :|||::|||
Db      244 CFQGSHVPWTFGGGTLEI 262

```

## RESULT 15

US-09-293-533--66  
: Sequence 66, Application US/09293533  
: Patent No. 6509016  
: GENERAL INFORMATION:  
: APPLICANT: Chatterjee, Malaya  
: APPLICANT: Foon, Kenneth A.  
: APPLICANT: Chatterjee, Sunil K.  
: TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
: TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
: NUMBER OF SEQUENCES: 66  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: MORRISON & FOERSTER  
: STREET: 755 PAGE MILL ROAD  
: CITY: PALO ALTO  
: STATE: CA  
: COUNTRY: USA  
: ZIP: 94304-1018  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/293,533  
: FILING DATE:  
: CLASSIFICATION:  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US/08/752,844  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Schiff, J. Michael  
: REGISTRATION NUMBER: 40,253  
: REFERENCE/DOCKET NUMBER: 30414-20002.21  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (415) 813-5600  
: TELEFAX: (415) 494-0792  
: TELEX: 706141  
: INFORMATION FOR SEQ ID NO: 66:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 263 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: US-09-293-533--66

Query Match	43.9%;	Score 592.5;	DB 4;	Length 263;
Best Local Similarity	51.7%;	Pred. No. 3.1e-37;		
Matches 134;	Conservative 30;	Mismatches 72;	Indels 23;	Gaps 7;
QY	1	QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLASINWDDKC	60	
		:             : : :    :    :                   :		
Db	20	QVQVKESGPTLVPPSQSLSTICTVSGFSLTITYGVS--WIRQPPGKLEWLGAI-WGDGTT	76	
QY	61	-YSPSLKSRLTITKDTPEKNQVLAAMSNMDDPATATYSCALDMPHDSGPQSPDASDVWGP	119	
		:          :    :       :                :		

Db 77 NYHSALISRLSISKDNSKSVFLKLNLSLQTDDTATYYCA-----KLGNLYDALDYWGQ 128

QY 120 GTMTVSSGGGGSGGGSGGGSGGGSSYELMQLP-SVSVPGQTASITCSGD-----N 173

Db 129 GTSVTVS-----SGGGSGGGSGGGSGGGSDVMTQTPLSLPVSLGDQASISCRSSQSIVHS 183

QY 174 LGDKYACWYQOKPGRSPVLVIYGDNKRPSGILPERFSGSNSGNTATLTISGTAMDADYY 233

Db 184 NGNTLYLEWYLOKPGQSPNLLITYFVSNRFGSVDRFSGSGSGTDFTLKISRVEADLGVYY 243

QY 234 QAMDSTAVFGTGTCLTV 252

Db 244 CFQGSHPVMTFGGGLTLEI 262

Search completed: May 13, 2004, 15:10:48  
Job time : 13.8782 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:07:07 ; Search time 37.4587 Seconds  
(without alignments)  
1879.405 Million cell updates/sec

Title: US-10-072-301-25  
Perfect score: 1351  
Sequence: 1 QVTLKESGPTLVKPTQTTLT.....CQAWDTSTAVFGTGTKLTVL 253

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1351	100.0	253	14 US-10-072-301-17	Sequence 17, Appl
2	1351	100.0	253	14 US-10-072-301-25	Sequence 25, Appl
3	1351	100.0	253	14 US-10-071-866-17	Sequence 17, Appl
4	1351	100.0	253	14 US-10-071-866-25	Sequence 25, Appl
5	1351	100.0	253	15 US-10-360-828-17	Sequence 17, Appl
6	1351	100.0	253	15 US-10-360-828-25	Sequence 25, Appl
7	794	58.8	253	14 US-10-072-301-23	Sequence 23, Appl
8	794	58.8	253	14 US-10-072-301-31	Sequence 31, Appl
9	794	58.8	253	14 US-10-071-866-23	Sequence 23, Appl
10	794	58.8	253	14 US-10-071-866-31	Sequence 31, Appl
11	794	58.8	253	15 US-10-360-828-23	Sequence 23, Appl
12	794	58.8	253	15 US-10-360-828-31	Sequence 31, Appl
13	783	58.0	250	10 US-09-880-748-1548	Sequence 1548, Ap
14	783	58.0	250	12 US-10-293-418-1548	Sequence 1548, Ap
15	779.5	57.7	247	10 US-09-880-748-1651	Sequence 1651, Ap

16	779.5	57.7	247	12 US-10-293-418-1651	Sequence 1651, Ap
17	771.5	57.1	249	13 US-10-039-785-53	Sequence 53, Appl
18	771.5	57.1	249	14 US-10-139-785-53	Sequence 53, Appl
19	747	55.3	254	10 US-09-880-748-1966	Sequence 1966, Ap
20	747	55.3	254	12 US-10-293-418-1966	Sequence 1966, Ap
21	742	54.9	250	10 US-09-880-748-1480	Sequence 1480, Ap
22	742	54.9	250	12 US-10-293-418-1480	Sequence 1480, Ap
23	739.5	54.7	258	14 US-10-072-301-27	Sequence 27, Appl
24	739.5	54.7	258	15 US-10-071-866-27	Sequence 27, Appl
25	739.5	54.7	258	15 US-10-360-828-27	Sequence 27, Appl
26	736	54.5	256	10 US-09-880-748-1607	Sequence 1607, Ap
27	736	54.5	256	12 US-10-293-418-1607	Sequence 1607, Ap
28	734.5	54.4	251	10 US-09-880-748-990	Sequence 990, App
29	734.5	54.4	251	12 US-10-293-418-990	Sequence 990, App
30	733	54.3	252	10 US-09-880-748-1329	Sequence 1329, Ap
31	733	54.3	252	12 US-10-293-418-1329	Sequence 1329, Ap
32	731	54.1	254	10 US-09-880-748-844	Sequence 844, App
33	731	54.1	254	12 US-10-293-418-844	Sequence 844, App
34	730	54.0	252	14 US-10-120-414-73	Sequence 73, Appl
35	728.5	53.9	247	10 US-09-880-748-1018	Sequence 1018, Ap
36	728.5	53.9	247	12 US-10-293-418-1018	Sequence 1018, Ap
37	723.5	53.6	251	10 US-09-880-748-1316	Sequence 1316, Ap
38	723.5	53.6	251	12 US-10-293-418-1316	Sequence 1316, Ap
39	723.5	53.6	253	10 US-09-880-748-1619	Sequence 1619, Ap
40	723.5	53.6	253	12 US-10-293-418-1619	Sequence 1619, Ap
41	722.5	53.5	251	10 US-09-880-748-952	Sequence 952, App
42	722.5	53.5	251	12 US-10-293-418-952	Sequence 952, App
43	721.5	53.4	255	10 US-09-880-748-841	Sequence 841, App
44	721.5	53.4	255	12 US-10-293-418-841	Sequence 841, App
45	721	53.4	248	10 US-09-880-748-1995	Sequence 1995, Ap

ALIGNMENTS

RESULT 1  
US-10-072-301-17  
; Sequence 17, Application US/10072301  
; Publication No. US20030152913A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODE.  
; FILE REFERENCE: 25636-718  
; CURRENT APPLICATION NUMBER: US/10/072,301  
; CURRENT FILING DATE: 2002-02-08  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.186.35  
US-10-072-301-17

Query Match	100.0%;	Score 1351;	DB 14;	Length 253;
Best Local Similarity	100.0%;	Pred. No. 2.8e-87;		
Matches 253;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	QVTLKESGPTLVKPTQTTLTCTISGFSLS	SGSVGVMIRQPPGKALEWLASINWDDKC	60
QY	61	YSPSLKRLTITKDTPKNQVILANSNMDPADTATYSCALDMPHDSGFS	FDASDVWGPG	120
Db	61	YSPSLKRLTITKDTPKNQVILANSNMDPADTATYSCALDMPHDSGFS	FDASDVWGPG	120
QY	121	TMWTVSSGGGSGGGGSGGGGSSYELMQLPSVSVSPGQTASITCSGDN	LGDKYAC	180
Db	121	TMWTVSSGGGSGGGGSGGGGSSYELMQLPSVSVSPGQTASITCSGDN	LGDKYAC	180

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QY      181 WYQOKPGRSPLYVLYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAWDTS 240
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QY      241 TAVFGTGTKLTVL 253
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Db      241 TAVFGTGTKLTVL 253
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## RESULT 2

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US-10-072-301-25
; Sequence 25, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.186.35 Variant
US-10-072-301-25
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Query Match      100.0%; Score 1351; DB 14; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.8e-87;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSSTSGSVSGWIRQPPGKALEWLASINWDDKC 60
      |||||||
QY      61 YSPSLKSRLLTTTKDTPKNQVVLAMSNMDDPADTATYSCALDMPPHDSGPOSFDASDVWGP 120
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Db      61 YSPSLKSRLLTTTKDTPKNQVVLAMSNMDDPADTATYSCALDMPPHDSGPOSFDASDVWGP 120
      |||||||
QY      121 TMVTVSSGGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 180
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Db      121 TMVTVSSGGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 180
      |||||||
QY      181 WYQOKPGRSPLYVLYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAWDTS 240
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Db      181 WYQOKPGRSPLYVLYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAWDTS 240
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QY      241 TAVFGTGTKLTVL 253
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Db      241 TAVFGTGTKLTVL 253
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## RESULT 3

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US-10-071-866-17
; Sequence 17, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST H
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.186.35
US-10-071-866-17
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Query Match      100.0%; Score 1351; DB 14; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.8e-87;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSSTSGSVSGWIRQPPGKALEWLASINWDDKC 60
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QY      61 YSPSLKSRLLTTTKDTPKNQVVLAMSNMDDPADTATYSCALDMPPHDSGPOSFDASDVWGP 120
      |||||||
Db      61 YSPSLKSRLLTTTKDTPKNQVVLAMSNMDDPADTATYSCALDMPPHDSGPOSFDASDVWGP 120
      |||||||
QY      121 TMVTVSSGGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 180
      |||||||
Db      121 TMVTVSSGGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 180
      |||||||
QY      181 WYQOKPGRSPLYVLYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAWDTS 240
      |||||||
Db      181 WYQOKPGRSPLYVLYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAWDTS 240
      |||||||
QY      241 TAVFGTGTKLTVL 253
      |||||||
Db      241 TAVFGTGTKLTVL 253
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## RESULT 4

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US-10-071-866-25
; Sequence 25, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST P
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.186.35 Variant
US-10-071-866-25
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Query Match      100.0%; Score 1351; DB 14; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.8e-87;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSSTSGSVSGWIRQPPGKALEWLASINWDDKC 60
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QY      61 YSPSLKSRLLTTTKDTPKNQVVLAMSNMDDPADTATYSCALDMPPHDSGPOSFDASDVWGP 120
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Db      61 YSPSLKSRLLTTTKDTPKNQVVLAMSNMDDPADTATYSCALDMPPHDSGPOSFDASDVWGP 120
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      |||||||
Db      121 TMVTVSSGGGGSGGGSGGGSGGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 180
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Db 181 WYQKPGRSPLVIYGDNRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDTS 240  
QY 241 TAVFGTGTKLTVL 253  
Db 241 TAVFGTGTKLTVL 253

RESULT 5

US-10-360-828-17  
; Sequence 17, Application US/10360828  
; Publication No. US20030206909A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shaobing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS  
; FILE REFERENCE: 25636-727  
; CURRENT APPLICATION NUMBER: US/10/360,828  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: US 10/071,866  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/072,301  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/133,978  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.186.35  
US-10-360-828-17

Query Match 100.0%; Score 1351; DB 15; Length 253;  
Best Local Similarity 100.0%; Pred. No. 2.8e-87;  
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTSGSVSGWIRQPPGKALEWLASINWDDKC 60  
Db 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTSGSVSGWIRQPPGKALEWLASINWDDKC 60  
QY 61 YSPSLKSRLLTTKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGPGSFDASDVWGP 120  
Db 61 YSPSLKSRLLTTKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGPGSFDASDVWGP 120  
QY 121 TMVTVSSGGGGSGGGGGGGGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 180  
Db 121 TMVTVSSGGGGSGGGGGGGGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 180  
QY 181 WYQKPGRSPLVIYGDNRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDTS 240  
Db 181 WYQKPGRSPLVIYGDNRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDTS 240  
QY 241 TAVFGTGTKLTVL 253  
Db 241 TAVFGTGTKLTVL 253

RESULT 6

US-10-360-828-25  
; Sequence 25, Application US/10360828  
; Publication No. US20030206909A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shaobing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS  
; FILE REFERENCE: 25636-727  
; CURRENT APPLICATION NUMBER: US/10/360,828  
; CURRENT FILING DATE: 2003-02-07

; PRIOR APPLICATION NUMBER: US 10/071,866  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/072,301  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/133,978  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.186.35 Variant  
US-10-360-828-25

Query Match 100.0%; Score 1351; DB 15; Length 253;  
Best Local Similarity 100.0%; Pred. No. 2.8e-87;  
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTSGSVSGWIRQPPGKALEWLASINWDDKC 60  
Db 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTSGSVSGWIRQPPGKALEWLASINWDDKC 60  
QY 61 YSPSLKSRLLTTKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGPGSFDASDVWGP 120  
Db 61 YSPSLKSRLLTTKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGPGSFDASDVWGP 120  
QY 121 TMVTVSSGGGGSGGGGGGGGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 180  
Db 121 TMVTVSSGGGGSGGGGGGGGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 180  
QY 181 WYQKPGRSPLVIYGDNRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDTS 240  
Db 181 WYQKPGRSPLVIYGDNRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDTS 240  
QY 241 TAVFGTGTKLTVL 253  
Db 241 TAVFGTGTKLTVL 253

RESULT 7

US-10-072-301-23  
; Sequence 23, Application US/10072301  
; Publication No. US20030152913A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF  
; FILE REFERENCE: 25636-718  
; CURRENT APPLICATION NUMBER: US/10/072,301  
; CURRENT FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.24  
US-10-072-301-23

Query Match 58.8%; Score 794; DB 14; Length 253;  
Best Local Similarity 62.8%; Pred. No. 3.5e-48;  
Matches 159; Conservative 24; Mismatches 68; Indels 2; Gaps 2;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTSGSVSGWIRQPPGKALEWLASINWDDKC 60  
Db 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSRTTGEVGVWVQPPGKALEWLASINWDDDKR 60  
QY 61 YSPSLKSRLLTTKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGPGSFDASDVWGP 120

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Db      61 YSPSLKSRLLITTKDTSKKQVLLTMTNVDPADTATYYCTHEQYYYDTSGQPY-YFDWGG 119
QY      121 TMTVSSGGGGSGGGSGGGSGGGSSYELMQLP-SVSVSPGQTASITCSGDNLGDKYA 179
Db      120 TLVTVSSGGGGSGGGSGGGSGGGSNIQVTQSPSSLASVGDRTVMTCRASQDIRKNL 179
QY      180 CMYQOKPGRSPVLVIYGDNKRPSGIPERFSGSNSGNTATLITISGTQAMDEADYYCQAWDT 239
Db      180 NMWYQOKPGKAPKVLIDASDLGTGIPSRFSGSGSGTDFILITISLQPEDIAITYCCQSDY 239
QY      240 STAVFGTGTKLTV 252
Db      240 LPLTFGGGTKVDI 252
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RESULT 8
US-10-072-301-31
; Sequence 31, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24 Variant
US-10-072-301-31
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Query Match      58.8%; Score 794; DB 14; Length 253;
Best Local Similarity 62.8%; Pred. No. 3.5e-48;
Matches 159; Conservative 24; Mismatches 68; Indels 2; Gaps 2;

QY      1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSGVSVGWIRQPPGKALEWLASINWDDKC 60
Db      1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSRTGEGVWVRQPPGKALEWLALIIYWDDKR 60
QY      61 YSPSLKSRLLITTKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGQSFSDASDVWGP 120
Db      61 YSPSLKSRLLITTKDTSKKQVLLTMTNVDPADTATYYCTHEQYYYDTSGQPY-YFDWGG 119
QY      121 TMTVSSGGGGSGGGSGGGSGGGSSYELMQLP-SVSVSPGQTASITCSGDNLGDKYA 179
Db      120 TLVTVSSGGGGSGGGSGGGSGGGSNIQVTQSPSSLASVGDRTVMTCRASQDIRKNL 179
QY      180 CMYQOKPGRSPVLVIYGDNKRPSGIPERFSGSNSGNTATLITISGTQAMDEADYYCQAWDT 239
Db      180 NMWYQOKPGKAPKVLIDASDLGTGIPSRFSGSGSGTDFILITISLQPEDIAITYCCQSDY 239
QY      240 STAVFGTGTKLTV 252
Db      240 LPLTFGGGTKVDI 252
```

```
RESULT 9
US-10-071-866-23
; Sequence 23, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST H
```

```
; TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24
US-10-071-866-23
```

```
Query Match      58.8%; Score 794; DB 14; Length 253;
Best Local Similarity 62.8%; Pred. No. 3.5e-48;
Matches 159; Conservative 24; Mismatches 68; Indels 2; Gaps 2;

QY      1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSGVSVGWIRQPPGKALEWLASINWDDKC 60
Db      1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSRTGEGVWVRQPPGKALEWLALIIYWDDKR 60
QY      61 YSPSLKSRLLITTKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGQSFSDASDVWGP 120
Db      61 YSPSLKSRLLITTKDTSKKQVLLTMTNVDPADTATYYCTHEQYYYDTSGQPY-YFDWGG 119
QY      121 TMTVSSGGGGSGGGSGGGSGGGSSYELMQLP-SVSVSPGQTASITCSGDNLGDKYA 179
Db      120 TLVTVSSGGGGSGGGSGGGSGGGSNIQVTQSPSSLASVGDRTVMTCRASQDIRKNL 179
QY      180 CMYQOKPGRSPVLVIYGDNKRPSGIPERFSGSNSGNTATLITISGTQAMDEADYYCQAWDT 239
Db      180 NMWYQOKPGKAPKVLIDASDLGTGIPSRFSGSGSGTDFILITISLQPEDIAITYCCQSDY 239
QY      240 STAVFGTGTKLTV 252
Db      240 LPLTFGGGTKVDI 252
```

```
RESULT 10
US-10-071-866-31
; Sequence 31, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST P
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24 Variant
US-10-071-866-31
```

```
Query Match      58.8%; Score 794; DB 14; Length 253;
Best Local Similarity 62.8%; Pred. No. 3.5e-48;
Matches 159; Conservative 24; Mismatches 68; Indels 2; Gaps 2;

QY      1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSGVSVGWIRQPPGKALEWLASINWDDKC 60
Db      1 QVTLKESGPTLVKPTQTLLTCTLSGFSLSRTGEGVWVRQPPGKALEWLALIIYWDDKR 60
QY      61 YSPSLKSRLLITTKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGQSFSDASDVWGP 120
Db      61 YSPSLKSRLLITTKDTSKKQVLLTMTNVDPADTATYYCTHEQYYYDTSGQPY-YFDWGG 119
```

```
QY 121 TMVTSSGGGGSGGGSGGGSSYELMQLP-SVSVSPGQTASITCSGDNLGDKYA 179
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 TLVTSSGGGGSGGGSGGGSSNIQVTSPLSASVGDRTWTCRASQDIRKNL 179
QY 180 CWYQQRKGRSPVLVIYGDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYCCQAWDT 239
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 NWYQQRKGRKAPKVLIDASDLETGIPSRFSGSGGTDFTLTISLQPEDIAITYCCQOSDY 239
QY 240 STAVFGTGKLTIV 252
|:|||||:
Db 240 LPLTFGGGTVKVDI 252
```

RESULT 11  
US-10-360-828-23

```
; Sequence 23, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24
US-10-360-828-23
```

Query Match 58.8%; Score 794; DB 15; Length 253;  
Best Local Similarity 62.8%; Pred. No. 3.5e-48;  
Matches 159; Conservative 24; Mismatches 68; Indels 2; Gaps 2;

```
QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVGWIRPPGKALEWLASINWDDKC 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSRTGEGVGMWRQPPGKALEWLALITYWDDDKR 60
QY 61 YSPSLKSRLLITTKDTPKNOVLAMSNMADPADTATYSCALDMPHDSGPQSFSDASDVWGPG 120
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YSPSLKSRLLITTKDTSKKQVLTMTNVDPADTATYCTHEQYYVDTSGQPY-YFDWGGG 119
QY 121 TMVTSSGGGGSGGGSGGGSSYELMQLP-SVSVSPGQTASITCSGDNLGDKYA 179
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 TLVTSSGGGGSGGGSGGGSSNIQVTSPLSASVGDRTWTCRASQDIRKNL 179
QY 180 CWYQQRKGRSPVLVIYGDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYCCQAWDT 239
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 NWYQQRKGRKAPKVLIDASDLETGIPSRFSGSGGTDFTLTISLQPEDIAITYCCQOSDY 239
QY 240 STAVFGTGKLTIV 252
|:|||||:
Db 240 LPLTFGGGTVKVDI 252
```

RESULT 12  
US-10-360-828-31  
; Sequence 31, Application US/10360828  
; Publication No. US20030206909A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shaobing

```
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24 Variant
US-10-360-828-31
```

Query Match 58.8%; Score 794; DB 15; Length 253;  
Best Local Similarity 62.8%; Pred. No. 3.5e-48;  
Matches 159; Conservative 24; Mismatches 68; Indels 2; Gaps 2;

```
QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVGWIRPPGKALEWLASINWDDKC 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSRTGEGVGMWRQPPGKALEWLALITYWDDDKR 60
QY 61 YSPSLKSRLLITTKDTPKNOVLAMSNMADPADTATYSCALDMPHDSGPQSFSDASDVWGPG 120
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YSPSLKSRLLITTKDTSKKQVLTMTNVDPADTATYCTHEQYYVDTSGQPY-YFDWGGG 119
QY 121 TMVTSSGGGGSGGGSGGGSSYELMQLP-SVSVSPGQTASITCSGDNLGDKYA 179
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 TLVTSSGGGGSGGGSGGGSSNIQVTSPLSASVGDRTWTCRASQDIRKNL 179
QY 180 CWYQQRKGRSPVLVIYGDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYCCQAWDT 239
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 NWYQQRKGRKAPKVLIDASDLETGIPSRFSGSGGTDFTLTISLQPEDIAITYCCQOSDY 239
QY 240 STAVFGTGKLTIV 252
|:|||||:
Db 240 LPLTFGGGTVKVDI 252
```

RESULT 13  
US-09-880-748-1548  
; Sequence 1548, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1548  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-880-748-1548

Query Match 58.0%; Score 783; DB 10; Length 250;  
Best Local Similarity 63.5%; Pred. No. 2e-47;  
Matches 162; Conservative 29; Mismatches 56; Indels 8; Gaps 4;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLASINWDDKC 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCAVSGYSIS-SGYTWGMIRQPPGKGLEWIGSIYHSGSTY 59  
QY 61 YSPSLKSRLLTITKDTPKNQVVLAMSNMADPATATYSCALDMPPHDSGQSFDAADVWGPG 120  
Db 60 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAIYYCA--RVHYDILTGYLWAFDIWGG 117  
QY 121 TMVTVSSGGGSGGGSGGGSGGGSSYELMQLPSVSPGQTASITCSGDNLGDKYAC 180  
Db 118 TMVTVSSGGGSGGGSGGGSGGGSSYELMQLPSVSPGQTASITCSGDNLGDKYAC 180  
QY 181 WYQOKPGRSPVLVIYGDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDTS 240  
Db 175 WYQOKPQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGTQAEADYCYCNRDSS 234  
QY 241 --TAVFGTGTCLTVL 253  
Db 235 GNHVVFGGGTQLTVL 249

RESULT 14

US-10-293-418-1548  
; Sequence 1548, Application US/10293418  
; Publication No. US20030223996A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PFS23P2  
; CURRENT APPLICATION NUMBER: US/10/293,418  
; PRIOR FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1548  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-1548

Query Match 58.0%; Score 783; DB 12; Length 250;  
Best Local Similarity 63.5%; Pred. No. 2e-47;  
Matches 162; Conservative 29; Mismatches 56; Indels 8; Gaps 4;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLASINWDDKC 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCAVSGYSIS-SGYTWGMIRQPPGKGLEWIGSIYHSGSTY 59  
QY 61 YSPSLKSRLLTITKDTPKNQVVLAMSNMADPATATYSCALDMPPHDSGQSFDAADVWGPG 120  
Db 60 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAIYYCA--RVHYDILTGYLWAFDIWGG 117  
QY 121 TMVTVSSGGGSGGGSGGGSGGGSSYELMQLPSVSPGQTASITCSGDNLGDKYAC 180

Db 118 TMVTVSSGGGSGGGSGGGSGGGSSYELMQLPSVSPGQTASITCSGDNLGDKYAC 174  
QY 181 WYQOKPGRSPVLVIYGDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDTS 240  
Db 175 WYQOKPQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGTQAEADYCYCNRDSS 234  
QY 241 --TAVFGTGTCLTVL 253  
Db 235 GNHVVFGGGTQLTVL 249

RESULT 15

US-09-880-748-1651  
; Sequence 1651, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PFS23  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1651  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1651

Query Match 57.7%; Score 779.5; DB 10; Length 247;  
Best Local Similarity 60.5%; Pred. No. 3.5e-47;  
Matches 161; Conservative 28; Mismatches 44; Indels 33; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLASINWDDKC 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCAVSGYSIS-SGYTWGMIRQPPGKGLEWIGSIYHSGSTY 59  
QY 61 YSPSLKSRLLTITKDTPKNQVVLAMSNMADPATATYSCA-----LMPPHDSGPQ 109  
Db 60 YNPSLKSRTVISVDTSKNQPSLKLSSVTAADTAIYYCARFRYDILTGYYDM----- 111  
QY 110 SFDASDVWGPDTMTVSSGGGSGGGSGGGSSYELMQLPSVSPGQTASITC 169  
Db 112 -----DVMGRGTLTVSSGGGSGGGSGGGSS-----ELTQDPAVSVALGQTVRITC 160  
QY 170 SGNLGDYKACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGSNSGNTATLTISGTQAMDE 229  
Db 161 QGDSLSRSYASWYQOKPQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDE 220  
QY 230 ADYYCQAWDTS--TAVFGTGTCLTVL 253  
Db 221 ADYYCNSRDSGNHVVFGGGTQLTVL 246

Search completed: May 13, 2004, 15:43:33  
Job time : 38.4587 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:50:27 ; Search time 11.4218 Seconds  
(without alignments)  
2130.694 Million cell updates/sec

**Title:** US-10-072-301-25

**Perfect score:**

Sequence: 1 QVTLKESGPTLVKPTQTLL...CQAMDSTAVFGTGTCLTVL 253

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

```
Database : PIR_78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query				ID	Description
No.	Score	Match	Length	DB		
1	516	38.2	231	2	S25738	Ig lambda chain -
2	494.5	36.6	120	2	S30525	Ig lambda chain V
3	486.5	36.0	249	2	S41374	single chain Fv anti-SS-A/Ro 60K F
4	485	35.9	107	2	PC4283	Ig heavy chain V r
5	483.5	35.8	124	2	A49002	Ig heavy chain V r
6	483	35.8	268	2	A56446	Ig heavy chain V r
7	479	35.5	151	2	S25739	Ig lambda chain -
8	478	35.4	231	2	S25751	Ig lambda chain -
9	474	35.1	106	1	L4HUBU	Ig lambda chain V-
10	474	35.1	114	2	S16440	Ig lambda chain -
11	472	34.9	231	2	S25753	Ig lambda chain -
12	470	34.8	95	2	S36065	Ig lambda chain -
13	470	34.8	106	1	L4HUX	Ig lambda chain V-
14	469	34.7	138	2	S31513	Ig heavy chain - h
15	466	34.5	374	2	S69339	Ig heavy chain V r
16	462.5	34.2	105	2	S44124	Ig lambda chain V
17	457	33.8	125	1	MHHUMC	Ig heavy chain V-I
18	455	33.7	119	2	S18555	Ig heavy chain V r
19	451	33.4	121	2	A36005	Ig heavy chain V r
20	441	32.6	106	1	L4HURL	Ig lambda chain V-
21	436	32.3	121	1	G1HUME	Ig heavy chain V-I
22	427.5	31.6	233	2	JC5322	p53 specific singl
23	423.5	31.3	120	1	G1HUCO	Ig heavy chain V-I
24	419.5	31.1	118	2	S18556	Ig heavy chain V r
25	418	30.9	107	1	L4HURL	Ig lambda chain V-
26	417	30.9	119	2	S30526	Ig lambda chain V
27	415.5	30.8	232	2	S25756	Ig lambda chain -
28	415	30.7	96	2	S26924	Ig heavy chain V r
29	412	30.5	120	2	S30527	Ig lambda chain V

30	411	30.4	96	2	S26923	Ig heavy chain V
31	403.5	29.9	106	2	S38495	Ig lambda chain -
32	403	29.8	106	1	L4HUKN	Ig lambda chain V-
33	400	29.6	132	2	S09713	Ig lambda chain V
34	398.5	29.5	143	2	PT0174	Ig heavy chain pre
35	398.5	29.5	147	1	G2HUCS	Ig heavy chain pre
36	395	29.2	128	2	S24319	Ig lambda chain pr
37	393	29.1	108	1	LSHUDL	Ig lambda chain V-
38	389	28.8	233	2	S25747	Ig lambda chain -
39	388	28.7	105	2	S49533	anti-Sm antibody V
40	386.5	28.6	122	2	S11740	Ig heavy chain pre
41	384	28.4	119	1	GIHUDW	Ig heavy chain V-I
42	380	28.1	96	2	S26922	Ig heavy chain V
43	378	28.0	127	2	S70444	Ig lambda chain pr
44	375	27.8	108	2	S47184	Ig lambda chain -
45	375	27.8	109	2	S19663	Ig lambda chain V

## ALIGNMENTS

## RESULT 1

Ig lambda chain - human  
 C/Species: Homo sapiens (man)  
 C/Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C/Accession: S25738  
 R/Combriato, G.; Klobeck, H.G.  
 Eur. J. Immunol. 21, 1513-1522, 1991  
 A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda  
 A/Reference number: S16439; MUID:91257162; PMID:1904362  
 A/Accession: S25738  
 A/Status: preliminary; translation not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-231 <COM>  
 A/Cross-references: EMBL:X57802; NID:g33701; PIDN:CAA40940.1; PID:g33702  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F,146-214/Domains: immunoglobulin homology <IMM>

Query Match	38.2%;	Score 516;	DB 2;	Length 231;
Best Local Similarity	89.1%;	Pred. No. 1.1e-27;		
Matches 98;	Conservative 4;	Mismatches 8;	Indels 0;	Gaps 0;

**Qy** 144 GGGSSYELMQLPSVSVPQGTAITCSGDNLGDKYACWYQQKPGRSPVLVIYGDNKRPSG 203  
:  
**Dd** 16 GSVA SYELTPPSVSVSPGQTASITCSGDTLGDKYACWYQQKPGHSPVLVIFQDSKRPSG 75  
:  
**Qy** 204 IPRFSGNSGNATLTISGTQAMDEADYYCQAMDSTAVFGTGKLTVL 253  
:  
**Dd** 76 IPRFSGNSGNATLTISGTQAMDEADYYCQAMDSSTAVFGGCKLTVL 125

## RESULT 2

Ig lambda chain V region - human  
 C/Species: Homo sapiens (man)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C/Accession: S30525  
 R/Mariette, X.  
 submitted to the EMBL Data Library, October 1992  
 A/Reference number: S30520  
 A/Accession: S30525  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-120 <MAR>  
 A/Cross-references: EMBL:Z18331  
 C/Suprafamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F,15-89/Domain: immunoglobulin homology <IMM>

Query Match	36.6%;	Score 494.5;	DB 2;	Length 120;
Best Local Similarity	88.8%;	Pred. No. 1.6e-26;		

Matches 95; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 148 SYELMQLPSVSVSPGQTASITCSGDNLDGKYACWYQOKPGRSPVLVIYGDNKRPSGIPER 207  
Db 1 SYELTPPSVSVSPGQTASITCSGDKGNKYACWYQOKPGQSPVVIYODSKRPSGIPER 60

QY 208 FSGNSGNTATLTISGTQAMDEADYYCQAWDTST-AVFGTGTCLTVL 253  
Db 61 FSGNSGNTATLTISGTQAMDEADYYCQAWDSITYVFGGTTCLTVL 107

#### RESULT 3

S41374  
single chain Fv antibody - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995

C/Accession: S41374

R/Artsenko, O.; Weller, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A/Description: Construction and functional characterization of a single chain Fv antibod

A/Reference number: S41374

A/Accession: S41374

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-249 <ART>

A/Cross-references: EMBL:Z29480

Query Match 36.0%; Score 486.5; DB 2; Length 249;  
Best Local Similarity 43.6%; Pred. No. 1.1e-25;  
Matches 112; Conservative 34; Mismatches 90; Indels 21; Gaps 7;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTSGSVGWIROPKALEWLASI-NWNDK 59  
Db 1 QVQLQSGAEIVRPGASVKLSCTASGFNFKD--YIMHWKQRPKEGLEWIAPIAPASGNV 58

QY 60 CYSPSLKSRLLTTKDTPKNQVVLAMSNMADPADATATYSCALDMPHDSGPGSFDASDVWGP 119  
Db 59 KYVPRFDKATITADTSMNTAVLLLSLTSEDYAYYCA-----RRDTLYTSLGYWQ 111

QY 120 GTMYTVSSGGGSGGGSGGGSSYEIMQL-PSVSVSPGQTASITC-SGDNL--- 174  
Db 112 GSTVTVS-----SRGGSGGGSGGGSGGSDIELTQSPPSVVIPEGESVISCRSSKSLYS 166

QY 175 -GDKYACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYY 233  
Db 167 DGDSYLFWFILQRPQSPQLLIYRMSNLASGVDPDRFSGSGSGTSTFLIRISVFAEDVGYY 226

QY 234 CQAWDTSTAVFGTGTCL 250  
Db 227 CMQHREYPLTFGAGTKL 243

#### RESULT 4

PC4283

anti-S5-A/Ro 60K peptide light chain E-60 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 07-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 16-Jul-1999

C/Accession: PC4283

R/Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.

Biochem. Biophys. Res. Commun. 232, 101-106, 1997

A/Title: Molecular cloning of anti-S5-A/Ro 60-kDa peptide fab fragments from infiltratin

A/Reference number: PC4279; MUID:97236289; PMID:9125110

A/Accession: PC4283

A/Molecule type: protein

A/Residues: 1-107 <SUZ>

C/Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjog

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

F/13-87/Domain: immunoglobulin homology <IMM>

Query Match 35.9%; Score 485; DB 2; Length 107;  
Best Local Similarity 87.7%; Pred. No. 6e-26;  
Matches 93; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 150 ELMQLPSVSVSPGQTASITCSGDNLDGKYACWYQOKPGRSPVLVIYGDNKRPSGIPER 209  
Db 1 ELLQPPSVSVSPGQTASITCSGDKLGDKYTCWYQOKPGQSPVVIYQDNKRPSGIPGRS 60

QY 210 GNSGNTATLTISGTQAMDEADYYCQAWDT--STAVFGTGTCLTVL 253  
Db 61 GNSGNTATLTISGTQAMDEADYYCQAWDSNNTVFGGTTCLTVL 106

#### RESULT 5

A49002

Ig heavy chain V region, rheumatoid factor RF antibody - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999

C/Accession: A49002

R/Stuber, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, H.W.J.; Gaeklin, R

Arthritis Rheum. 35, 900-904, 1992

A/Title: A rheumatoid factor from a normal individual encoded by VH2 and V kappa II ger

A/Reference number: A49002; MUID:92352481; PMID:1322670

A/Accession: A49002

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-124 <STU>

A/Cross-references: GB:M90808; NID:9185515; PIDN:AAA52989.1; PID:9567176

A/Experimental source: EBV-transformed lymphoblastoid cell line SSH23

A/Note: sequence extracted from NCBI backbone (NCBIN:110261, NCBIPI:110262)

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/15-99/Domain: immunoglobulin homology <IMM>

Query Match 35.8%; Score 483.5; DB 2; Length 124;  
Best Local Similarity 74.6%; Pred. No. 8.8e-26;  
Matches 97; Conservative 7; Mismatches 17; Indels 9; Gaps 2;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTSGSVGWIROPKALEWLASINWDDK 60  
Db 1 QITLKESGPTLVKPTQTLTLTCTLSGFSLSSTSGVGVWIRQPKALEWLAIIYWNDDR 60

QY 61 YSPSLKSRLLTTKDTPKNQVVLAMSNMADPADATATYSCA--LDMPHDSGPGSFDASDVW 117  
Db 61 YSPSLKSRLLTTKDTSKNQVVLTMNMDPVDATATYCAHWTVDSGGYLG-----FDYW 114

QY 118 GPGTMVTSS 127  
Db 115 GQGTIVTVSS 124

#### RESULT 6

A56446

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C/Species: Mus musculus (house mouse)

C/Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996

C/Accession: A56446

R/Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally identic

A/Reference number: A56446; MUID:95229583; PMID:7713873

A/Accession: A56446

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-268 <TAN>

A/Cross-references: GB:U20617

C/Keywords: heterotetramer; immunoglobulin

Query Match 35.8%; Score 483; DB 2; Length 268;  
Best Local Similarity 42.0%; Pred. No. 2.1e-25;  
Matches 108; Conservative 38; Mismatches 87; Indels 24; Gaps 7;

QY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSLSSTSGSVGWIROPKALEWLASI-NWNDK 59  
Db 3 QVQLQSGAEIVRPGASVKLSCTTSGFNKDT--YIMHWKQRPKEGLEWIGRIAPANGIT 60

QY 60 CYSPSLKSRLLTTKDTPKNQVVLAMSNMADPADATATYSCALDMPHDSGPGSFDAS---DV 116

Db 61 KYDPKFGKATIAADTSSNTAYLQLSLTSEDYAVYYCA-----SYLLTRYENY 109

Qy 117 WPGPTMYTVSSGGGSGGGGSGGGSSYELMQLPSV-SVSPGQTASITCSGDNLG 175

Db 110 WGQGTTVTVS-----SGGGSGGGGSDSGGGSDIELTQSPAIMSASLGEKVTMSCRASS-S 163

Qy 176 DKYACWYQOKPGRSPVLVIYGDNKRPSGIPEFRFGSGNSGNTATLTISGTQAMDEADYYCQ 235

Db 164 VNFYIYWYQOKSDASPKLMVYTTSHLPQGVPAFSGSGSGNSYSTLTISMEGEDAATYYCQ 223

Qy 236 AWDSTAVFGTGTCLTV 252

Db 224 QFTSSPFTFGSGTKLEI 240

RESULT 7

S25739

Ig lambda chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C/Accession: S25739

R/Combriato, G.; Klobbeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam

A/Reference number: S16439; MUID:91257162; PMID:1904362

A/Accession: S25739

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-151 <COM>

A/Cross-references: EMBL:X57803; NID:g33703; PIDN:CAA40941.1; PID:g33704

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/34-108/Domain: immunoglobulin homology <IMM>

Query Match 35.5%; Score 479; DB 2; Length 151;

Best Local Similarity 84.5%; Pred. No. 2.2e-25;

Matches 93; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 144 GGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYACWYQOKPGRSPVLVIYGDNKRPSG 203

Db 16 GSVASYELTQPPSVSVSPGQTASITCSGDTLGDKYACWYQOKPGHSPVLVIYQDSKRPSG 75

Qy 204 IPEFRFGSGNSGNTATLTISGTQAMDEADYYCOAWDTSTAVFGTGTCLTVL 253

Db 76 IPEFRFGSGNSGNTATLTISGTQAMDEADYYCOALGQHCVFSGGTCLTVL 125

RESULT 8

S25751

Ig lambda chain - human

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C/Accession: S25751

R/Combriato, G.; Klobbeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam

A/Reference number: S16439; MUID:91257162; PMID:1904362

A/Accession: S25751

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-231 <COM>

A/Cross-references: EMBL:X57816; NID:g33731; PIDN:CAA40953.1; PID:g33732

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/146-214/Domain: immunoglobulin homology <IMM>

Query Match 35.4%; Score 478; DB 2; Length 231;

Best Local Similarity 83.6%; Pred. No. 3.9e-25;

Matches 92; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Db 16 GSVASYELTQPPSVSVSPGKTASITCSGDKLGDKYASWYQOKAGOSPVLVIYRHSKRPSG 75

Qy 204 IPEFRFGSGNSGNTATLTISGTQAMDEADYYCOAWDTSTAVFGTGTCLTVL 253

Db 76 IPEFRFGSGNSGNTATLTISGTQVMEADYYCOAWDSIVVFGGGTCLTVL 125

RESULT 9

I4HUBU

Ig lambda chain V-IV region (Bau) - human

C/Species: Homo sapiens (man)

C/Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 02-Sep-1997

C/Accession: A01981

R/Baczko, K.; Braun, D.; Hilschmann, N.

Hope-Seyler's Z. Physiol. Chem. 355, 131-154, 1974

A/Title: Pattern of antibody structure. The primary structure of a monoclonal immunoglob

A/Reference number: A01981; MUID:75059189; PMID:4435717

A/Accession: A01981

A/Molecule type: protein

A/Residues: 1-106 <BAC>

C/Comment: This is a Bence Jones protein.

C/Genetics:

A/Gene: GDB:IGLV@

A/Cross-references: GDB:119342; OMIM:147240

A/Map position: 22q11.2-22q11.2

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer

F/14-88/Domain: immunoglobulin homology <IMM>

F/21-86/Disulfide bonds: #status predicted

Query Match 35.1%; Score 474; DB 1; Length 106;

Best Local Similarity 83.8%; Pred. No. 3.2e-25;

Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 149 YELMQLPSVSVSPGQTASITCSGDNLGDKYACWYQOKPGRSPVLVIYGDNKRPSGIPERF 208

Db 1 YGLTQPPSLSVSPGQTASITCSGDKLGQYVCWYQOKPGOSPVLVIYHDSKRPSGIPERF 60

Qy 209 SGSNSGNTATLTISGTQAMDEADYYCOAWDTSTAVFGTGTCLTVL 253

Db 61 SGSNSGTTATLTISGTQAMDEADYYCOAWDSYTVIFGGGTCLTVL 105

RESULT 10

S16440

Ig lambda chain - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000

C/Accession: S16440

R/Combriato, G.; Klobbeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin la

A/Reference number: S16439; MUID:91257162; PMID:1904362

A/Accession: S16440

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-114 <COM>

A/Cross-references: EMBL:X57826

C/Genetics:

A/Introns: 16/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/34-108/Domain: immunoglobulin homology <IMM>

Query Match 35.1%; Score 474; DB 2; Length 114;

Best Local Similarity 89.9%; Pred. No. 3.5e-25;

Matches 89; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 144 GGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYACWYQOKPGRSPVLVIYGDNKRPSG 203

Db 16 GSVASYELTQPPSVSVSPGQTASITCSGDKLGDKYACWYQOKPGOSPVLVIYQDSKRPSG 75



OY 204 IPERFSGNSGNTATLTISGTQAMDEADYCCQAWDTSTA 242  
Db 76 IPERFSGNSGNTATLTISGTQAMDEADYCCQAWDSSTA 114

RESULT 11  
Ig lambda chain - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C/Accession: S25753  
R/Combiarto, G.; Klobbeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam  
A/Reference number: S16439; MUID:91257162; PMID:1904362  
A/Accession: S25753  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-231 <COM>  
A/Cross-references: EMBL:X57818; NID:g33735; PIDN:CAA40955.1; PID:g33736  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/146-214/Domain: immunoglobulin homology <IMM>

Query Match 34.9%; Score 472; DB 2; Length 231;  
Best Local Similarity 80.9%; Pred. No. 9.8e-25;  
Matches 89; Conservative 7; Mismatches 14; Indels 0; Gaps 0;  
OY 144 GGGSSYELMQLPSVSPGQTASITCSGDNIGDKYACWYQOKPGRSPVLVIYGNKRPSGIPER 203  
Db 16 GSVASYELTQPPSVSPGQTASITCFGDKIGDKYSSWYQOKPGRSPVLVIYQDNRSGIPERF 60  
OY 204 IPERFSGNSGNTATLTISGTQAMDEADYCCQAWDTSTA 253  
Db 76 IPERFSGNSGNTATLTISGTQAMDEADYCCQAWDSNTVVFEGGTTLTVL 125

RESULT 12  
Ig lambda chain - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 01-Dec-1995 #text\_change 21-Jan-2000  
C/Accession: S36065  
R/Williams, S.C.  
submitted to the EMBL Data Library, April 1993  
A/Reference number: S36046  
A/Accession: S36065  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-95 <WIL>  
A/Cross-references: EMBL:Z22208; NID:g312871; PIDN:CAA80216.1; PID:g312872  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-89/Domain: immunoglobulin homology <IMM>

Query Match 34.8%; Score 470; DB 2; Length 95;  
Best Local Similarity 92.6%; Pred. No. 5.3e-25;  
Matches 88; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
OY 148 SYELMQLPSVSPGQTASITCSGDNIGDKYACWYQOKPGRSPVLVIYGNKRPSGIPER 207  
Db 1 SYELTQPPSVSPGQTASITCSGDKIGDKYACWYQOKPGRSPVLVIYQDSKRPSGIPER 60  
OY 208 FSGNSGNTATLTISGTQAMDEADYCCQAWDTSTA 242  
Db 61 FSGNSGNTATLTISGTQAMDEADYCCQAWDSSTA 95

RESULT 13  
Ig lambda chain V-IV region (X) - human  
C/Species: Homo sapiens (man)

C/Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 02-Sep-1997  
C/Accession: A01982  
R/Milstein, C.; Clegg, J.B.; Jarvis, J.M.  
Biochem. J. 110, 631-652, 1968  
A/Title: Immunoglobulin lambda-chains. The complete amino acid sequence of a Bence-Jon  
A/Reference number: A90243; MUID:69088380; PMID:4883841  
A/Accession: A01982  
A/Molecule type: protein  
A/Residues: 1-106 <MIL>  
C/Comment: This is a Bence Jones protein.  
C/Genetics:  
A/Gene: GDB:IGLV@  
A/Cross-references: GDB:119342; OMIM:147240  
A/Map position: 22q11.2-22q11.2  
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer  
F/14-88/Domain: immunoglobulin homology <IMM>  
F/21-86/Disulfide bonds: #status predicted

Query Match 34.8%; Score 470; DB 1; Length 106;  
Best Local Similarity 83.8%; Pred. No. 5.9e-25;  
Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;  
OY 149 YELMQLPSVSPGQTASITCSGDNIGDKYACWYQOKPGRSPVLVIYGNKRPSGIPERF 208  
Db 1 YDLTQPPSVSPGQTASITCSGDKIGDKYDCWYQQRPGSPVLVIYQDNRSSGIPERF 60  
OY 209 SGSNSGNTATLTISGTQAMDEADYCCQAWDTSTA 253  
Db 61 SGSNSGNTATLTISGTQAMDEADYCCQAWDSMSVVFEGGTTLTVL 105

RESULT 14  
Ig heavy chain - human  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C/Accession: S31513  
R/Chastagner, P.; Demaison, C.; There, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A/Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA aut  
A/Reference number: S31509  
A/Accession: S31513  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-138 <CHA>  
A/Cross-references: EMBL:X69861; NID:g33084; PIDN:CAA49495.1; PID:g33085  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/30-114/Domain: immunoglobulin homology <IMM>

Query Match 34.7%; Score 469; DB 2; Length 138;  
Best Local Similarity 74.0%; Pred. No. 9.1e-25;  
Matches 94; Conservative 7; Mismatches 20; Indels 6; Gaps 2;  
OY 1 QVTLKESGPTLVKPTQTLTLTCTLSGFSISTSGSVGWIROPKALEWLASINWDDKC 60  
Db 16 QITLKESGPTLVKPTQTLTLTCSFSGFSISTSGVGWIRPCKTLEWLAITYWDDDKR 75  
OY 61 YSPSLKRLITTKDTPKQOVVLAMSNMADPADTATYSCALDMPHDSGPQSPDAS-DWGP 119  
Db 76 YSPSLKRLITTKDTSQNVVLTMTNMDPVDATYCA-----HRPGIAVTGQNFQYMQ 130  
OY 120 GTMTVVS 126  
Db 131 GTLVTVS 137

RESULT 15  
Ig heavy chain V region precursor - human  
S69339



C:Species: Homo sapiens (man)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C:Accession: S69339; S72664  
R:Khamlich, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; MUID:95262687; PMID:7744049  
A:Accession: S69339  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <KHA>  
A:Cross-references: EMBL:X81695  
R:Khamlich, A.A.  
submitted to the EMBL Data Library, September 1994  
A:Reference number: S72664  
A:Accession: S72664  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140, 'C', 142-374 <KH2>  
A:Cross-references: EMBL:X81695  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 34.5%; Score 466; DB 2; Length 374;  
Best Local Similarity 71.7%; Pred. No. 4.1e-24;  
Matches 91; Conservative 11; Mismatches 21; Indels 4; Gaps 1;

Qy 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVGWIRQPPGKALEWLASINWDDKC 60  
|:|||||  
Db 20 QITLKESGPTLVKPTQTTLTCTPSGFSLSKSGVGWIRQPPGQALEWLALIFWDDDKR 79  
61 YSPSLKSRLLTITKDTPKNQVVLAMSNMDPADTATYSCALDMPPHDSGPQSFDAVDWGP 120  
|||:|||||  
Db 80 YSPSLKSRLLTITKDTSKNQVVLMTNVDPADTATYCGYSVEGYGGYRFRHS----WGOG 135  
121 TMVTVSS 127  
|:|||||  
Db 136 TLVTVSS 142

Search completed: May 13, 2004, 15:08:43  
Job time : 11.4218 secs

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DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-IV region X.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=69088380; PubMed=4883841;  
RA Milestein C., Clegg J.B., Jarvis J.M.;  
RT "Immunoglobulin lambda-chains. The complete amino acid sequence of a  
RT Bence-Jones protein.";  
RL Biochem. J. 110:631-652(1968).  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01982; L4HDX.  
DR HSSP; P80748; 2LOI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 102 IG-LIKE.  
FT NON\_TER 106 106  
SQ SEQUENCE 106 AA; 11334 MW; 24D04344AA812855 CRC64;

Query Match 34.8%; Score 470; DB 1; Length 106;  
Best Local Similarity 83.8%; Pred. No. 1.4e-27;  
Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;  
  
QY 149 YELMQLPSVSVSPGQTASITCSGDNLGDKYACWYQOKPGRSPVLVIYGDNKRPSGIPERF 208  
DB 1 YDLTQPPSVSVSPGQTASITCSGDKLGDKVCWYQQRPGQSPVLVIYQDNQRSSGIPERF 60  
  
QY 209 SGSNSGNTATLTISGTQAMDEADYYCQAWDSTAVFGTGTCLTVL 253  
DB 61 SGSNSGNTATLTISGTQAMDEADYYCQAWDSMSVVFGGGTRTLTVL 105

RESULT 3  
HV2D HUMAN STANDARD; PRT; 125 AA.  
ID HV2D\_HUMAN  
AC P01817;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-II region MCE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81118242; PubMed=6780622;  
RA Gerber-Jenson B., Kazin A., Kehoe J.M., Scheffel C., Erickson B.W.,  
RA Liltman G.W.;  
RT "Molecular basis for the temperature-dependent insolubility of  
RT cryoglobulin. X. The amino acid sequence of the heavy chain variable  
RT region of MCE.";  
RL J. Immunol. 126:1212-1216(1981).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM  
CC CRYOIMMUNOGLOBULIN.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A02092; MHHMC.  
DR HSSP; P01825; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Pyridolone carboxylic acid.  
FT DOMAIN 1 113  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT NON\_TER 125 125  
SQ SEQUENCE 125 AA; 13783 MW; 7A1ADF4C40F47BB5 CRC64;  
  
Query Match 33.8%; Score 457; DB 1; Length 125;  
Best Local Similarity 70.9%; Pred. No. 1.5e-26;  
Matches 90; Conservative 11; Mismatches 24; Indels 2; Gaps 1;  
  
QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSGVSVGWIRQPPGKALEWLASINWDDKC 60  
DB 1 QITLKESGPTLVKPTETTLTCTFSGFSLSGVSVGWIRQPPGKALEWLAFTNWDDNR 60  
  
QY 61 YSPSLKRLTITKDTPKQVVLAMSNMADPATYVSCALDMPPHDSGPQSFASDVWGP 120  
DB 61 YSPSLRSRLTGTCTKDSRNQVVLTTNMDPVDSGTYFCARHPFRFTG--NIGGFDXWGG 118  
  
QY 121 TMVTYSS 127  
DB 119 TLVTYSS 125

RESULT 4  
LV4E HUMAN STANDARD; PRT; 106 AA.  
ID LV4E\_HUMAN  
AC P06889;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-IV region MOL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=87156515; PubMed=3103603;  
RA Holm E., Sletten K., Husby G.;  
RT "Structural studies of a carbohydrate-containing  
RT immunoglobulin-lambda-light-chain amyloid-fibril protein (AL) of  
RT variable subgroup IIL.";  
RL Biochem. J. 239:545-551(1986).  
CC -1- MISCELLANEOUS: RESIDUES 29-30 AND 56-58 WERE POSITIONED BY  
CC HOMOLOGY.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A26019; L4HDM.  
DR HSSP; P80748; 2LOI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Amyloid; Glycoprotein.  
FT DOMAIN 1 103  
FT DISULFID 21 86 BY SIMILARITY.  
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (PROBABLE).  
FT NON\_TER 106 106  
SQ SEQUENCE 106 AA; 11272 MW; D9BB77D4797D2123 CRC64;

Query Match 32.6%; Score 441; DB 1; Length 106;  
Best Local Similarity 77.1%; Pred. No. 1.7e-25;  
Matches 81; Conservative 13; Mismatches 11; Indels 0; Gaps 0;  
  
QY 149 YELMQLPSVSVSPGQTASITCSGDNLGDKYACWYQOKPGRSPVLVIYGDNKRPSGIPERF 208  
DB 1 YDLTQPPSVSVSPGQTASITCSGDKLGDKVCWYQQRPGQSPVLVIYQDNQRSSGIPERF 60



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Db      1 YELTOPPSVSPGQTATISCSGDKLGESYYDWYQSPGSPLLVIYEGDKRPSGIPZRF 60
Qy      209 SGSNSGNTATLTISGTQAMDEADYYCQAMDTSTAVFGTGKLTVL 253
        |||||
Db      61 SGSNSGNTATLTISGTESMDEADYYCQAMSSSVLFGGKLTVL 105

RESULT 5
HV2B_HUMAN
ID      HV2B_HUMAN      STANDARD;      PRT;      121 AA.
AC      P01818;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Ig heavy chain V-II region HE.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      MEDLINE=70114712; PubMed=5264153;
RX      Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.;
RT      "Subgroups of amino acid sequences in the variable regions of
RT      immunoglobulin heavy chains.";
RL      Proc. Natl. Acad. Sci. U.S.A. 64:997-1003(1969).
CC      -1- MISCELLANEOUS: THIS GAMMA-1 CHAIN WAS ISOLATED FROM A MYELOMA
CC      PROTEIN.
CC      -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR      PIR; A02093; GIHUCF.
DR      HSSP; P01825; 7FAB.
DR      GO; GO:0005576; C:extracellular; NAS.
DR      GO; GO:0003823; F:antigen binding; NAS.
DR      GO; GO:0006955; P:immune response; NAS.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; Ig_1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG LIKE; 1.
KW      Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT      DOMAIN 1 120 IG-LIKE.
FT      MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT      NON_TER 121 121
SQ      SEQUENCE 121 AA; 13483 MW; 88A5082C273753B4 CRC64;

Query Match      32.3%; Score 436; DB 1; Length 121;
Best Local Similarity 68.8%; Pred. No. 4.6e-25;
Matches 88; Conservative 13; Mismatches 19; Indels 8; Gaps 3;

Qy      1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLA-SINMNDK 59
        |||||
Db      1 QVTLKESGPTLVKPTETTLTCTLSGSLTDTGVAVMIRQPPGKALEWLA-LYWDGDK 60
Qy      60 CYSPLSKRLTTKDTPKNQVTLAMSNMDDPADTATYSCALDMPHDSGPQSFDAADVWGP 119
        :|||
Db      61 RFSPLSKRLTIVTRDTSKNQVLTMTNMDPVDATYYCV-----HRHPTL-AFDVWGQ 113
Qy      120 GTMVTWSS 127
        |||||
Db      114 GTKVAVSS 121

RESULT 6
HV2B_HUMAN
ID      HV2B_HUMAN      STANDARD;      PRT;      120 AA.
AC      P01815;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Ig heavy chain V-II region COR.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX      NCBI_TaxID=9606;
RN      [1]
RP      MEDLINE=70258837; PubMed=5449120;
RX      Press E.M., Hogg N.M.;
RT      "The amino acid sequences of the Fd fragments of two human gamma-1
RT      heavy chains.";
RL      Biochem. J. 117:641-660(1970).
CC      -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC      PROTEIN.
CC      -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR      PIR; A02089; GIHUCO.
DR      HSSP; P01825; 7FAB.
DR      GO; GO:0005576; C:extracellular; NAS.
DR      GO; GO:0003823; F:antigen binding; NAS.
DR      GO; GO:0006955; P:immune response; NAS.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; Ig_1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG LIKE; 1.
KW      Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.
FT      DOMAIN 1 110 IG-LIKE.
FT      MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT      DISULFID 22 94
FT      CARBOHYD 62 62 N-LINKED (GLCNAC. . .).
FT      NON_TER 120 120
SQ      SEQUENCE 120 AA; 13226 MW; 158A8B29AE7EB98 CRC64;

Query Match      31.3%; Score 423.5; DB 1; Length 120;
Best Local Similarity 67.2%; Pred. No. 3.6e-24;
Matches 86; Conservative 14; Mismatches 19; Indels 9; Gaps 3;

Qy      1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLASINMNDKC 60
        |||||
Db      1 QVTLRESGPAVKPTQTTLTCTFSGFSLSSTGMCVMIRQPPGKLEWLARIDWDGDKY 60
Qy      61 YSPSLSKRLTTKDTPKNQVTLAMSNMDDPADTATYSCA-LDMPHDSGPQSFDAADVWGP 119
        :|||
Db      61 YNTSLERLTLSKDTSRNQVLT--TMDPVDATYYCARITVTPADG-----YMDVWGR 112
Qy      120 GTMVTWSS 127
        |||||
Db      113 GTPVTWSS 120

RESULT 7
LV4C_HUMAN
ID      LV4C_HUMAN      STANDARD;      PRT;      107 AA.
AC      P01717;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Ig lambda chain V-IV region H11.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      MEDLINE=78187276; PubMed=418804;
RX      Lopez de Castro J.A., Chiu Y.-Y.H., Poljak R.J.;
RT      "Amino acid sequence of the variable region of the light (lambda)
RT      chain from human myeloma cryoimmunoglobulin IgG H11.";
RL      Biochemistry 17:1718-1723(1978).
CC      -1- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS APPARENTLY
CC      IDENTICAL WITH THAT OF HUMAN SH LAMBDA CHAIN EXCEPT IN HAVING
CC      155-ILE (HIL NUMBERING) INSTEAD OF VAL.
CC      -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC      -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR      PIR; A01983; L4HULH.
DR      HSSP; P80748; 2LOI.
DR      GO; GO:0005576; C:extracellular; NAS.
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DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 97 IG-LIKE.  
FT NON TER 107 107  
SQ SEQUENCE 107 AA; 11517 MW; ASC8AFBE0CC590A CRC64;

Query Match 30.9%; Score 418; DB 1; Length 107;  
Best Local Similarity 74.5%; Pred. No. 7.9e-24;  
Matches 79; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 148 SYELMQLPSVSPGQTASITCSGDNLGDKYACWYQOKPGRSPVLYIGDNKRPSGIPER 207  
DB 1 SYELTOPPSVSPGQTARITCSANALPNQYAYWYQOKPGRAPVWYTKDTPRPSGIPOR 60  
QY 208 FSGSNSGNTATLTISGTQAMDEADYCCQAMDSTAVFGTKLTVL 253  
DB 61 FSSSTSGTWTLTISGVQAEADYCCQAMDNSASIFGGTKLTVL 106

RESULT 8  
LV4D\_HUMAN  
ID LV4D\_HUMAN STANDARD; PRT; 106 AA.  
AC P01718;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE IG lambda chain V-IV region Kern.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71150336; Pubmed=5549568;  
RA Ponsingl H., Hess M., Hilschmann N.;  
RT "Structural rule of antibodies. Primary structure of a monoclonal immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-protein Kern). V. The complete amino acid sequence and its genetic interpretation.";  
RT Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).  
RL -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ MARKER.  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01984; L4HUKN.  
DR HSSP; P80748; 2LOT.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 102 IG-LIKE.  
FT DISULFID 21 86 BY SIMILARITY.  
FT NON TER 106 106  
SQ SEQUENCE 106 AA; 11277 MW; C8B4A05B9CB43CBE CRC64;

Query Match 29.8%; Score 403; DB 1; Length 106;  
Best Local Similarity 72.4%; Pred. No. 9.4e-23;  
Matches 76; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 149 YELMQLPSVSPGQTASITCSGDNLGDKYACWYQOKPGRSPVLYIGDNKRPSGIPER 208  
DB 1 YALTOPPSVSPGQTAVITCSGDNLEKTFVSWFQORPGOSPPLVITYHTSERPSEIPERF 60

QY 209 SGSNSGNTATLTISGTQAMDEADYCCQAMDSTAVFGTKLTVL 253  
DB 61 SGSSSGATATLTISGAQSVDEADYFCQGTWDTITITIFGGTKLTVL 105

RESULT 9  
HV2H\_HUMAN  
ID HV2H\_HUMAN STANDARD; PRT; 147 AA.  
AC P0438;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V-II region SESS precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84298107; Pubmed=6089186;  
RA Takahashi N., Noma T., Honjo T.;  
RT "Rearranged immunoglobulin heavy chain variable region (VH) pseudogene that deletes the second complementarity-determining region.";  
RT Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).  
RL PIR; A02090; G2HUCS.  
DR HSSP; P01825; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 147 IG HEAVY CHAIN V-II REGION SESS.  
FT DOMAIN 20 118 V SEGMENT.  
FT DOMAIN 119 132 D SEGMENT.  
FT DOMAIN 133 147 J SEGMENT.  
FT NON TER 147 147  
SQ SEQUENCE 147 AA; 16323 MW; FCBCDB3D00FB6666 CRC64;

Query Match 29.5%; Score 398.5; DB 1; Length 147;  
Best Local Similarity 63.9%; Pred. No. 2.8e-22;  
Matches 78; Conservative 16; Mismatches 27; Indels 1; Gaps 1;

QY 1 QVTLKESGPTLVKPTQTLTTLTSGFSLSTGSVGVIRQPPGKALEWLASINWDDKC 60  
DB 20 QVNLRESGPALVKATHTLTLTCTFSGLSVNTRGMSVSWIRQPPGKALEWLAIDWDDKY 79  
QY 61 YSPSLKRLTITKTPKQVVLAMSNMPPADTATYSCA-LDMPPHDSGPQSFDAVDWGP 119  
DB 80 YGTSLETRLTISKDTSKNQVVLKVTNMDPADTATYCCARMQVTMVRVWITSNAFDIWGQ 139  
QY 120 GT 121  
DB 140 GT 141

RESULT 10  
LV5A\_HUMAN  
ID LV5A\_HUMAN STANDARD; PRT; 108 AA.  
AC P01719;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE IG lambda chain V-V region DEL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;

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RN [1]
RP SEQUENCE.
RX MEDLINE=75112179; PubMed=4452363;
RA Eultz M.;
RT "A new subgroup of human I-chains of the lambda-type. Primary
RL structure of Bence-Jones protein DEL.";
RL Eur. J. Biochem. 50:49-69(1974).
CC -1- MISCELLANEOUS: THIS IS THE FIRST SEQUENCED V REGION OF LAMBDA
CC CHAIN SUBGROUP V.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01985; LSHUDL.
DR HSSP; P80748; 2LOI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 97 IG-LIKE.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11342 MW; B8E8ED9C09C9E451 CRC64;

Query Match
Best Local Similarity 29.1%; Score 393; DB 1; Length 108;
Matches 76; Conservative 9; Mismatches 20; Indels 2; Gaps 1;

QY 149 YELMQLPSVSVSPGQTASITCSGDNLGDKYACWYQOKPGRSPVLYIGDNKRPSGIPERF 208
DB 1 YVLSQPPSVSVAPGQTARITCGGDGIGKSVHWYQOKPGQAPVLVHEDNDRPAGIPERF 60

QY 209 SGSNSGNTATLTISGTQAMDEADYYCOAWDTSTA--VFGTGTLTVL 253
DB 61 SGSNSGNTATLTISRVEAGDEADYYCEWDDRTAHVFGGTGTLTVL 107

RESULT 11
LV3B_HUMAN
ID LV3B_HUMAN STANDARD; PRT; 111 AA.
AC P80748;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE Ig lambda chain V-III region LOI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, SUBUNIT, DISEASE, AND 3D-STRUCTURE MODELLING.
RC TISSUE=Urine;
RX MEDLINE=99441384; PubMed=10510403;
RA Jokiranta T.S., Solomon A., Pangburn M.K., Zipfel P.F., Meri S.;
RT "Nephritogenic lambda light chain dimer: a unique human
RL miniautoantibody against complement factor H.";
RL J. Immunol. 163:4590-4596(1999).
CC -1- FUNCTION: ACTIVATES THE ALTERNATIVE COMPLEMENT PATHWAY BY BINDING
CC TO THE SHORT CONSENSUS REPEAT DOMAIN 3 (SCR3) OF FACTOR H.
CC -1- SUBUNIT: Homodimer.
CC -1- DISEASE: The blocking of factor H by LOI protein leads to the
CC developmental of membranoproliferative glomerulonephritis (MPGN).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PDB; 2LOI; 29-DEC-99.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
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DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; 3D-structure.
FT DOMAIN 1 97 IG-LIKE.
FT BINDING 15 15 SCR3.
FT BINDING 25 25 SCR3.
FT BINDING 29 29 SCR3.
FT BINDING 48 51 SCR3.
FT BINDING 94 94 SCR3.
FT DISULFID 21 86 BY SIMILARITY.
FT STRAND 4 4
FT STRAND 8 8
FT TURN 13 14
FT STRAND 16 22
FT STRAND 32 37
FT TURN 38 40
FT STRAND 41 46
FT TURN 49 50
FT STRAND 54 54
FT TURN 55 55
FT TURN 58 59
FT STRAND 60 61
FT STRAND 64 65
FT TURN 66 67
FT STRAND 68 74
FT TURN 78 79
FT STRAND 82 88
FT TURN 91 93
FT STRAND 97 98
FT STRAND 102 104
FT TURN 107 108
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11935 MW; 69498BEFEDE82053 CRC64;

Query Match
Best Local Similarity 28.8%; Score 389; DB 1; Length 111;
Matches 75; Conservative 12; Mismatches 18; Indels 2; Gaps 1;

QY 149 YELMQLPSVSVSPGQTASITCSGDNLGDKYACWYQOKPGRSPVLYIGDNKRPSGIPERF 208
DB 1 YVLTQPPSVSVAPGETARLTICGNDIGSESVHWYQOKPGQAPVLVYFDRDRPSGIPERF 60

QY 209 SGSNSGNTATLTISGTQAMDEADYYCOAWDTST--AVFGTGTGTLTVL 253
DB 61 SGSNSGNTATLTISRVEAGDEADYYCOLWDSSEHVVFPGGTGTLTVL 107

RESULT 12
HV2C_HUMAN
ID HV2C_HUMAN STANDARD; PRT; 119 AA.
AC P01816;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE Ig heavy chain V-II region DAW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;
RA Press B.M., HOGS N.M.;
RT "The amino acid sequences of the Fd fragments of two human gamma-1
RT heavy chains.";
RL Biochem. J. 117:641-660(1970).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE
CC SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02091; GLHWDW.
DR HSSP; P01789; IMCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
```



DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.  
FT DOMAIN 1 113  
FT MOD\_RES 1 113 IG-LIKE.  
FT NON\_TER 1 119 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 119 AA; 13045 MW; 4E13E00214BAD789 CRC64;

Query Match 28.4%; Score 384; DB 1; Length 119;  
Best Local Similarity 62.2%; Pred. No. 2.5e-21;  
Matches 79; Conservative 12; Mismatches 28; Indels 8; Gaps 2;

QY 1 QVTLKESGPTLVKPTQTLTLTCTSGFSLSTSGVSGVWIRPPGKALEWLASINWDDKC 60  
DB 1 QVTLRESGPAALVRPTQTLTLTCTSGFSLSTSGVSGVWIRPPGKALEWLASINWDDKC 60  
QY 61 YSPSLKSRLLTITKDTPKNOVVLAMSNMDDPADTATYSCALDMPPHDSGQSFSDASDVWGP 120  
DB 61 YGASLETRLAVSKDTSKNQVVLAMNTVGPGRATYYCA-----RSCGSQYF--DYWGQG 112  
QY 121 TMTVVS 127  
DB 113 ILTVVS 119

RESULT 13  
HV2A\_HUMAN STANDARD; PRT; 126 AA.  
ID HV2A\_HUMAN  
AC P01814;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-II region OU.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=74005511; PubMed=4742735;  
RA Putnam F.W., Florent G., Paul C., Shinoda T., Shimizu A.;  
RT "Complete amino acid sequence of the mu heavy chain of a human Igm  
RT immunoglobulin.";  
RL Science 182:287-291 (1973).  
CC -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S  
CC MACROGLOBULIN.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A02088; MHUOU.  
DR HSSP; P01825; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.  
FT DOMAIN 1 113  
FT MOD\_RES 1 113 IG-LIKE.  
FT DISULFID 22 97 PYRROLIDONE CARBOXYLIC ACID.  
FT NON\_TER 126 126  
SQ SEQUENCE 126 AA; 14276 MW; A85C0BE0DAB6296F CRC64;

Query Match 27.4%; Score 369.5; DB 1; Length 126;  
Best Local Similarity 62.5%; Pred. No. 2.9e-20;  
Matches 80; Conservative 15; Mismatches 30; Indels 3; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTLTLTCTSGFSLSTSGVSGVWIRPPGKALEWLASINWDDKC 60  
DB 1 QVTLRESGPAALVRPTQTLTLTCTSGFSLSTSGVSGVWIRPPGKALEWLASINWDDKC 60

DB 1 QVTLRESGPAALVRPPKQPLTLTCTSGFSLSTSGVSGVWIRPPGKALEWLASINWDDKC 59  
QY 61 Y-SPSLKSRLLTITKDTPKNOVVLAMSNMDDPADTATYSCALDMPPHDSGQSFSDASDVWGP 119  
DB 60 YNSTSLTRLISISKDSKNQVVLIMINVPYDTATYYCARVSVNAG-YYYYMDVWVK 118  
QY 120 GTMTVVS 127  
DB 119 GTTVVS 126

RESULT 14  
LV3A\_HUMAN STANDARD; PRT; 108 AA.  
ID LV3A\_HUMAN  
AC P01714;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-III region SH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=70166723; PubMed=4909564;  
RA Titani K., Wikler M., Shinoda T., Putnam F.W.;  
RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The  
RT complete amino acid sequence and the location of the disulfide  
RT bridges.";  
RL J. Biol. Chem. 245:2171-2176 (1970).  
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01980; L3HUSH.  
DR HSSP; P80748; 2LOI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 97  
FT DISULFID 21 86 IG-LIKE.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;

Query Match 26.0%; Score 351; DB 1; Length 108;  
Best Local Similarity 66.0%; Pred. No. 5.2e-19;  
Matches 70; Conservative 14; Mismatches 20; Indels 2; Gaps 1;

QY 150 ELMQLPSVSVSPQGTASITCSGDNIGDKYACWYQKPGKSPVLYIGDNKRPSGIPRFS 209  
DB 2 ELTQDPVAVSVALGQTVRITCGDLSRGYDAANYQKPGQAPLLVYGRNRPSPGIPDRFS 61  
QY 210 GSNNGTATLTISGTQAMDEADYYQAMDTS--TAVFGTGTXTLVL 253  
DB 62 GSSSGHTASLTITGAQAEDADYYCNSRDSGKHTVLFGGSTKLTVL 107

RESULT 15  
LV7A\_HUMAN STANDARD; PRT; 111 AA.  
ID LV7A\_HUMAN  
AC P01720;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-VII region MOT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.



OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81122740; PubMed=6780787;  
RA Kojima M., Odani S., Ikenaka T.;  
RT "Amino acid sequence of the lambda type light chain of a human IgG1  
RT myeloma protein (MOT) with unusual antigenicity: a possible new  
RT subgroup of lambda chain having a unique N-terminal sequence.";  
RL Mol. Immunol. 17:1407-1414(1980).  
CC -1- MISCELLANEOUS: THIS SEQUENCE REPRESENTS A NEW LAMBDA CHAIN  
CC SUBGROUP. IT HAS AN AMINO-TERMINAL EXTENSION OF THREE RESIDUES  
CC COMPARED WITH OTHER HUMAN LAMBDA CHAINS.  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+  
CC MARKERS.  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01986; L7HUMT.  
DR HSSP; P80748; 2LOI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 105 IG-LIKE.  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 11942 MW; 140A28A2F86A6911 CRC64;  
  
Query Match 26.0%; Score 351; DB 1; Length 111;  
Best Local Similarity 61.7%; Pred. No. 5.4e-19;  
Matches 66; Conservative 17; Mismatches 22; Indels 2; Gaps 1;  
  
QY 149 YELMQLPSVSVSPGQTASITCSGDNLGDKYACWYQKPGRSPVLYIGDNKRPSGIPERF 208  
||| ||| ||| : ||| ||| ||| : ||| ||| ||| : ||| ||| ||| : ||| ||| |||  
Db 4 YELTQPPSVSLAAGQTAMITCEGNDIGERSVHWYQKPGQAPVPVYDDADRPSPGVPARF 63  
  
QY 209 SGSNSGNTALTITISGTQAMDEADYYCQAMDIST--AVFGTGTKLTVL 253  
||| ||| ||| : ||| ||| ||| : ||| ||| ||| : ||| ||| ||| : ||| ||| |||  
Db 64 SGYNSGNSAIIITINRVEAGDEADYFCQSWDNGSYEVVFGTGTMTVL 110

Search completed: May 13, 2004, 15:02:05  
Job time : 7.1233 secs

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Db 40 QVKLQSGGGLVKPGSLKLSGSAASGSDFSRYWMS--WVRQAPGKGLWIGEINPDSSTI 97  
QY 61 -YSPSLKSRLLTTKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGQSPDASDVWGP 119  
Db 98 NYTPSLKDKFIRSDNAKNTLYLQMSKVRSEDTALYYCA-----RASYYGHSAYWQG 149  
QY 120 GTMTVTVSSGGGGSGGGSGGGSSSYELMQLP-SVSVSPGQTASITCSGDNLDGKY 178  
Db 150 GTTVTVS-----SGGGSGGGGGSGGGSDIELTQSPASLSASVGETVITTCRASGNINHY 204  
QY 179 ACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAMD 238  
Db 205 LAMWQOKQKSPQLLVVNAKTLADGVPSRFSGSGSGTQYSLKINSIQPEDFGSYCCQHFV 264  
QY 239 TSTA VFGTGTCLTV 252  
Db 265 TTPYTFGGGTKEI 278

RESULT 2  
Q921A6  
ID Q921A6 PRELIMINARY; PRT; 241 AA.  
AC Q921A6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Anti-CEA 79 single chain Fv fragment (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98170165; PubMed=9509426;  
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,  
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;  
RT "Cloning and characterization of cDNAs encoding VH and VL of a  
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and  
RT generation of a single-chain Fv molecule (scFv).";  
RL Mol. Cells 7:816-819(1997).  
DR EMBL; U88067; AAB48044.1; -.  
DR InterPro; IPR007110; IG-1like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG\_2.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PSS0835; IG\_LIKE; 2.  
FT NON\_TER 1  
FT NON\_TER 241  
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

QY 1 QVTLKESGPTLVKPTQTLLTCTLGSFSLSTSGVSVGWIRQPPGKALEWLASIN-WNDK 59  
Db 1 QVKLQSGGPELKKPGETVKISCKASGYTFDYGNN--WVQAPEGKGLKMMGMINTYTGEP 58  
QY 60 CYSPSLKSRLLTTKDTPKNQVVLAMSNMDDPADTATYSCA-LDMPPHDSGQSPDASDVWG 118  
Db 59 TYADDFKGRFAFSLSTASTAVLIQINLNKEDTATYFCARKDLRY-----FDYWG 109  
QY 119 PGTMVTVSSGGGGSGGGSGGGSSSYELMQLP-SVSVSPGQTASITCSGDNLDGDK 177  
Db 110 QGTVTVS-----SGGGSGGGGGSGGGSDIELTQSPASLSASVGETVITTCRASQDINK 164  
QY 178 YACWYQOKPGRSP---VLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEADYY 233  
Db 165 YIAMYQHKPGKGPRAHTLHIY----IQGPISRFSGSGSGRDYSPSISNLEPEDIATYY 220  
QY 234 QQAMDSTAVFGTGTCL 250  
Db 221 CLHYD-NLHTFGGTCL 236

RESULT 3  
Q9UL96  
ID Q9UL96 PRELIMINARY; PRT; 121 AA.  
AC Q9UL96;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035018; AAD56254.1; -.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; IG-1like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 121  
SQ SEQUENCE 121 AA; 13695 MW; D582D450596BDD35 CRC64;

Query Match 34.0%; Score 460; DB 4; Length 121;  
Best Local Similarity 73.2%; Pred. No. 9.1e-30;  
Matches 93; Conservative 7; Mismatches 21; Indels 6; Gaps 2;  
QY 1 QVTLKESGPTLVKPTQTLLTCTLGSFSLSTSGVSVGWIRQPPGKALEWLASINWDDK 60  
Db 1 QITLKESGPTLVKPTQTLLTCTLGSFSLSTSGMDVGIWIRQPPGKALEWLASINWDDK 60  
QY 61 YSPSLKSRLLTTKDTPKNQVVLAMSNMDDPADTATYSCALDMPHDSGQSPDASDVWGP 120  
Db 61 YSPSLKSRLLTTKDTSPKNQVVLAMSNMDDPADTATYSCA-----HRKSGDGY-YFDYWGQ 114  
QY 121 TMVTVSS 127  
Db 115 TLVTVSS 121

RESULT 4  
Q7QM2  
ID Q7QM2 PRELIMINARY; PRT; 243 AA.  
AC Q7QM2;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE scFv 6H8 protein (Fragment).  
GN scFv 6H8.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Balb/C;  
RA Peter J.C., Eftekhari P., Billfeld P., Wallukat G.;  
RT "scFv single chain antibody variable fragment as inverse agonist for  
RT the beta-2 adrenergic receptor.";  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ574851; CAE00495.1; -.  
FT NON\_TER 1



SQ SEQUENCE 243 AA; 25976 MW; BEFF64D2DC4F76 CRC64;  
Query Match 33.6%; Score 454; DB 11; Length 243;  
Best Local Similarity 40.5%; Pred. No. 6.5e-29;  
Matches 106; Conservative 42; Mismatches 78; Indels 36; Gaps 10;  
QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLASI----- 53  
DB 1 QVQLQSGSELVKPGASVSLCKASGTYFTTYMMH--WVKQRHGGGLEWIGNITYPGSGIT 58  
QY 54 NMNDKCYSPSLKSRLLTITKDPKQNVVLAMSNMDPADTATYSCALDMPHDSGPQSFDA 113  
DB 59 N-----YDEKFKNKGILTVDTSSSTAYMHLSSLASDSAVYYCA-----RGRG 102  
QY 114 SDVWPGTMTVTVSSGGSGGGSGGGSSYLEMQ-LPSVSVSPGQTASITC-SG 171  
DB 103 LDVWGAGTTLTVS-----SGGGSGGGSGGGSGGSDIQMTQSSSFSVSLGDRVTITCKAS 157  
QY 172 DNLGDKVACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTISGTQAMDEAD 231  
DB 158 EDIYNRLA-WYQOKPGNAPRLILISGATSLGTGVPSPRFSGSGSGKDYTLISLTQTEDVAT 216  
QY 232 YCCQA-WDTSTAVFGTGKTLTV 252  
DB 217 YCCQYWSITRT--FGGCTKLEI 236

RESULT 5

Q925S1 PRELIMINARY; PRT; 218 AA.  
AC Q925S1;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE MRP5 (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX PubMed=11819679;  
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X., Su C.;  
RT "Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after irradiation in mice.";  
RL World J. Gastroenterol. 6:709-717(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Cui D., Zeng G., Yan X., Li X., Su C.;  
RT "Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same strain.";  
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
DR EMBL; AF240168; AAK43733.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON TER 218  
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 31.1%; Score 419.5; DB 11; Length 218;  
Best Local Similarity 41.9%; Pred. No. 3.5e-26;  
Matches 95; Conservative 37; Mismatches 74; Indels 21; Gaps 7;  
QY 1 QVTLKESGPTLVKPTQTTLTCTLSGFSLSSTGVSVMIRQPPGKALEWLASINMND-K 59  
DB 3 QVQLQSGSELVKPGETVRISCKASGYFTTAAQM--WVQKMPGKGLKMWIGINTHSGVP 60

QY 60 CYSPLSKRLTITKDPKQNVVLAMSNMDPADTATYSCALDMPHDSGPQSFASDVWGP 119  
DB 61 KYAEFEKGRFAFSLETSASTAYLQISNLKNEDTATYFCM--RWDYDGG-----PAYWQG 112  
QY 120 GTWTVVSSGGSGGGSGGGSGGGSSYLEMQLP-SVSVSPGQTASITC---SGDNL 174  
DB 113 GTTVTVS-----SGGGSGGGSGGGSGGSDIVLTQSPASLAVSLGQRATISCRASESVNI 167  
QY 175 GDKVACWYQOKPGRSPVLVIYGDNKRPSGIPERFSGNSGNTATLTI 221  
DB 168 GISFNMWFQOKPGQPKLLIYASKQSGVPAGLLASGSGITDLSNI 214

RESULT 6

Q8TBC9 PRELIMINARY; PRT; 233 AA.  
AC Q8TBC9;  
DT 01-JUN-2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell;  
RA Strausberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC022823; AAH22823.1; -.  
DR PIR; S12442; S12442.  
DR PIR; S30526; S30526.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;

Query Match 30.9%; Score 417; DB 4; Length 233;  
Best Local Similarity 75.0%; Pred. No. 6e-26;  
Matches 84; Conservative 8; Mismatches 18; Indels 2; Gaps 1;

QY 144 GGGSSYLEMQLPVSVPSPGQTASITCSGDNLGDKYACWYQOKPGRSPVLVIYGDNKRPSG 203  
DB 16 GSEASYELTQPPSVSVSPGQTARITCSGDALPKQYAYWYQOKPGQAPVLVIYKDNERPSSG 75  
QY 204 IPRRSGNSGNTATLTISGTQAMDEADYYCQAMDTSTA--VFGTGKTLTVL 253  
DB 76 IPRRSGSSGTTVTLTISGVQAEDEADYYCQASDSSGTYWVFGGCTKTLTVL 127

RESULT 7

Q8N355 PRELIMINARY; PRT; 234 AA.  
AC Q8N355;  
DT 01-OCT-2002 (Tremblrel. 22, Created)  
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC028090; AAH28090.1; -.  
DR PIR; S12441; S12441.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig\_1like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KM Hypothetical protein.  
SQ SEQUENCE 234 AA; 24792 MW; CC848CAEBA4A9D63 CRC64;

Query Match 30.4%; Score 410.5; DB 4; Length 234;  
Best Local Similarity 70.8%; Pred. No. 2e-25;  
Matches 80; Conservative 10; Mismatches 20; Indels 3; Gaps 1;

QY 144 GGGSSYELMQLPSVSVSPGQTASITCGDNLGDKYACWYQKPGRSPVLVIYGDNRKPSG 203  
DB 16 GSVTSYVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQKPGQAPLVVYDSDRPSG 75  
QY 204 IPERFSGNSGNTATLTISGTQAMDEADYYCQAWDTST--AVFGTGTKLTVL 253  
DB 76 IPERFSGNSGNTATLTISRVDAGDEADYYCQLMDSSDHPVVFVGGTKLTVL 128

RESULT 8  
Q81IUS PRELIMINARY; PRT; 118 AA.  
ID Q81IUS  
AC Q81IUS;  
DT 01-JUN-2003 (TREMBLrel. 24, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Anti-human Fc gamma receptor III 3G8 gamma heavy chain variable region (Fragment).  
DE Mus musculus (Mouse).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Bruenke J., Valerius T., Repp R., Fey G.H.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY173025; AA018227.1; -  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig\_1like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KM Receptor.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 118 AA; 12979 MW; F57BB07033742E99 CRC64;

Query Match 28.9%; Score 390.5; DB 11; Length 118;  
Best Local Similarity 61.4%; Pred. No. 3.7e-24;  
Matches 78; Conservative 17; Mismatches 23; Indels 9; Gaps 2;

QY 1 QVTLKESGPTLVKPTOTLTTLTSLGFSLSGVSVMIRQPGKALEWLASINMNDKC 60  
DB 1 QVTLKESGPGIQLPQSQTLSLTCFSFGSLRRTSGMGVIRQPSGKGLEWLAHIWDDDKR 60  
QY 61 YSPSLKSLRLTITKTPKNOVVLAMSNMDDPATATYSCALDMPHDSGQSFDAADVWGP 120  
DB 61 YNPALKSLRLTISKDTSSNQVFLKIASVDLTATYCA-----QINAWF---AYWGG 111

QY 121 TMVTVSS 127  
DB 112 TLVTVSA 118

RESULT 9  
Q8NSF4 PRELIMINARY; PRT; 233 AA.  
ID Q8NSF4  
AC Q8NSF4;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain, and Lung;  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC032452; AAH32452.1; -  
DR PIR; S12441; S12441.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig\_1like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KM Hypothetical protein.  
SQ SEQUENCE 233 AA; 24961 MW; F092CFB6A6E3A9A CRC64;

Query Match 28.8%; Score 389; DB 4; Length 233;  
Best Local Similarity 72.5%; Pred. No. 1.1e-23;  
Matches 79; Conservative 8; Mismatches 20; Indels 2; Gaps 1;

QY 147 SSYELMQLPSVSVSPGQTASITCGDNLGDKYACWYQKPGRSPVLVIYGDNRKPSGIP 206  
DB 19 ASYELTQPPSVSVSPGQTARITCGDALPKKYAWYQKSGQTPVLVIYDTERPSGIP 78  
QY 207 RFSGSGSGNTATLTISGTQAMDEADYYCQAWDTSTA--VFGTGTKLTVL 253  
DB 79 RFSGSGSGNTATLTLSGAQVEDADYYCYSSDSSGNHWVFGGTKLTVL 127

RESULT 10  
Q9UL82 PRELIMINARY; PRT; 107 AA.  
ID Q9UL82  
AC Q9UL82;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RT Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
DR EMBL; AF035032; AAD56268.1; -.

DR HSSP; P01703; 7EAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1  
RC NON\_TER 107  
SQ SEQUENCE 107 AA; 11445 MW; 52F0CC1AB26821DC CRC64;

Query Match 28.3%; Score 382.5; DB 4; Length 107;  
Best Local Similarity 72.0%; Pred. No. 1.4e-23;  
Matches 77; Conservative 8; Mismatches 21; Indels 1; Gaps 1;

QY 148 SYELMQLPSVSVSPGQTASITCSGDNIGDKYACWYQOKPGRSPVLYIGDNKRPPSGIPER 207  
DB 1 SYELTQPSVSVSPGQTARITCSGDLAKKYARWFQOKPGQAPLVIKPTERPSGIPER 60

QY 208 FSGSNGTATLTISGTQAMDEADYYC-QAWDTSTAVFGTGTCLTVL 253  
DB 61 FSGSSSGTIVTLTISGAQVEADYYCYSASDNNGRVFGGTCLTVL 107

RESULT 11  
O43234 PRELIMINARY; PRT; 97 AA.

AC O43234;  
DT 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Rheumatoid factor RF-ET13 (Fragment).

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Borretzen M., Natvig J.B., Thompson K.M.;  
RT "Heterogenous RF structures between and within healthy individuals are  
RT not related to HLA DRB1\*0401.";  
RL Mol. Immunol. 0:0-0(1997).

DR EMBL; AF035802; AAB8534.1; -.  
DR HSSP; P01789; IMCP.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.

FT NON\_TER 1  
FT NON\_TER 97  
SQ SEQUENCE 97 AA; 10748 MW; DDC0BF47B9AA812D CRC64;

Query Match 27.8%; Score 376; DB 4; Length 97;  
Best Local Similarity 76.0%; Pred. No. 4.3e-23;  
Matches 73; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 3 TLKESGPTLVKPTQTTLTCTLSGFSISTSGVSVGWIRQPPGKALEWLASINWDDKCY 62  
DB 1 TLKESGPTLVKPTETTLTCTVSGFISNRRMGVSWIRQPPGKAVELAHIFANDEKSYS 60

QY 63 PSLKSLRLLTKDTPKNQVLAISNMDPADTATYSCA 98  
DB 61 TSLKSLRLLTKDTPKNQVLAISNMDPADTATYSCA 96

RESULT 12  
Q9NSD6 PRELIMINARY; PRT; 107 AA.

AC Q9NSD6;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein (Fragment).

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;

RP SEQUENCE FROM N.A.  
RC TISSUE=Lymphocytes;  
RA Hohnann A.;  
RT "Autoimmunity.";  
RT Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; L43092; AAA69746.2; -.  
DR HSSP; P01709; 2MCG.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.

FT NON\_TER 1  
FT NON\_TER 107  
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match 27.7%; Score 374; DB 4; Length 107;  
Best Local Similarity 70.8%; Pred. No. 7e-23;  
Matches 75; Conservative 10; Mismatches 19; Indels 2; Gaps 1;

QY 150 ELMQLPSVSVSPGQTASITCSGDNIGDKYACWYQOKPGRSPVLYIGDNKRPPSGIPER 209  
DB 1 ELTQDPVSVVALGQTVRITCGDLSRYSYASWYQOKPGQAPVLYIGKNRPPSGIPDRFS 60

QY 210 GSNSGNTATLTISGTQAMDEADYYCQAWDTS--TAVFGTGTCLTVL 253  
DB 61 GSSSGNTATLTITGAQAEADYYCNSRDSGNHAFVFGGTCLTVL 106

RESULT 13  
O7Z2U7 PRELIMINARY; PRT; 234 AA.

AC O7Z2U7;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22388257; Pubmed=12477932;  
RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC054883; AAH54883.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 234 AA; 25015 MW; 9A5723ABC93A06F CRC64;

Query Match  
Best Local Similarity 27.3%; Score 368.5; DB 4; Length 234;  
Matches 72; Conservative 12; Mismatches 23; Indels 3; Gaps 1;

QY 147 SSYELMQLPSVSVSPGQTASITCSGDNLGDKYACWYQOKPGRSPVLVIYGDNKRPSGIPE 206  
Db 19 ASYVLTQPPSVSVAPGKTARITCGADNIGAKSVHWYQOKTDQAPVLVHDDNDRPSGIPE 78

QY 207 RFGSGNSGNTATLTISGTQAMDEADYYCQAMDSTA--VFGTGKLTVL 253  
Db 79 RFGSGNSGNTATLTISRVEPGDEADYFCQVWDNSGGQLMMFGGKLTVL 128

RESULT 14

ID Q96169 PRELIMINARY; PRT; 233 AA.  
AC Q96169;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell;  
RA Strausberg R;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC007782; AAH07782.1; -  
DR PIR; S12440; S12440.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004812; F:RNA ligase activity; IEA.  
DR GO; GO:0006418; P:amino acid activation; IEA.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR InterPro; IPR001412; tRNA-synt\_1.  
DR Pfam; PF00047; IG\_2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00178; AA\_TRNA\_LIGASE\_1; 1.  
DR PROSITE; PS50835; IG\_LIKE\_2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 233 AA; 24802 MW; C694F8397B27650B CRC64;

Query Match  
Best Local Similarity 26.1%; Score 353; DB 4; Length 233;  
Matches 68; Conservative 15; Mismatches 27; Indels 2; Gaps 1;

QY 144 GGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYACWYQOKPGRSPVLVIYGDNKRPSG 203  
Db 16 GSGTSYVLTQPPASVSAPGQTARITCGSNLGSKSVNMYQLRPGQAPILVYENKERPAAG 75

QY 204 IPERFSGNSGNTATLTISGTQAMDEADYYCQAMDSTA--VFGTGKLTVL 253  
Db 76 IPERLSALTSEETATLTISSVAGDEADYFCQVWDTSQYVFGTGTQVTVL 127

RESULT 15

ID Q72374 PRELIMINARY; PRT; 492 AA.  
AC Q72374;  
DT 01-OCT-2003 (Tremblrel. 25, Created)  
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein DKFZp686C02218 (Fragment).  
GN DKFZp686C02218.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RA Bloeker H., Boeche M., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fob G., Han M., Wiemann S.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX538077; CAD98001.1; -  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match  
Best Local Similarity 25.6%; Score 346; DB 4; Length 492;  
Matches 91; Conservative 26; Mismatches 84; Indels 38; Gaps 6;

QY 1 QVTLKESGPTLVKPTQTLTLCTLSGFSLSGVSVMIRQPPGKALEWLASINWDDKC 60  
Db 32 QVLQESGPGLVKPSFETSLTCTVSGSVSNRNYWGWIRQPPGKLEWISYINENTY 91  
QY 61 YSPSLKSLTITKDTPKNOVVLAMSNMPPADATYSCALDMPHDSGPGSFDASDVWPG 120  
Db 92 YSPSLKSLTITFVDTSKNHSRLTSTVADTAVYCV---RHVGPYGW--FDPWGG 145  
QY 121 TMVTYSSGGGGSGGGSGGGSGGSSYELMQLPSVSVSPGQTASITCSGDNLGDKYAC 180  
Db 146 TLVTYSSASP-----TSPKVFPPLSDSTPQDGNV---VAC 178  
QY 181 WYQOKPGRSPVLVIY---GDNKRPSGIP--ERFSGNSGNTATLTISGTQAMDEADYYC 234  
Db 179 LVQGFPPQEPFLSVTWSESGQNTARNPPPSQDASGDLTYTSSQLTLPATQCPDGKSYTC 237

Search completed: May 13, 2004, 15:06:59  
Job time : 35.0199 secs



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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:48:56 ; Search time 53.1029 Seconds  
(without alignments)  
1372.754 Million cell updates/sec

Title: US-10-072-301-27

Perfect score: 1371  
Sequence: 1 QVQLQESGPGLVKPSSETLSL.....AMDESLNGVVFSGGTKVTVL 258

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1031.5	75.2	252	5	ABP45212	Abp45212 Human Bly
2	1020.5	74.4	246	3	AAY15126	Aay15126 Anti-muri
3	1008.5	73.6	240	4	AAB46058	Aab46058 Human TF
4	1003.5	73.2	244	6	AAE36248	Aae36248 TRAIL rec
5	1002	73.1	241	4	AAB46061	Aab46061 Human TF
6	1002	73.1	255	5	ABP45631	Abp45631 Human Bly
7	1001.5	73.0	244	4	AAB46060	Aab46060 Human TF
8	997.5	72.8	244	2	AAY21883	Aay21883 Amino aci
9	994.5	72.5	252	5	ABP45983	Abp45983 Human Bly
10	987	72.0	251	5	ABP45499	Abp45499 Human Bly
11	987	72.0	255	5	ABP45586	Abp45586 Human Bly
12	985.5	71.9	250	6	AAE36254	Aae36254 TRAIL rec
13	984	71.8	239	4	AAB46059	Aab46059 Human TF
14	982	71.6	251	5	ABP45535	Abp45535 Human Bly
15	966	70.5	247	5	ABP45970	Abp45970 Human Bly
16	963	70.2	243	4	AAB46056	Aab46056 Human TF
17	947	69.1	242	4	AAB46057	Aab46057 Human TF
18	945	68.9	247	5	ABP45982	Abp45982 Human Bly
19	939.5	68.5	254	5	ABP45648	Abp45648 Human Bly
20	935	68.2	249	5	ABP45951	Abp45951 Human Bly
21	929	67.8	251	6	ABJ19829	Abj19829 Human VEG
22	927	67.6	247	5	ABP45987	Abp45987 Human Bly
23	925.5	67.5	256	5	ABP45596	Abp45596 Human Bly
24	921	67.2	251	5	ABP45527	Abp45527 Human Bly
25	915.5	66.8	244	2	AAY06718	Aay06718 Antibody

26	915.5	66.8	258	5	ABP46072	Abp46072 Human Bly
27	915.5	66.8	266	5	ABG97835	Abg97835 Single ch
28	915.5	66.8	266	5	ABG35336	Abg35336 Thrombopo
29	905	66.0	251	5	ABP44979	Abp44979 Human Bly
30	898	65.5	245	5	ABP45853	Abp45853 Human Bly
31	896	65.4	253	5	ABP45608	Abp45608 Human Bly
32	890.5	65.0	254	5	ABP45947	Abp45947 Human Bly
33	888.5	64.8	254	5	ABP45567	Abp45567 Human Bly
34	886	64.6	247	5	ABP45182	Abp45182 Human Bly
35	883	64.4	247	5	ABP45755	Abp45755 Human Bly
36	881.5	64.3	256	5	ABP45734	Abp45734 Human Bly
37	881	64.3	251	5	ABP45531	Abp45531 Human Bly
38	880.5	64.2	252	5	ABP45318	Abp45318 Human Bly
39	879.5	64.2	250	5	ABP45402	Abp45402 Human Bly
40	877	64.0	253	6	ABJ19830	Abj19830 Human VEG
41	876.5	63.9	248	5	ABP45879	Abp45879 Human Bly
42	874	63.7	253	5	ABP45328	Abp45328 Human Bly
43	874	63.7	253	5	ABP44943	Abp44943 Human Bly
44	872	63.6	255	5	ABP44830	Abp44830 Human Bly
45	871	63.5	247	5	ABP45389	Abp45389 Human Bly

ALIGNMENTS

RESULT 1						
ID	ABP45212	standard; protein; 252 AA.				
XX	AC	ABP45212;				
DT	19-AUG-2002	(first entry)				
XX	DE	Human Blys binding scFv SEQ ID 1223.				
XX	KW	Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;				
KW	tumour necrosis factor; B cell proliferation; B cell differentiation;					
KW	immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;					
KW	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;					
KW	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;					
XX	common variable immunodeficiency; acquired immunodeficiency syndrome.					
OS	Homo sapiens.					
XX	PN	WO200202641-A1.				
XX	PD	10-JAN-2002.				
XX	PF	15-JUN-2001; 2001WO-US019110.				
XX	PR	16-JUN-2000; 2000US-0212210P.				
PR	17-OCT-2000; 2000US-0240816P.					
PR	16-MAR-2001; 2001US-0276248P.					
PR	21-MAR-2001; 2001US-0277379P.					
PR	25-MAY-2001; 2001US-0293499P.					
XX	PA	(HUMA-) HUMAN GENOME SCI INC.				
PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.					
XX	PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;				
XX	WPI; 2002-114799/15.					
PT	Antibodies against B lymphocyte Stimulating polypeptides, useful for the					
PT	diagnosis and treatment of cancers and immune disorders.					
XX	PS	Claim 1; Page 1861-1862; 3148pp; English.				
XX	This invention describes novel antibodies that immunospecifically bind to					
CC	B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the					
CC	tumour necrosis factor (TNF) super family and induces B cell					
CC	proliferation and differentiation. The antibodies of the invention have					
CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,					

CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 252 AA;

Query Match 75.2%; Score 1031.5; DB 5; Length 252;  
Best Local Similarity 78.1%; Pred. No. 1.1e-56;  
Matches 203; Conservative 15; Mismatches 31; Indels 11; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIH--DYMSWIRQPPGEGLEWIGFIFFDGSIN 58  
Db 1 QVQLQESGPGVVKPSSETLSLTCTVSGGFISSRTSYMGWIRQPPGKLEWIGNIYTGKTY 60  
QY 59 YNPISLNGRVITISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVW 118  
Db 61 YSPSLKSRVTISADTSKQLSLKLSVTAADTAVYCARAGYDLLTGYPFYF-----DSW 115  
QY 119 GGGTTVTSSGGGSGGGSGGGSGGGSGGNFMLTOPPSASGTPGQRVISICSGSSSDIG 178  
Db 116 GKGTMTVTSSGGGSGGGSGGGSGGGG-----AQSVLTQPPSASGTPGQRTVIECGSSSNIG 171  
QY 179 SNTVNMWYQQLPGTAPKLLIYSNNQRPSPGVPDRFSGFKSGTSASLVISGLQSEDEADYYCA 238  
Db 172 SNTVNMWYQQLPGTAPKLLIYNNQRPSPGVPDRFSGSKGTSASLSISGLQSEDEADYYCL 231  
QY 239 AWDESLNGVVFSGGTKVTVL 258  
Db 232 TWDDSLNGVPVFGGTKVTVL 251

RESULT 2  
AAY15126  
ID AAY15126 standard; protein; 246 AA.  
AC AAY15126;  
XX  
DT 07-FEB-2000 (first entry)  
XX  
DE Anti-murine CTLA-4 M3 sFv.  
XX  
KW Anti-murine CTLA-4 sFv; M3 sFv; single chain antibody; murine CTLA4;  
KW membrane-associated protein; chimeric construct; extracellular domain;  
KW human CD8; ligand; activated T-cell; co-stimulatory signal; donor B7;  
KW xenograft-specific immunosuppression.  
XX  
OS Mus sp.  
OS Synthetic.  
OS  
XX  
PN WO9957266-A2.  
XX  
PD 11-NOV-1999.  
XX  
PF 30-APR-1999; 99WO-GB001350.  
XX  
PR 30-APR-1998; 98GB-00009280.  
XX  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX  
PI Lechler IR, Dorling A;  
XX  
DR WPI; 2000-038815/03.  
DR N-PSDB; AA228998.

XX  
PT Inhibiting T-cell mediated rejection of xenotransplanted organs.  
XX  
PS Claim 9; Fig 11; 43pp; English.  
XX

CC The present sequence is the anti-murine CTLA-4 sFv (M3 sFv). This is a  
CC membrane-associated protein which binds to CTLA-4. Chimeric constructs  
CC comprising DNA sequences encoding the extracellular domain of murine  
CC CTLA4 and human CD8 were used for the study of anti-CTLA4-sFv protein.  
CC The anti-hCTLA4 sFv functions as a ligand binding to CTLA-4 on activated  
CC T-cells and antagonises the co-stimulatory signal provided by the  
CC interaction between donor B7 and recipient CD28. Cells expressing the  
CC anti-hCTLA4 sFv failed to stimulate T-cell proliferation. This is used in  
CC xenograft-specific immunosuppression  
XX  
SQ Sequence 246 AA;

Query Match 74.4%; Score 1020.5; DB 3; Length 246;  
Best Local Similarity 76.9%; Pred. No. 5.3e-56;  
Matches 200; Conservative 17; Mismatches 22; Indels 21; Gaps 4;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSI--GHDYMSWIRQPPGEGLEWIGFIFFDGSIN 58  
Db 3 QVQLQESGPGLVKPSSETLSLTCTVSGSVSSGSYYMSWIRQPPGKLEWIGIYISGSIN 62  
QY 59 YNPISLNGRVITISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVW 118  
Db 63 YNPISLKSRTVISDTISKNQFLKLSVTAADTAVYFCARMR-----KDKFDYV 110  
QY 119 GGGTTVTSSGGGSGGGSGGGSGGGSGGNFMLTOPPSASGTPGQRVISICSGSSSDIG 178  
Db 111 GGGTLVTVS-----SGGGSGGGSGGGSGGSAQSVLTQPPSASGTPGQRTVIECGSSSNIG 165  
QY 179 SNTVNMWYQQLPGTAPKLLIYSNNQRPSPGVPDRFSGFKSGTSASLVISGLQSEDEADYYCA 238  
Db 166 SNTVNMWYQQLPGTAPKLLIYNNQRPSPGVPDRFSGSKGTSASLSISGLQSEDEADYYCA 225  
QY 239 AWDESLNGVVFSGGTKVTVL 258  
Db 226 AWDDSL--FVFGGTKLTVL 243

RESULT 3  
AAB46058  
ID AAB46058 standard; peptide; 240 AA.  
AC AAB46058;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Human TF anti-1-idiotype antibody fragment Z44.  
XX  
KW MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer;  
KW antidiotytic antibody; cytostatic; virucidal; antibacterial; TF antigen;  
KW antiparasitic; infectious disease.  
XX  
OS Homo sapiens.  
OS  
XX  
PN WO200073430-A2.  
XX  
PD 07-DEC-2000.  
XX  
PF 29-MAY-2000; 2000WO-DE001809.  
XX  
PR 27-MAY-1999; 99DE-01024405.  
PR 09-SEP-1999; 99DE-01043016.  
XX  
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.  
XX  
PI Goletz S, Karsten U;  
XX  
DR WPI; 2001-049937/06.  
DR

PT Vaccines against conformation-dependent or non-peptide antigens, based on  
PT DNA encoding peptide which mimics the antigen, useful e.g. as antitumor  
PT vaccines.  
XX  
PS Disclosure; Page 13; 36pp; German.  
XX  
CC This invention describes a novel vaccine (V1) against conformation-  
CC dependent antigen (CDA) comprising DNA (I) and/or an antibody, or  
CC peptide which immunologically imitates CDA, is new. (I) encodes a region  
CC of an antiidiotypic antibody (Ab2) or another peptide which: (a)  
CC specifically binds to the binding site of an antibody (Ab1) or an antigen  
CC binding molecule; and (b) immunologically mimics the initial antigen. The  
CC epitope is partially or completely conformation-dependent, and has an  
CC immunogenic structure defined by a specific spatial conformation of amino  
CC acids. (I) is used in the form of linear or circular naked DNA and/or  
CC with a viral vector and/or adjuvants. The products of the invention have  
CC cytostatic, virucidal, antibacterial and antiparasitic. The invention  
CC also describes (1) a corresponding vaccine (V2) against antigens which  
CC are not proteins or peptides, as defined above but which have epitopes  
CC which show an immunogenic structure; (2) preparing (V1) and (V2); (3)  
CC human antiidiotypic antibody fragments against the MUC1-conformation  
CC epitope having one of 31 approximately 60 residue amino acids sequences,  
CC all fully defined in the specification; (4) MUC1-conformation epitope  
CC mimics having one of 16 9-17 residue amino acid sequences, all fully in  
CC the specification; (5) antiidiotypic antibody fragments against the TF  
CC antigen having one of 24 approximately 200 residue amino acid sequences,  
CC fully defined in the specification; (6) TF carbohydrate epitope mimetics  
CC having one of 25 7-13 residue amino acid sequences, all fully defined in  
CC the specification; and (7) DNA sequences encoding the fragments and  
CC derivatives defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat  
CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria  
CC and parasites. The vaccines are effective in cases where vaccination has  
CC previously not been possible  
XX  
SQ Sequence 240 AA;  
  
Query Match 73.6%; Score 1008.5; DB 4; Length 240;  
Best Local Similarity 76.4%; Pred. No. 2.9e-55;  
Matches 198; Conservative 15; Mismatches 25; Indels 21; Gaps 3;  
  
QY 1 QVQLQESGPGLVKPSETLSLTCTVSGGSI-GHDYWSMIRQPPGEGLEWIGFIFPDGSTNY 59  
Db 1 QVQLQESGPGLVKPSGTLSTLCAVSGGSISSNMWSWVRQPPGKGLEWIGEITYHSGSTNY 60  
  
QY 60 NPSLNGRYTISLDTSKNQLSLRTSVTAADTAVYFCARLKGAMLSEPPYFSSDGMVWG 119  
Db 61 NPSLKSRYTISVDKSKNQPSLKLSSVTAADTAVYCAR-----DDKGGWG 105  
  
QY 120 QGTTVTVSSGGGSGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRVISCSGSSSDIGS 179  
Db 106 QGTLVTVS-----SGGGSGGGGSGGSGALQSVLTQPPSASGTPGQRVITISCSGSSSNIGS 160  
  
QY 180 NTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCAA 239  
Db 161 NTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGSKSGTSASLAISGLQSEDEADYYCAA 220  
  
QY 240 WDESLNGVVFGGGTKVTVL 258  
Db 221 WDDSLRLSLVFGGKTLTVL 239  
  
RESULT 4  
AAE36248  
ID AAE36248 standard; protein; 244 AA.  
XX  
AC AAE36248;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE TRAIL receptor protein binding scFv protein, T1014A02.  
XX  
KM TRAIL receptor; TR4; cancer; Kaposi's sarcoma; cerebellar degeneration;  
KM hyperproliferative disorder; neurodegenerative disorder; immune disorder;  
KM

KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
KW retinitis pigmentosa; Huntington's disease; Hashimoto's thyroiditis;  
KW rheumatoid arthritis; multiple sclerosis; Sjogren's syndrome; asthma;  
KW biliary cirrhosis; Behcet's disease; Crohn's disease; allergic disorder;  
KW glomerulonephritis; immune deficiency syndrome; myasthenia gravis;  
KW polymyositis; inflammatory disorder; rheumatoid arthritis; septic shock;  
KW infectious disease; acquired immunodeficiency syndrome; viral infection;  
KW AIDS; proliferative disorder; myelodysplastic syndrome; aplastic anaemia;  
KW ischaemic injury; myocardial infarction; reperfusion injury; cachexia;  
KW anorexia; stroke; cardiovascular disorder; peripheral artery disease;  
KW limb ischaemia; arrhythmia; congestive heart failure; neovascularisation;  
KW ocular disorder; wound healing; angiogenesis; transplantation.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Domain 1. .118  
FT /note= "VH domain"  
FT 26. .35  
FT /note= "VH domain complementarity determining region 1  
FT (CDR1)"  
FT 50. .65  
FT /note= "VH domain complementarity determining region 2  
FT (CDR2)"  
FT 98. .105  
FT /note= "VH domain complementarity determining region 3  
FT (CDR3)"  
FT 134. .244  
FT /note= "VL domain"  
FT 156. .168  
FT /note= "VL domain complementarity determining region 1  
FT (CDR1)"  
FT 184. .190  
FT /note= "VL domain complementarity determining region 2  
FT (CDR2)"  
FT 223. .233  
FT /note= "VL domain complementarity determining region 3  
FT (CDR3)"  
PN WO200297033-A2.  
PD 05-DEC-2002.  
XX  
PF 07-MAY-2002; 2002WO-US014268.  
XX  
PR 25-MAY-2001; 2001US-0293473P.  
PR 04-JUN-2001; 2001US-0294981P.  
PR 02-AUG-2001; 2001US-0309176P.  
PR 21-SEP-2001; 2001US-0323807P.  
PR 09-OCT-2001; 2001US-0327364P.  
PR 07-NOV-2001; 2001US-0331044P.  
PR 14-NOV-2001; 2001US-0331310P.  
PR 20-DEC-2001; 2001US-0341237P.  
PR 05-APR-2002; 2002US-0369860P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Salcedo T, Ruben SM, Rosen CA, Albert VR, Dobson CL, Vaughan TJ;  
PI WPI; 2003-140454/13.  
XX DR N-PSDB; AAD54849.  
DR  
XX  
PT Novel antibody useful for treating cancers and other hyperproliferative  
PT disorders, immunospecifically binds to TRAIL receptor and comprises  
PT variable heavy or light chain complementarity determining regions.  
XX  
XX  
PS Claim 1; Page 285-286; 301pp; English.  
XX  
CC The present invention relates to novel antibodies that immunospecifically  
CC bind to TRAIL receptor (TR4). Sequences of the invention are useful for  
CC treating, preventing or ameliorating cancer (e.g. colon, breast, uterine,  
CC pancreatic, lung, gastrointestinal or central nervous system cancer e.g.  
CC medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in



CC human. They are useful for detecting expression of TR4 polypeptide and  
CC detecting, diagnosing, prognosing or monitoring cancers and other hyper-  
CC proliferative disorders. Antibodies of the invention are useful for  
CC treating, preventing or ameliorating neurodegenerative disorders (e.g.  
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,  
CC retinitis pigmentosa, cerebellar degeneration and Huntington's disease),  
CC immune disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis,  
CC Sjogren's syndrome, biliary cirrhosis, Behcet's disease, Crohn's disease,  
CC polymyositis, immune-related glomerulonephritis, myasthenia gravis,  
CC Hashimoto's thyroiditis and immune deficiency syndrome), inflammatory  
CC disorders (e.g. asthma, allergic disorders and rheumatoid arthritis),  
CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS),  
CC herpes viral infections and other viral infections) and proliferative  
CC disorders. They are also useful for treating myelodysplastic syndromes  
CC (e.g. aplastic anaemia), ischaemic injury (such as that caused by stroke,  
CC myocardial infarction and reperfusion injury), septic shock, cachexia,  
CC anorexia and toxin-induced liver diseases (such as alcohol). They are  
CC also useful for treating cardiovascular disorders including peripheral  
CC artery diseases such as limb ischaemia, arrhythmia, congestive heart  
CC failure and cardiovascular tuberculosis, diseases or disorders associated  
CC with neovascularisation and ocular disorders, for wound healing, for  
CC promoting angiogenesis and as adjuvants to enhance immune responsiveness  
CC to specific antigen e.g. viral antigen. They are also useful in the  
CC preparation or recovery from surgery, trauma, radiation therapy and  
CC transplantation. The present sequence is T1014A02 single chain Fv (scFv)  
CC antibody that immunospecifically bind to TR4 protein. This sequence is  
CC used in the invention

CC SQ Sequence 244 AA;

Query Match 73.2%; Score 1003.5; DB 6; Length 244;  
Best Local Similarity 75.2%; Pred. No. 6e-55;  
Matches 194; Conservative 18; Mismatches 31; Indels 15; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGISGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGISDYMSWIRQSPGKLEWIGSIDYAGSTNYN 60  
QY 61 PSLNGRVTISLDTSKNQLSLRLTSVTADTAVFYFCARLKGAWLLSEPPYFSSDGMVWGQ 120  
DB 61 PSLSRVTMTIDSKSKQFPKIDSVTAADTAMYYCARQLGRI-----SDYWGQ 108  
QY 121 GTVTVSSGGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGGRVVISCSGSSSDIGSN 180  
DB 109 GTLVTVSSGGGSGGGSGGGSGGGSG--ALSYVLTPPSASGTPGGRVTISCSGSSSNIGCN 165  
QY 181 TVNMWYQQLPGTAPKLLIYSNNQRPSPGVDRPFGSKGTSASLVISGLQSEDEADYYCAAW 240  
DB 166 TVNMWYQQLPATAPKLLIYSNNQRPSPGVDRPFGSGSKGTSASLVISGLQSEDEADYYCATW 225  
QY 241 DESLNGVVFPGGGTKVTVL 258  
DB 226 DDSRGGWVFPGGGTKLTVL 243

RESULT 5  
AAB46061  
ID AAB46061 standard; peptide; 241 AA.  
XX  
AC AAB46061;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Human TF anti-idiotype antibody fragment Z9.  
XX  
KW MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer;  
KW anti-idiotypic antibody; cytosstatic; virucidal; antibacterial; TF antigen;  
XX anti-parasitic; infectious disease.  
OS Homo sapiens.  
XX  
PN WO200073430-A2.  
XX

PD 07-DEC-2000.  
XX  
XX 29-MAY-2000; 2000WO-DE001809.  
PF  
XX  
PR 27-MAY-1999; 99DE-01024405.  
PR 09-SEP-1999; 99DE-01043016.  
XX  
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.  
XX  
PI Goletz S, Karsten U;  
XX  
DR WPI; 2001-049937/06.  
XX

Vaccines against conformation-dependent or non-peptide antigens, based on  
PT DNA encoding peptide which mimics the antigen, useful e.g. as antitumor  
PT vaccines.  
XX  
PS Disclosure; Page 14; 36pp; German.

This invention describes a novel vaccine (V1) against conformation-  
CC dependent antigens (CDA) comprising DNA (I) and/or an antibody, or  
CC peptide which immunologically imitates CDA, is new. (I) encodes a region  
CC of an anti-idiotypic antibody (Ab2) or another peptide which: (a)  
CC specifically binds to the binding site of an antibody (Ab1) or an antigen  
CC binding molecule; and (b) immunologically mimics the initial antigen. The  
CC epitope is partially or completely conformation-dependent, and has an  
CC immunogenic structure defined by a specific spatial conformation of amino  
CC acids. (I) is used in the form of linear or circular naked DNA and/or  
CC with a viral vector and/or adjuvants. The products of the invention have  
CC cytostatic, virucidal, antibacterial and antiparasitic. The invention  
CC also describes (1) a corresponding vaccine (V2) against antigens which  
CC are not proteins or peptides, as defined above but which have epitopes  
CC which show an immunogenic structure; (2) preparing (V1) and (V2); (3)  
CC human anti-idiotypic antibody fragments against the MUC1-conformation  
CC epitope having one of 31 approximately 60 residue amino acids sequences,  
CC all fully defined in the specification; (4) MUC1-conformation epitope  
CC mimics having one of 16 9-17 residue amino acid sequences, all fully in  
CC the specification; (5) anti-idiotypic antibody fragments against the TF  
CC antigen having one of 24 approximately 200 residue amino acid sequences,  
CC fully defined in the specification; (6) TF carbohydrate epitope mimics  
CC having one of 25 7-13 residue amino acid sequences, all fully defined in  
CC the specification; and (7) DNA sequences encoding the fragments and  
CC derivatives defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat  
CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria  
CC and parasites. The vaccines are effective in cases where vaccination has  
CC previously not been possible

CC SQ Sequence 241 AA;

Query Match 73.1%; Score 1002; DB 4; Length 241;  
Best Local Similarity 77.5%; Pred. No. 7.3e-55;  
Matches 200; Conservative 13; Mismatches 27; Indels 18; Gaps 4;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGISGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
DB 1 QVQLQESGAGLLKPSSETLSLTCAVYGGSFSGYMSWIRQPPGKLEWIGIHNHSGSTNYN 60  
QY 61 PSLNGRVTISLDTSKNQLSLRLTSVTADTAVFYFCARLKGAWLLSEPPYFSSDGMVWGQ 120  
DB 61 PSLSRVTISVDTSKNQFSLKLSVTADTAVFYCAR-KG--LNFGP-----WGQ 107  
QY 121 GTVTVSSGGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGGRVVISCSGSSSDIGSN 180  
DB 108 GTLVTVS-----SGGGSGGGSGGSGSALQSVLTQPPSASGTPGGRVTISCSGSSSNVGSN 162  
QY 181 TVNMWYQQLPGTAPKLLIYSNNQRPSPGVDRPFGSKGTSASLVISGLQSEDEADYYCAAW 240  
DB 163 TVNMWYQQLPGTAPKLLIYSNNQRPSPGVDRPFGSGSKGTSASLVISGLQSEDEADYYCAAW 222  
QY 241 DESLNGVVFPGGGTKVTVL 258  
DB 223 DDSLRSYVFPGGGTKLTVL 240



```

RESULT 6
ABP45631
ID ABP45631 standard; protein; 255 AA.
XX
XX AC ABP45631;
XX
XX DT 19-AUG-2002 (first entry)
XX
XX DE Human BlyS binding scFv SEQ ID 1642.
XX
XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
OS Homo sapiens.
XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX 17-OCT-2000; 2000US-0240816P.
XX 16-MAR-2001; 2001US-0276248P.
XX 21-MAR-2001; 2001US-0277379P.
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
XX Claim 1; Page 2362-2363; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of BlyS. The antibodies bind to BlyS
XX and so may be used to detect and quantitate the presence of BlyS in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of BlyS. They may also be
XX administered to treat diseases associated with aberrant BlyS expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
XX the antibodies and fragments of the antibodies described in the method of
XX the invention
XX
XX Sequence 255 AA;
XX
XX Query Match 73.1%; Score 1002; DB 5; Length 255;
XX Best Local Similarity 75.7%; Pred. No. 7.7e-55;
XX Matches 196; Conservative 23; Mismatches 34; Indels 6; Gaps 2
XX
XX 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGISGHDYMSWIRQPPGEGLEWIGTIFFDGSTNNY 60
XX |||||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 1 QVQLQGWAGLLKPSSETLSLTCAVYGGSFSGYYMSWIRQSPGKLEWIGETINHGGSNNY 60
XX
XX PSINGRVITISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAW-LLSEPPYSSSDGMDVWG 119

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Db	61	PSLSKSRVTISVDASKNQFSLKLSSTVTAADTA VVYCCARERSYDILTGVSPRSKYGMDVWG	120
QY	120	QGTIVTVSSGGGGSGGGGGSGGGGSGNFMLT	179
Db	121	RGTLVTVS-----SGGGSGGGGGSGGGGSQSVL	175
QY	180	NTVNWYQQLPGTAPKLLIYSNNQRPSPGV	239
Db	176	NTVNWYQRLPGAAPQLLIYNNDQRPSPGIP	235
QY	240	WDESLNGVFEFGGTKVTVL	258
Db	236	WDSLNGRVFEGGTKLTVL	254
RESULT 7			
AAB46060	ID	AAB46060 standard; peptide; 244 AA.	
XX	AC	AAB46060;	
XX	DT	23-MAR-2001 (first entry)	
XX	DE	Human TF anti-idiotypic antibody fragment ZA14.	
XX	KW	MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer;	
XX	KW	antidiabetic antibody; cytostatic; virucidal; antibacterial; TF antigen;	
XX	OS	antiparasitic; infectious disease.	
XX	PN	Homo sapiens.	
XX	PD	WO200073430-A2.	
XX	PF	07-DEC-2000.	
XX	PR	29-MAY-2000; 2000WO-DE001809.	
XX	PR	27-MAY-1999; 99DE-01024405.	
XX	PR	09-SEP-1999; 99DE-01043016.	
XX	PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.	
XX	PI	Goletz S, Karsten U;	
XX	DR	WPI; 2001-049937/06.	
XX	PT	Vaccines against conformation-dependent or non-peptide antigens, based on	
XX	PT	DNA encoding peptide which mimics the antigen, useful e.g. as antitumor	
XX	PT	vaccines.	
XX	PS	Disclosure; Page 14; 36pp; German.	
XX	XX	This invention describes a novel vaccine (V1) against conformation-	
CC	CC	dependent antigens (CDA) comprising DNA (I) and/or an antibody, or	
CC	CC	peptide which immunologically imitates CDA, is new. (I) encodes a region	
CC	CC	of an antiidiotypic antibody (Ab2) or another peptide which: (a)	
CC	CC	specifically binds to the binding site of an antibody (Ab1) or an antigen	
CC	CC	binding molecule; and (b) immunologically mimics the initial antigen. The	
CC	CC	epitope is partially or completely conformation-dependent, and has an	
CC	CC	immunogenic structure defined by a specific spatial conformation of amino	
CC	CC	acids. (I) is used in the form of linear or circular naked DNA and/or	
CC	CC	with a viral vector and/or adjuvants. The products of the invention have	
CC	CC	cytostatic, virucidal, antibacterial and antiparasitic. The invention	
CC	CC	also describes (1) a corresponding vaccine (V2) against antigens which	
CC	CC	are not proteins or peptides, as defined above but which have epitopes	
CC	CC	which show an immunogenic structure; (2) preparing (V1) and (V2); (3)	
CC	CC	human antiidiotypic antibody fragments against the MUC1-conformation	
CC	CC	epitope having one of 31 approximately 60 residue amino acids sequences,	
CC	CC	all fully defined in the specification; (4) MUC1-conformation epitope	
CC	CC	mimics having one of 16 9-17 residue amino acid sequences, all fully in	
CC	CC	the specification; (5) antiidiotypic antibody fragments against the TF	
CC	CC	antigen having one of 24 approximately 200 residue amino acid sequences,	

CC fully defined in the specification; (6) TF carbohydrate epitope mimetics  
CC having one of 25 7-13 residue amino acid sequences, all fully defined in  
CC the specification; and (7) DNA sequences encoding the fragments and  
CC derivatives defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat  
CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria  
CC and parasites. The vaccines are effective in cases where vaccination has  
CC previously not been possible  
XX

Sequence 244 AA;

Query Match 73.0%; Score 1001.5; DB 4; Length 244;  
Best Local Similarity 76.1%; Pred. No. 7.9e-55;  
Matches 197; Conservative 17; Mismatches 28; Indels 17; Gaps 4;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSI-GHDYWSWIRQPPGEGLEWIGFIFFDGSTNY 59  
Db 1 QVQLQESGPGLVKPSGTSILTCVAVSGSISSSNWSWVRQPPGKGLHWIGEIVHSGSTNY 60  
QY 60 NPSINGRVTISLDTSKNQSLRLTSVTADTAIVYFCARLKGAWLSEPPYFSSDGMVWG 119  
Db 61 NPSLKSRTVISVXKSKNQFSLKLSVTAXDTAVYYCAR-----PSHNA--GTHTWG 109  
QY 120 QGTTVTVSSGGGSGGGGSGGGSGGGSNFMLTQPPSASGTPGQRVVISCSGSSSDIGS 179  
Db 110 QGTLVTVS-----SGGGSGGGGSGGSGSALQSVLTPPPSASGTPGQRTVISCSGSSSNIGS 164  
QY 180 NTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCAA 239  
Db 165 NTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGSKSGTSASLAIISGLQSEDEADYYCAA 224  
QY 240 WDESLNGVVFQGGTKVTVL 258  
Db 225 WDLSLRALVFGGTKLTVL 243

RESULT 8  
AAY21883  
ID AAY21883 standard; protein; 244 AA.  
AC AAY21883;  
XX  
DT 24-SEP-1999 (first entry)  
DE Amino acid sequence of antibody BIOA8.  
XX  
KW Prostate-specific antigen; PSA; anti-chymotrypsin; ACT; antibody;  
KW diagnostic assay; PSA-ACT; prostate cancer; tumour; immunotherapy; BIOA8.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 201 /label= unknown  
FT /note= "encoded by TST"  
XX  
PN EP934953-A2.  
XX  
PD 11-AUG-1999.  
XX  
PF 01-DEC-1998; 98BP-00122546.  
XX  
PR 03-DEC-1997; 97US-0067428P.  
XX  
PA (BOEF ) BOEHRINGER MANNHEIM CORP.  
XX  
PI Winter GP, Mahoney W, Sawyer JR;  
XX  
DR WPI; 1999-432068/37.  
DR N-PSDB; AAX86940.  
XX  
PT New anti-complex antibody useful for diagnosing prostate cancer.  
XX  
PS Claim 28; Page 25-27; 42pp; English.

XX The invention relates to an antibody that binds a complex between  
CC prostate-specific antigen (PSA) and anti-chymotrypsin (ACT), and has an  
CC affinity for the complex which is at least 10 fold higher than the  
CC affinity for either PSA or ACT alone. The antibody is used in diagnostic  
CC assays to detect PSA-ACT in serum samples from patients. The levels of  
CC PSA-ACT complex increase in patients suffering from prostate cancer  
CC compared to the levels in patients with benign or no growths in the  
CC prostate. Therefore detection of PSA in complex with ACT is useful for  
CC the early detection of prostate tumours, by distinguishing between benign  
CC and malignant conditions of the prostate as well as for the management of  
CC patients with prostate cancer, such as the disclosure of metastasis and  
CC the monitoring of the PSA levels after treatment. The antibodies may also  
CC be used in immunotherapy, affinity chromatography and isolation or  
CC purification of PSA-ACT. Unlike prior art antibodies which bind to PSA-  
CC ACT complexes but may also bind PSA or ACT alone, the present antibody is  
CC specific for PSA-ACT alone. Diagnostic assays using the antibodies are  
CC more accurate in diagnosing prostate cancer as they only detect the  
CC intact complex of PSA-ACT. Sequences AAY21880-884 represent specific  
CC examples of antibodies directed against PSA-ACT. The present sequence  
CC represents the amino acid sequence of antibody BIOA8  
XX

Sequence 244 AA;

Query Match 72.8%; Score 997.5; DB 2; Length 244;  
Best Local Similarity 76.0%; Pred. No. 1.4e-54;  
Matches 196; Conservative 14; Mismatches 31; Indels 17; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIGHDYWSWIRQPPGEGLEWIGFIFFDGSTNY 60  
Db 3 QVQLQESGAGLKPSETLSLTCAVVGSGFSGYWSWIRQPPGKGLHWIGEIVHSGSTNYN 62  
QY 61 PSINGRVTISLDTSKNQSLRLTSVTADTAIVYFCARLKGAWLSEPPYFSSDGMVWGQ 120  
Db 63 PSLKSRTVISVDTSKNQFSLKLSVTADTAIVYYCARM--WSLK-----FDYWGQ 110  
QY 121 GTTVTVSSGGGSGGGGSGGGSGGGSNFMLTQPPSASGTPGQRVVISCSGSSSDIGSN 180  
Db 111 GTLVTVS-----SGGGSGGGGSGGSGSALQSVLTPPPSASGTPGQRTVISCSGSSSNIGSN 165  
QY 181 TVNMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCAAW 240  
Db 166 YVYMWYQQLPGTAPKLLIYRNQRPSPGVDRFSGSKSGTSASLAIISGLRSEDEADYYCAAW 225  
QY 241 WDESLNGVVFQGGTKVTVL 258  
Db 226 DDSLRLGIVFGGTKLTVL 243

RESULT 9  
ABP45983  
ID ABP45983 standard; protein; 252 AA.  
XX  
AC ABP45983;  
XX  
DT 19-AUG-2002 (first entry)  
DE Human Blys binding scFv SEQ ID 1994.  
XX  
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US019110.

XX 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX  
DR WPI; 2002-114799/15.  
XX  
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.  
XX  
PS Claim 1; Page 2779-2780; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 252 AA;  
  
Query Match 72.5%; Score 994.5; DB 5; Length 252;  
Best Local Similarity 74.6%; Pred. No. 2.2e-54;  
Matches 194; Conservative 21; Mismatches 34; Indels 11; Gaps 3;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSI--GHDYMSWIRQPPGEGLEWIGFIFPDGSTN 58  
DB 1 QLQLQESGPGLVKPSQTLSTLTCTVSGSGSISSGDYMSWIRQHPGEGLEWIGYIYHSGSTY 60  
  
QY 59 YNPSLNGRVTISLDTSKNQLSRLTSVTAADTAVYFCARLKGAWLSEBPYFSSDGMVW 118  
DB 61 YNPSLKSRVMSVDTSKNQYSLKLSVTADTAVYYCARLR-----PDADYGDYGFDPYW 114  
  
QY 119 GGGTTVTVSSGGGGSGGGGGSGGGGSNFMLTQPPSASGTPGQRVISICSGSSSDIG 178  
DB 115 GGGTMVTVSSGGGGSGGGGGSGGGGS--ALSYVLTOPPSASATPGQRTVITISCSGSRNIG 171  
  
QY 179 SNTVNMVYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCA 238  
DB 172 SNTYVMYQQPPGAAPKLLIYRSYQRPSPGVDRFSGSKSGTSASLAISGLRSEDEADYYCA 231  
  
QY 239 AWDESLNGVVFEGGKTQTVL 258  
DB 232 TWDDRLRGLVFGGKTQTVL 251  
  
RESULT 10  
ABP45499 standard; protein; 251 AA.  
XX  
AC ABP45499;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scFv SEQ ID 1510.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US019110.  
XX  
PR 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX  
DR WPI; 2002-114799/15.  
XX  
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.  
XX  
PS Claim 1; Page 2205-2206; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 251 AA;  
  
Query Match 72.0%; Score 987; DB 5; Length 251;  
Best Local Similarity 75.8%; Pred. No. 6.5e-54;  
Matches 197; Conservative 20; Mismatches 31; Indels 12; Gaps 4;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGIGH--DYMSWIRQPPGEGLEWIGFIFPDGSTN 58  
DB 1 QLQLQESGPGVVKPSSETLSLTCTVSGSGFISRTSYMGWIRQPPGEGLEWIGNITYTGKTY 60  
  
QY 59 YNPSLNGRVTISLDTSKNQLSRLTSVTAADTAVYFCARLKGAWLSEBPYFSSDGMVW 118  
DB 61 YSPSLKSRVTISADTSKNQLSRLKLSVTADTAVYYCARAGYDILLTGYPFYF-----DSW 115  
  
QY 119 GGGTTVTVSSGGGGSGGGGGSGGGGSNFMLTQPPSASGTPGQRVISICSGSSSDIG 178  
DB 116 GRGTLVTVSSGGGGSGGGGGSGGGGS---AAVLTQPPSASGTPGQRTVITISCSGSSNIG 171  
  
QY 179 SNTVNMVYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCA 238  
DB 172 STTVAMVYQVPGTAPKLLIYSNDRRPSGVDRFSGSKSGTSASLAISGLQSEDEADYYCA 231



Qy	239	AMDESLNGVFGGCTKVTTL	258
		:  : :       :	
Db	232	SMWDSPH-VVFGGCTKLTVL	250

RESULT	11
ABP45586	
ID	ABP45586
XX	standard; protein; 255 AA.

Human Blys binding scFv SEQ ID 1597.

Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

16-JUN-2000; 2000US-02112210P  
17-OCT-2000; 2000US-0240816P  
16-MAR-2001; 2001US-0276248P  
21-MAR-2001; 2001US-0277379P  
25-MAY-2001; 2001US-0293499P

(HUMA-) HUMAN GENOME SCI INC.  
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

WPI; 2002-114799/15.

antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.

Claim 1; Page 2308-2309; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to  
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytototoxic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, and  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency Syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention

**SQ Sequence 255 AA;**

Query Match	72.0%;	Score 987;	DB 5;	Length 255;
Best Local Similarity	73.4%;	Pred. No. 6.6e-54;		
Matches 196;	Conservative 20;	Mismatches 29;	Indels 22;	Gaps 4;

```

QY      1  QVQLQESGGPGLVKPKSETLTSLTCTVSSGSI--GHDIYMSWIRQPPGEGLEWIGFIFFDGSTN  58
Db      1  QVQLQESGPGLVKSSGTLSTLTCSVSGASILESDYFWTWIRQPPGKGLEWIGEINHRGDIN  60
QY      59  YNPSSLNGRVTISLDTSSKNQLSLRLTSVTAADTAVYFCAR-----LKGAWLSEPPYFS  111
Db      61  YNPSSLKSRVTILVDTSKNQSLSLKLNSTVTAADTAVYYCARHVRDYDILTG-----YYR  112
QY      112  SDGMDVMVGQGTIVTVSSGGGGSGGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRVASISCS  171
Db      113  GHYFDYWGKGLTVTS-----SGGGSGGGGGSGGGSGSGSVLTQPPSASGTPGQRTVTSICS  167
QY      172  GSSSDIGSNITVMWYQQLPGTAPKLLITYNNQRPSPGVDFRFSGFKSGTSASLVISGLQSED  231
Db      168  GSSSNIGSNITVMWYQRLPGAAPQLLIYNNQRPSPGIPDRFSGSKSGTSGLVISGLQSED  227
QY      232  EADYYCAAMDESLNGVVFGGGRTKTVL  258
Db      228  EADYYCASWDDSLNGRVFGGGRTKTVL  254

```

RESULT 12  
AAE36254

ID	AAE36254	standard; protein; 250 AA.
XX		

AC AAEE36254;

DT 26-JUN-2003 (first entry)

DE TRAIL receptor protein binding scFv protein, T1015A02.  
XX

KM hyperproliferative disorder; cancer; Kaposi's sarcoma; cerebellar degeneration;  
KM Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
KM retinitis pigmentosa; Huntington's disease; Hashimoto's thyroiditis;  
KM rheumatoid arthritis; multiple sclerosis; Sjogren's syndrome; asthma;  
KM biliary cirrhosis; Behcet's disease; Crohn's disease; allergic disorder;  
KM glomerulonephritis; immune deficiency syndrome; myasthenia gravis;  
KM polymyositis; inflammatory disorder; rheumatoid arthritis; septic shock;  
KM infectious disease; acquired immunodeficiency syndrome; viral infection;  
KM AIDS; proliferative disorder; myelodysplastic syndrome; aplastic anaemia;  
KM ischaemic injury; myocardial infarction; reperfusion injury; cachexia;  
KM anorexia; stroke; cardiovascular disorder; peripheral artery disease;  
KM limb ischaemia; arrhythmia; congestive heart failure; neovascularisation;  
KM ocular disorder; wound healing; angiogenesis; transplantation.

OS Unidentified.

Key	Location/Qualifiers
FH	
FT	1. .123

FT		
Misc-difference	23	

```

ET      /note= "Encoded by RGT"
ET      26 37
Region

```

```

/note= "VH domain complementarity determining region 1
(CDR1)"

```

```

/notes= "VH domain complementarity determines

```

Region	100. .112
100. .112	

```
(CDR3) =
140 CCG
Dcmajin
```

Region	/note= "VL domain"
162	174

```

/ note= "VL domain complementarity determining region 1
(CDR1) "

```

```
/note= "VL domain complementarity determining region 3
```



FT (CDR3) "  
XX WO200297033-A2.  
PN  
XX 05-DEC-2002.  
PD  
XX 07-MAY-2002; 2002WO-US014268.  
PF  
XX 25-MAY-2001; 2001US-0293473P.  
PR 04-JUN-2001; 2001US-0294981P.  
PR 02-AUG-2001; 2001US-0309176P.  
PR 21-SEP-2001; 2001US-0323807P.  
PR 09-OCT-2001; 2001US-0327364P.  
PR 07-NOV-2001; 2001US-0331044P.  
PR 14-NOV-2001; 2001US-0331310P.  
PR 20-DEC-2001; 2001US-0341237P.  
PR 05-APR-2002; 2002US-0369860P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Salcedo T, Ruben SM, Rosen CA, Albert VR, Dobson CL, Vaughan TJ;  
PI  
XX WPI; 2003-140454/13.  
DR N-PSDB; AAD54855.  
XX  
XX Novel antibody useful for treating cancers and other hyperproliferative  
PT disorders, immunospecifically binds to TRAIL receptor and comprises  
PT variable heavy or light chain complementarity determining regions.  
XX  
XX Claim 1; Page 291-292; 301pp; English.  
XX  
CC The present invention relates to novel antibodies that immunospecifically  
CC bind to TRAIL receptor (TR4). Sequences of the invention are useful for  
CC creating, preventing or ameliorating cancer (e.g. colon, breast, uterine,  
CC pancreatic, lung, gastrointestinal or central nervous system cancer e.g.  
CC medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in  
CC human. They are useful for detecting expression of TR4 polypeptide and  
CC detecting, diagnosing, prognosing or monitoring cancers and other hyper-  
CC proliferative disorders. Antibodies of the invention are useful for  
CC treating, preventing or ameliorating neurodegenerative disorders (e.g.  
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,  
CC retinitis pigmentosa, cerebellar degeneration and Huntington's disease),  
CC immune disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis,  
CC Sjogren's syndrome, biliary cirrhosis, Behcet's disease, Crohn's disease,  
CC polymyositis, immune-related glomerulonephritis, myasthenia gravis,  
CC Hashimoto's thyroiditis and immune deficiency syndrome), inflammatory  
CC disorders (e.g. asthma, allergic disorders and rheumatoid arthritis),  
CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS),  
CC herpes viral infections and other viral infections) and proliferative  
CC disorders. They are also useful for treating myelodysplastic syndromes  
CC (e.g. aplastic anaemia), ischaemic injury (such as that caused by stroke,  
CC myocardial infarction and reperfusion injury), septic shock, cachexia,  
CC anorexia and toxin-induced liver diseases (such as alcohol). They are  
CC also useful for treating cardiovascular disorders including peripheral  
CC artery diseases such as limb ischaemia, arrhythmia, congestive heart  
CC failure and cardiovascular tuberculosis, diseases or disorders associated  
CC with neovascularisation and ocular disorders, for wound healing, for  
CC promoting angiogenesis and as adjuvants to enhance immune responsiveness  
CC to specific antigen e.g. viral antigen. They are also useful in the  
CC preparation or recovery from surgery, trauma, radiation therapy and  
CC transplantation. The present sequence is T1015A02 single chain Fv (scFv)  
CC antibody that immunospecifically bind to TR4 protein. This sequence is  
CC used in the invention  
XX  
SQ Sequence 250 AA;

Query Match 71.9%; Score 985.5; DB 6; Length 250;  
Best Local Similarity 74.2%; Pred. No. 8e-54;  
Matches 193; Conservative 24; Mismatches 30; Indels 13; Gaps 5;  
Qy 1 QVQLQESGPGLVKPSETLSLTCTVSGSGSIGHD--YMSWIRQPPGEGLEWIGFIFPDGSTN 58  
Db 1 QVQLQESGPGLVKPSETLSLTCTVSGSGSIGHD--YMSWIRQPPGEGLEWIGFIFPDGSTN 58

Qy 59 YNPSLNGRVITSLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVW 118  
Db 61 YKPSLRSLRVTSMDTSRNQFSLKLTSTVTAADTALYYCVR---EW--ANGDHWSA--FDLW 113  
Qy 119 GGGTTVTVSSGGGGSGGGGGSGGGGSGNFMLTQPPSASGTPGGRVVISCSGSSSDIG 178  
Db 114 GGGTLVTVSSGGGGSGGGGGSGGGGSG---AQAVLTQPPSASGTPGGRVTVIPCSGSSSNIG 169  
Qy 179 SNTVNWYQQLPGTAPKLLIYSNNQRPSPGVDRFSFGKSGTSASLVISGLQSEDEADYYCA 238  
Db 170 GNTVNWYQQLPGTAPKLLIYGNDRPSGVDPDRFSGSKSGTSASLALITGLQSEDEADYYCA 229  
Qy 239 AWDESLNGVVEGGGKTQTVL 258  
Db 230 AWDDSLIGYVFGTGTQTLTVL 249

RESULT 13  
AAB46059  
ID AAB46059 standard; peptide; 239 AA.  
XX  
AC AAB46059;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Human TF anti-idiotypic antibody fragment ZA36.  
XX  
KW MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer;  
KW anti-idiotypic antibody; cytostatic; virucidal; antibacterial; TF antigen;  
KW antiparasitic; infectious disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200073430-A2.  
XX  
PD 07-DEC-2000.  
XX  
PF 29-MAY-2000; 2000WO-DE001809.  
XX  
PR 27-MAY-1999; 99DE-01024405.  
PR 09-SEP-1999; 99DE-01043016.  
XX  
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.  
XX  
PI Goletz S, Karsten U;  
XX  
DR WPI; 2001-049937/06.  
XX  
PT Vaccines against conformation-dependent or non-peptide antigens, based on  
PT DNA encoding peptide which mimics the antigen, useful e.g. as antitumor  
PT vaccines.  
XX  
PS Disclosure; Page 14; 36pp; German.  
XX  
CC This invention describes a novel vaccine (V1) against conformation-  
CC dependent antigens (CDA) comprising DNA (I) and/or an antibody, or  
CC peptide which immunologically imitates CDA, is new. (I) encodes a region  
CC of an anti-idiotypic antibody (Ab2) or another peptide which: (a)  
CC specifically binds to the binding site of an antibody (Ab1) or an antigen  
CC binding molecule; and (b) immunologically mimics the initial antigen. The  
CC epitope is partially or completely conformation-dependent, and has an  
CC immunogenic structure defined by a specific spatial conformation of amino  
CC acids. (I) is used in the form of linear or circular naked DNA and/or  
CC with a viral vector and/or adjuvants. The products of the invention have  
CC cytostatic, virucidal, antibacterial and antiparasitic. The invention  
CC also describes (1) a corresponding vaccine (V2) against antigens which  
CC are not proteins or peptides, as defined above but which have epitopes  
CC which show an immunogenic structure; (2) preparing (V1) and (V2); (3)  
CC human anti-idiotypic antibody fragments against the MUC1-conformation  
CC epitope having one of 31 approximately 60 residue amino acid sequences,  
CC all fully defined in the specification; (4) MUC1-conformation epitope  
CC mimics having one of 16 9-17 residue amino acid sequences, all fully in

CC the specification; (5) antidiotypic antibody fragments against the TF  
CC antigen having one of 24 approximately 200 residue amino acid sequences,  
CC fully defined in the specification; (6) TF carbohydrate epitope mimetics,  
CC having one of 25 7-13 residue amino acid sequences, all fully defined in  
CC the specification; and (7) DNA sequences encoding the fragments and  
CC derivatives defined in (3, 4, 5, or 6). (VI) and (V2) are used to treat  
CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria  
CC and parasites. The vaccines are effective in cases where vaccination has  
CC previously not been possible  
XX  
SQ Sequence 239 AA;

Query Match 71.8%; Score 984; DB 4; Length 239;  
Best Local Similarity 74.5%; Pred. No. 9.5e-54;  
Matches 193; Conservative 17; Mismatches 27; Indels 22; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSI-GHDYMSWIRQPPGEGLEWIGFIFPDGSTNY 59  
DB 1 QVQLQESGPGLVKPSGTLSTLCAVSGSISSNMWSWVRQPPGKLEWIGEIVHSGSTNY 60  
QY 60 NPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLLSEPPYFSSDGMVWG 119  
DB 61 NPSLKSRTVTISVDKSKNQFSLKLSVTAADTAVYCAR-----PSSIWG 104  
QY 120 QGTTVTIVSSGGGSGGGSGGGSGGGSNFMLTQPPSASGTPGQRVVISGSGSSSDIGS 179  
DB 105 QGTLVTIVS-----SGGGSGGGSGGSGSALQSVLTQPPSASGTPGQRVTISGSGSSSNIGS 159  
QY 180 NTYVMYQQLPGTAPKLLIYSNNQRPSPGVPDRFSGFKSGTSASLVISGLQSEDEADYCAA 239  
DB 160 NYTYMYQQLPGTAPKLLIYRNNQRPSPGVPDRFSGFKSGTSASLAISGLREDEADYCAA 219  
QY 240 WDESLNGVVFEGGTKVTVL 258  
DB 220 WDSLRLSLVFGGTKLTVL 238

RESULT 14  
ABP45535  
ID ABP45535 standard; protein; 251 AA.  
XX  
AC ABP45535;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scFv SEQ ID 1546.  
XX  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US019110.  
XX  
PR 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-027379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX

DR WPI; 2002-114799/15.

XX Antibodies against B lymphocyte stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.

XX Claim 1; Page 2247-2249; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 251 AA;

Query Match 71.6%; Score 982; DB 5; Length 251;  
Best Local Similarity 74.2%; Pred. No. 1.3e-53;  
Matches 196; Conservative 18; Mismatches 30; Indels 20; Gaps 5;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSI-GHDYMSWIRQPPGEGLEWIGFIFPDGSTNY 59  
DB 1 QVQLQESGPGLVKPSGTLSTLCAVSGDSIRGHWNNWVRQPPGKLEWIGEIVHSGSTNS 60  
QY 60 NPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCAR-----LKGAWLLSEPPYFSSDG 114  
DB 61 NPSLKSRTVTLSADKSKNLFSLSLSVTAADTAVYCCARGDYDVLG-----YLK-- 110  
QY 115 MDVWGGTTVTIVSSGGGSGGGSGGGSGGGSNFMLTQPPSASGTPGQRVVISGSGSS 174  
DB 111 LDYWGKGLVTIVSSGGGSGGGSGGGSGGGS---AQPVLTQPPSASGTPGQRVTISGSGSS 166  
QY 175 SDIGSNTVMYQQLPGTAPKLLIYSNNQRPSPGVPDRFSGFKSGTSASLVISGLQSEDEAD 234  
DB 167 SNIGSRVTVMYQQLPGTAPKLLIYESTNLRLPSGVPDRFSGFKSGTSASLAISGLQSEDEAD 226  
QY 235 YYCAWDESLNGVVFEGGTKVTVL 258  
DB 227 YYCSAWDDSLNGVPVFEGGTKVTVL 250

RESULT 15  
ABP45970  
ID ABP45970 standard; protein; 247 AA.  
XX  
AC ABP45970;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scFv SEQ ID 1981.  
XX  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX

PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US019110.  
XX  
PR 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX  
DR WPI; 2002-114799/15.  
XX  
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
XX diagnosis and treatment of cancers and immune disorders.  
PS Claim 1; Page 2764-2765; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 247 AA;  
  
Query Match 70.5%; Score 966; DB 5; Length 247;  
Best Local Similarity 72.7%; Pred. No. 1.3e-52;  
Matches 189; Conservative 22; Mismatches 33; Indels 16; Gaps 4;  
  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGIG--HDYWSWIRQPPGEGLEWIGFIFPDGSTN 58  
Db 1 QQLQESGPGLVKPLETSLTCTVSGSGVSGRTHYWGWIRLPKGMEWIASLSFDGTPF 60  
  
QY 59 YNPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVW 118  
Db 61 YNPSLKSRYSVSRTSKNQFSLKVTSTVTAADTAVYYCAR-----HDVY--GDLFDYW 110  
  
QY 119 GGGTIVTVSSGGGGSGGGSGGGSGSNFMLTQPPSASGTPGQRVISCSGSSSDIG 178  
Db 111 GGGTIVTVSSGGGGSGGGSGGGSGGS----AQSVLTQPPSASGTPGQRPVISCSSGSGSNIG 166  
  
QY 179 SNTVNMVYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCA 238  
Db 167 SNSVSWYQOVPGTAPKLLIYNNNRPSGVDRFSASKSGTSASLAISGLQSEDEADYYCA 226  
  
QY 239 AWDESLNGVVFEGGKTATVL 258  
Db 227 SWDSDLTVPVFEGGKTATVL 246

Search completed: May 13, 2004, 15:01:00  
Job time : 54.1029 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:53:42 ; Search time 14.1524 Seconds  
(without alignments)  
941.146 Million cell updates/sec

Title: US-10-072-301-27  
Perfect score: 1371  
Sequence: 1 QVQLQESGPGLVKPSSETLSL.....AWDESLNGVVFGGTKVTVL 258

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1003.5	73.2	244	4	US-10-039-785-44 Sequence 44, Appl
2	985.5	71.9	250	4	US-10-039-785-50 Sequence 50, Appl
3	915.5	66.8	244	4	US-08-918-148-79 Sequence 79, Appl
4	815	59.4	278	3	US-09-260-527-3 Sequence 3, Appl
5	808	58.9	310	4	US-09-079-029-11 Sequence 11, Appl
6	800	58.4	258	2	US-08-665-202-5 Sequence 5, Appl
7	800	58.4	258	4	US-09-315-574-5 Sequence 5, Appl
8	728	53.1	334	4	US-09-646-028-53 Sequence 53, Appl
9	728	53.1	339	4	US-09-646-028-55 Sequence 55, Appl
10	728	53.1	348	4	US-09-646-028-51 Sequence 51, Appl
11	716	52.2	249	4	US-10-039-785-53 Sequence 53, Appl
12	698	50.9	249	4	US-08-918-148-74 Sequence 74, Appl
13	693	50.5	245	4	US-10-039-785-42 Sequence 42, Appl
14	689.5	50.3	309	4	US-09-079-029-9 Sequence 9, Appl
15	689	50.3	312	4	US-09-079-029-10 Sequence 10, Appl
16	677	49.4	245	4	US-10-039-785-46 Sequence 46, Appl
17	672	49.0	245	4	US-10-039-785-47 Sequence 47, Appl
18	672	49.0	245	4	US-10-039-785-48 Sequence 48, Appl
19	671	48.9	245	4	US-10-039-785-51 Sequence 51, Appl
20	669	48.8	245	4	US-10-039-785-49 Sequence 49, Appl
21	666	48.6	235	2	US-08-190-199A-61 Sequence 61, Appl
22	666	48.6	245	4	US-10-039-785-52 Sequence 52, Appl
23	666	48.6	280	3	US-09-260-527-1 Sequence 1, Appl
24	648	47.3	245	4	US-10-039-785-43 Sequence 43, Appl
25	643.5	46.9	248	2	US-08-887-352B-22 Sequence 22, Appl
26	643.5	46.9	248	3	US-09-109-207C-22 Sequence 22, Appl
27	643.5	46.9	248	3	US-09-296-005-22 Sequence 22, Appl

28	643.5	46.9	248	4	US-09-920-171-22 Sequence 22, Appl
29	641	46.8	245	4	US-10-039-785-45 Sequence 45, Appl
30	629	45.9	281	4	US-09-025-769B-178 Sequence 178, App
31	627	45.7	263	2	US-08-752-844-66 Sequence 66, Appl
32	627	45.7	263	4	US-09-293-533-66 Sequence 66, Appl
33	626.5	45.7	248	2	US-08-887-352B-23 Sequence 23, Appl
34	626.5	45.7	248	3	US-09-109-207C-23 Sequence 23, Appl
35	626.5	45.7	248	4	US-09-296-005-23 Sequence 23, Appl
36	626.5	45.7	248	3	US-09-920-171-23 Sequence 23, Appl
37	623	45.4	249	2	US-08-797-689-18 Sequence 18, Appl
38	623	45.4	249	4	US-09-984-186-18 Sequence 18, Appl
39	613	44.7	245	4	US-08-918-148-75 Sequence 75, Appl
40	610	44.5	245	4	US-08-918-148-76 Sequence 76, Appl
41	609.5	44.5	240	4	US-10-092-246-37 Sequence 37, Appl
42	609.5	44.5	240	4	US-10-092-246-37 Sequence 37, Appl
43	606.5	44.2	297	4	US-09-486-814A-2 Sequence 2, Appl
44	606.5	44.2	301	2	US-08-661-052-14 Sequence 14, Appl
45	606.5	44.2	301	3	US-09-188-082-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1  
US-10-039-785-44  
; Sequence 44, Application US/10039785  
; Patent No. 6538938  
; GENERAL INFORMATION:  
; APPLICANT: Salcedo et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL  
; FILE REFERENCE: PF550  
; CURRENT APPLICATION NUMBER: US/10/039, 785  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: 60/369, 860  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 60/341, 237  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 60/331, 310  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/331, 044  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/327, 364  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/323, 807  
; PRIOR FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 60/309, 176  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: 60/294, 981  
; PRIOR FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: 60/293, 473  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 44  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: T1014A02 scFv  
; US-10-039-785-44  
  
Query Match 73.2%; Score 1003.5; DB 4; Length 244;  
Best Local Similarity 75.2%; Pred. No. 3.1e-66;  
Matches 194; Conservative 18; Mismatches 31; Indels 15; Gaps 2;  
  
QY 1 QVQLQESGPGLVKPSSETLSLCTVSGSGISGHDYMSWIROPPEGLEWIGFIFPDGSTNYN 60  
DB 1 QVQLQESGPGLVKPSSETLSLCTVSGGSISDYMSWVRQSPGKLEWIGSIDYAGSTNYN 60  
QY 61 PSILGRVTISLDTSKNQLSIRLTSVTAADTAVYFCARLKGAWLLEPPYFSSDGMVWGQ 120  
DB 61 PSILSRVTMTIDSKKQFPLKIDSVTAADTAVYFCARLGRIRI-----SDVWGQ 108

QY 121 GTTIVSSGGGGSGGGSGGGGSGGGSNFMLTQPPSASGTPGQRVISICSSSSDIGN 180  
Db 109 GTLVTVSSGGGGSGGGSGGGGSGGGS--ALSYVLTPPSASGTPGQRTVISICAGSSSNIGN 165  
QY 181 TVNMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCAW 240  
Db 166 TVNMWYQQLPATAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCATW 225  
QY 241 DESLNGVVFEGGCTKTVL 258  
Db 226 DDSRGGWVFEGGCTKTVL 243

RESULT 2  
US-10-039-785-50  
; Sequence 50, Application US/10039785  
; Patent No. 6538938  
; GENERAL INFORMATION:  
; APPLICANT: Salcedo et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: PFS50  
; CURRENT APPLICATION NUMBER: US/10/039,785  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: 60/369,860  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 60/341,237  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 60/331,310  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/331,044  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/327,364  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/323,807  
; PRIOR FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 60/309,176  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: 60/294,981  
; PRIOR FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: 60/293,473  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 50  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: T1015A02 scFv  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (250)  
; OTHER INFORMATION: Xaa equals either Gly or Ser  
US-10-039-785-50

Query Match 71.9%; Score 985.5; DB 4; Length 250;  
Best Local Similarity 74.2%; Pred. No. 6.5e-65;  
Matches 193; Conservative 24; Mismatches 30; Indels 13; Gaps 5;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGIGHD--YMSWTRQPPGEGLEWIGTFPFDGSTN 58  
Db 1 QVQLQESGPGLVKPSQTLSTKCNVSGSGISGTGDIYMSWTRQPPGKGLWIGYTHSSGSTY 60  
QY 59 YNPSLNGRVITSLDTSKNQLSRLTSTVTAADTAVFCAFLKGAWLSEPPYFSSDGMVW 118  
Db 61 YKPSLRSLTVSMDTSRNQFSLKLTSTVTAADTAALYCYR---EW--ANGHWSA--FDLW 113  
QY 119 GGGTIVTVSSGGGGSGGGSGGGGSGGGSNFMLTQPPSASGTPGQRVISICSSSSSDIG 178  
Db 114 GGGTLVTVSSGGGGSGGGSGGGGSGGGS----AQAVLTQPSASGTPGQRTVITPCSSSSSNIG 169

QY 179 SNTVNMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCA 238  
Db 170 GNTVNMWYQQLPGTAPKLLIYGNDRPSPGVDRFSGFKSGTSASLVITGLQSEDEADYYCA 229  
QY 239 AWDESLNGVVFEGGCTKTVL 258  
Db 230 AWDSLIGYVFGTGTQTLTVL 249

RESULT 3  
US-08-918-148-79  
; Sequence 79, Application US/08918148A  
; Patent No. 6342220  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camellia  
; APPLICANT: W.  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Fendly, Brian M.  
; APPLICANT: Gurney, Austin L.  
; TITLE OF INVENTION: Agonist Antibodies  
; FILE REFERENCE: P0979  
; CURRENT APPLICATION NUMBER: US/08/918,148A  
; CURRENT FILING DATE: 1997-08-25  
; NUMBER OF SEQ ID NOS: 79  
; SEQ ID NO 79  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: artificial  
US-08-918-148-79

Query Match 66.8%; Score 915.5; DB 4; Length 244;  
Best Local Similarity 68.7%; Pred. No. 8.4e-60;  
Matches 178; Conservative 34; Mismatches 26; Indels 21; Gaps 5;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGIGHDYMSWTRQPPGEGLEWIGTFPFDGSTNYN 60  
Db 3 QVQLQESGPGLVKPSSETLSLTCTVSGDSISYYMSWTRQPPGKGLWIGYTHSSGSTNYN 62  
QY 61 PSLNGRVITSLDTSKNQLSRLTSTVTAADTAVFCAFLKGAWLSEPPYFSSDGMVWQ 120  
Db 63 PSLKSRVTISVDTSKSQFSLKLTSTVTAADTAVYCARGR-----YF-----DWGR 108  
QY 121 GTTIVSSGGGGSGGGSGGGGSGGGSNFMLTQPPSASGTPGQRVISICSSSDIGS- 179  
Db 109 GTMTVTS-----SGGGSGGGSGGGGSSVLTQPPSVSGSPQSITISCTGTSSDVCGY 163  
QY 180 NTVNMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCAA 239  
Db 164 NYVSWYQQLHPKAPKLMIEGSKRPSGVSNRFGSGSKGNTASLTISGLQAEDEADYYCSS 223  
QY 240 WDESLNGVVFEGGCTKTVL 258  
Db 224 Y-TTRSTRVVFEGGCTKTVL 241

RESULT 4  
US-09-260-527-3  
; Sequence 3, Application US/09260527A  
; Patent No. 6228599  
; GENERAL INFORMATION:  
; APPLICANT: Knox, J.P.  
; APPLICANT: Mikelsen, J.D.  
; APPLICANT: Willats, W.G.  
; TITLE OF INVENTION: ANTIBODY  
; FILE REFERENCE: DYOUI9.001AUS  
; CURRENT APPLICATION NUMBER: US/09/260,527A  
; CURRENT FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 278  
; TYPE: PRT  
; ORGANISM: UNKNOWN

FEATURE:  
OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected  
OTHER INFORMATION: from a naive phage display library known as the  
OTHER INFORMATION: Synthetic scfv library (#1) from the Centre for  
OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK  
US-09-260-527-3

Query Match 59.4%; Score 815; DB 3; Length 278;  
Best Local Similarity 63.3%; Pred. No. 2.2e-52;  
Matches 164; Conservative 24; Mismatches 49; Indels 22; Gaps 5;

QY 1 QVQLQESGPGLVKPESETLSLTCTVSGGSI-GHDYWSWIRQPPGEGLEWIGFIFFDGSTNY 59  
DB 23 QVQLQESGPGLVKPSDTLSLTCAVSGYSISSNMWGMIRQPPGKLEWIGYIYSGSTYY 82  
QY 60 NPSLNGRVTLSDTSKNQLSLRLTSVTADTAVYFCARLKGAWLSEPPYFSSDGMVWG 119  
DB 83 NPSLKSRTVMSVDTSKNQPSLKLSSVTAVDTAVYVCARF-----HPRVYD-----WG 129  
QY 120 QGTVTVSSGGGGSGGGSGGGSGGGSGNMLTQPPSASGTPGQRVISCSGSSSDIGS 179  
DB 130 QGTLVTVSRGGGGSGGGSGGGSGGGSS-----ELTQDPAVSVALGQTVRITCGDS--LRS 181  
QY 180 NTVNMYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCA 239  
DB 182 YYASWYQQLPGQAPVLVIYGNRRPSGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNS 241  
QY 240 WDESLLNGVVFEGGCTKVTVL 258  
DB 242 RDSGSHVVFEGGCTKLTVL 260

RESULT 5  
US-09-079-029-11

Sequence 11, Application us/09079029  
Patent No. 6342369  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilia W.  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Chundharapal, Anan  
APPLICANT: Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079, 029  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 310 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-079-029-11

Query Match 58.9%; Score 808; DB 4; Length 310;  
Best Local Similarity 61.9%; Pred. No. 7.9e-52;  
Matches 161; Conservative 31; Mismatches 50; Indels 18; Gaps 4;

QY 1 QVQLQESGPGLVKPESETLSLTCTVSGGSI-GHDYWSWIRQPPGEGLEWIGFIFFDGSTN-Y 59  
DB 40 QVQLVQSGGIVQPGRSRLRLSCAASGFIFSSYGMHWVRQAPGKLEWVAGIFYDGNKYY 99  
QY 60 NPSLNGRVTLSDTSKNQLSLRLTSVTADTAVYFCARLKGAWLSEPPYFSSDGMVWG 119  
DB 100 ADSVKGRFTISRDNKNTLYLQMSLRADDTAVYVCARDRGYYY-----MDVWG 148  
QY 120 QGTVTVSSGGGGSGGGSGGGSGGGSGNMLTQPPSASGTPGQRVISCSGSSSDIGS 179  
DB 149 KGTIVTVS-----SGGGSGGGSGGGSGGSLTQPPSVSGAPGQRTVISTGRSSNIGA 203  
QY 180 -NTVNMYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCA 238  
DB 204 GHDVHWYQQLPGTAPKLLIYDSSNRPSGVDRFSGRSRGSASLAIITGLQAEDEADYYCQ 263  
QY 239 AWDESLLNGVVFEGGCTKVTVL 258  
DB 264 SYDSLRGSVVFEGGCTKVTVL 283

RESULT 6  
US-08-665-202-5

Sequence 5, Application us/08665202  
Patent No. 5977322  
GENERAL INFORMATION:  
APPLICANT: Marks, James D.  
APPLICANT: Schier, Robert  
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to  
TITLE OF INVENTION: Tumor Antigens  
NUMBER OF SEQUENCES: 141  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/665,202  
FILING DATE: 13-JUN-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,238  
FILING DATE: 14-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,250  
FILING DATE: 15-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 02307B-061410  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 258 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-665-202-5

Query Match 58.4%; Score 800; DB 2; Length 258;

Best Local Similarity 61.5%; Pred. No. 2.5e-51;  
Matches 163; Conservative 32; Mismatches 52; Indels 18; Gaps 6;

```
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYW-SWIRQPPGEGLEWIGFI-FDGSTN 58
Db 1 QVQLQSGAELKKPGESLTKISCKSGSYSP-TSYWIAWVRQMPGKLEWIGLIYPGDSDTK 59
QY 59 YNPISLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSE-----PPYFSSD 113
Db 60 YSPSFGQVTTISVDKSVSTAYLQWSSLKPSDSAVYFCARHDVGYCSSSNCAMKPEYFQH- 118
QY 114 GMDVWGQGTITVTVSSGGGSGGGSGGGSGGGSNFMLTQPPSASGTPGQRVISICSGS 173
Db 119 ----WGQGLTVTS-----SGGGSGGGSGGGSGGGSQSVLTQPPSVSAAPGQKVTIISCSGS 169
QY 174 SSDIGSNTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEA 233
Db 170 SSNIGNNVSWYQQLPGTAPKLLIYHTNRPAGVDRFSGSKSGTSASLSAISGFRSEDEA 229
QY 234 DYCAAMDESLNGVFGGGTKVTVL 258
Db 230 DYCAAMDLSLGSWVFGGGTKLTVL 254
```

## RESULT 7

US-09-315-574-5  
Sequence 5, Application US/09315574  
Patent No. 6512097

## GENERAL INFORMATION:

APPLICANT: Marks, James D.  
APPLICANT: Schier, Robert  
TITLE OF INVENTION: No. 6512097e1 High Affinity Human Antibodies to  
TITLE OF INVENTION: Tumor Antigens  
NUMBER OF SEQUENCES: 141  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Majestic, Parsons, Siebert & Heue P.C.  
STREET: Four Embarcadero Center, Suite 1100  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4106  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/315,574  
FILING DATE: 20-MAY-99  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,238  
FILING DATE: 14-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,250  
FILING DATE: 15-JUN-1995  
APPLICATION NUMBER: US 08/665,202  
FILING DATE: 13-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 02307E-061411  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 258 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-315-574-5

## Query Match

Best Local Similarity 58.4%; Score 800; DB 4; Length 258;  
Matches 163; Conservative 32; Mismatches 52; Indels 18; Gaps 6;

```
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYW-SWIRQPPGEGLEWIGFI-FDGSTN 58
Db 1 QVQLQSGAELKKPGESLTKISCKSGSYSP-TSYWIAWVRQMPGKLEWIGLIYPGDSDTK 59
QY 59 YNPISLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSE-----PPYFSSD 113
Db 60 YSPSFGQVTTISVDKSVSTAYLQWSSLKPSDSAVYFCARHDVGYCSSSNCAMKPEYFQH- 118
QY 114 GMDVWGQGTITVTVSSGGGSGGGSGGGSGGGSNFMLTQPPSASGTPGQRVISICSGS 173
Db 119 ----WGQGLTVTS-----SGGGSGGGSGGGSGGGSQSVLTQPPSVSAAPGQKVTIISCSGS 169
QY 174 SSDIGSNTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEA 233
Db 170 SSNIGNNVSWYQQLPGTAPKLLIYHTNRPAGVDRFSGSKSGTSASLSAISGFRSEDEA 229
QY 234 DYCAAMDESLNGVFGGGTKVTVL 258
Db 230 DYCAAMDLSLGSWVFGGGTKLTVL 254
```

## RESULT 8

US-09-646-028-53  
Sequence 53, Application US/09646028  
Patent No. 6562347

## GENERAL INFORMATION:

APPLICANT: Kwak, Larry  
APPLICANT: Biragyn, Arya  
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF  
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES  
FILE REFERENCE: 14014.0316/P  
CURRENT APPLICATION NUMBER: US/09/646,028  
PRIOR FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: 60/077,745  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 53  
LENGTH: 334  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct  
US-09-646-028-53

## Query Match

Best Local Similarity 53.1%; Score 728; DB 4; Length 334;  
Matches 152; Conservative 30; Mismatches 60; Indels 22; Gaps 6;

```
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYWSWIRQPPGEGLEWIGFI-FDGSTN-Y 59
Db 80 EVQLLESQGLVQSGSLRLSCVASGLTFSSAITWVRQAPGKLEWVSGISFSGDTTY 139
QY 60 NPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDG---MD 116
Db 140 ADSVKGRFSASRDNSKNTVYLLQMNLRPNDAVYFCAN-----NQTGNFCLD 186
QY 117 VMGQGTITVTVSS-GGGSGGGSGGGSGGGSNFMLTQPPSASGTPGQRVISICSGSS 175
Db 187 NMGQGLTVTVSSRRGGSGGGSGGGSGGGS---GSQSVLTQPPSVSAAPGQKVTIISCTGSR 243
QY 176 DIGSN-TVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEA 234
Db 244 NIGAGYDVNMWYQKPEPTAPKLLIYSNNNRPSGVDRFSGSKSGTSASLSAISGLQLEDEGT 303
QY 235 YCAAMDESLNGVFGGGTKVTVL 258
Db 304 YCCQCNDSLSLGSWVFGGGTKLTVL 327
```



```
RESULT 9
US-09-646-028-55
; Sequence 55, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Birsagyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-55

Query Match          53.1%; Score 728; DB 4; Length 339;
Best Local Similarity 57.6%; Pred. No. 6.2e-46;
Matches 152; Conservative 30; Mismatches 60; Indels 22; Gaps 6;

QY      1 OVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIROPGEGLWIGFIFPDGSTN-Y 59
      :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      85 EVQLLESGGGLVQSGGSLRLSCVASGLTFSSSAITWVRQAPGKLEWVSGISFSGDTTY 144
QY      60 NPSLNGRVTISLDTSKNQLSLRLSVTAADTAVYFCARLKGAWLSEPPYFSSDG--MD 116
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      145 ADSVKGRFASRDNSKNTVYLQMNMLRPNDTAVYFCAN-----NOTGNFCLD 191
QY      117 VMGGGTTVTSS-GGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRVISICSGSSS 175
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      192 NMGGGLVTVSSRGGGSGGGSGGGSGS---GSQSVLTQPPSVSAAPGQRTVISTGSR 248
QY      176 DIGSN-TVNMWYQQLPGTAPKLLIYNNQRPSPGVDPDRFSGFKSGTSASLVISGLQSEDEAD 234
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      249 NIGAGYDVNMWYQKFPETAPKVLIIYNNRPSGVPDRFSGSKSGTSASLAITGLQLEDEGT 308
QY      235 YYCAAMDESLNGVFGGGTKVTVL 258
      ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      309 YYCQCNDDSLSGWLFGGGTKLTVL 332

RESULT 10
US-09-646-028-51
; Sequence 51, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Birsagyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
```

```
US-09-646-028-51

Query Match          53.1%; Score 728; DB 4; Length 348;
Best Local Similarity 57.6%; Pred. No. 6.4e-46;
Matches 152; Conservative 30; Mismatches 60; Indels 22; Gaps 6;

QY      1 OVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIROPGEGLWIGFIFPDGSTN-Y 59
      :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      94 EVQLLESGGGLVQSGGSLRLSCVASGLTFSSSAITWVRQAPGKLEWVSGISFSGDTTY 153
QY      60 NPSLNGRVTISLDTSKNQLSLRLSVTAADTAVYFCARLKGAWLSEPPYFSSDG--MD 116
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      154 ADSVKGRFASRDNSKNTVYLQMNMLRPNDTAVYFCAN-----NOTGNFCLD 200
QY      117 VMGGGTTVTSS-GGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRVISICSGSSS 175
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      201 NMGGGLVTVSSRGGGSGGGSGGGSGS---GSQSVLTQPPSVSAAPGQRTVISTGSR 257
QY      176 DIGSN-TVNMWYQQLPGTAPKLLIYNNQRPSPGVDPDRFSGFKSGTSASLVISGLQSEDEAD 234
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      258 NIGAGYDVNMWYQKFPETAPKVLIIYNNRPSGVPDRFSGSKSGTSASLAITGLQLEDEGT 317
QY      235 YYCAAMDESLNGVFGGGTKVTVL 258
      ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      318 YYCQCNDDSLSGWLFGGGTKLTVL 341

RESULT 11
US-10-039-785-53
; Sequence 53, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1006F07 scFv
US-10-039-785-53

Query Match          52.2%; Score 716; DB 4; Length 249;
Best Local Similarity 56.7%; Pred. No. 3.3e-45;
Matches 149; Conservative 30; Mismatches 64; Indels 20; Gaps 6;

QY      1 OVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIROPGEGLWIGFIFPDGSTNY 59
      :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      1 EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVASISGSGSTYY 60
```



## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,029  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-079-029-9

## Query Match

Best Local Similarity 50.3%; Score 689.5; DB 4; Length 309;  
Matches 144; Conservative 32; Mismatches 63; Indels 23; Gaps 6;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWI-GFIFPDGSTNY 59  
DB 40 EYQLVQSGGVERPGSLRLSCAASGFTFDYGMSTWRQAPGKLEWVSGINMGSGTGY 99  
QY 60 NPSLNGRVTISLDTSKNQLSLRLSVTAADTAVYFCARLKA---WLLSEPPYFSSDGM 116  
DB 100 ADSYGRVTISRDNKNSLYLQNSLRAEDTAVYYCAKILGARGW-----YF-----D 148  
QY 117 VMGGGTTVTSSGGGSGGGSGGGSGGSGGSGNFMLTQPPSASGTPGQRVISISCGSSSD 176  
DB 149 LMGKGTIVTVSSGGGSGGGSGGGSGSS-----ELTQDPAVSVALGQTVRITCCGDS-- 200  
QY 177 IGSNTVNWYQQLPGTAPKLLIYNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYY 236  
DB 201 LRSYYASWYQOKPGQAPVLVIYGNRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY 260  
QY 237 CAAMDESLNGVFGGGTKVTVL 258  
DB 261 CNSRDSSGNHVFGGGTKLTVL 282

## RESULT 15

US-09-079-029-10  
Sequence 10, Application US/09079029  
Patent No. 6342369  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilia W.  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Chuntharapai, Anan  
APPLICANT: Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,029

## FILING DATE:

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 312 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-079-029-10

## Query Match

Best Local Similarity 50.3%; Score 689; DB 4; Length 312;  
Matches 146; Conservative 28; Mismatches 66; Indels 22; Gaps 5;

QY 2 VQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGFIFPDGSTNY- 60  
DB 41 VQLVESGGGLVQPGSLRLSCAASGFTFSSYMSWVRQAPGKLEWVANIKQDSSEKYY 100  
QY 61 PSLNGRVTISLDTSKNQLSLRLSVTAADTAVYFCAR---LKAWLLSEPPYFSSDGM 116  
DB 101 DSVKGRVTISRDNKNSLYLQNSLRAEDTAVYYCARDLLKVGK-----SSGWF 151  
QY 117 VMGGGTTVTSSGGGSGGGSGGGSGGSGGSGNFMLTQPPSASGTPGQRVISISCGSSSD 176  
DB 152 PMGRGTTVTSSGGGSGGGSGGGSGSS-----ELTQDPAVSVALGQTVRITCCGDS-- 203  
QY 177 IGSNTVNWYQQLPGTAPKLLIYNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYY 236  
DB 204 LRSYYASWYQOKPGQAPVLVIYGNRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY 263  
QY 237 CAAMDESLNGVFGGGTKVTVL 258  
DB 264 CNSRDSSGNHVFGGGTKLTVL 285

Search completed: May 13, 2004, 15:10:49  
Job time : 15.1524 secs

**This Page Blank (uspto)**



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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:07:07 ; Search time 38.199 Seconds  
(without alignments)  
1879.405 Million cell updates/sec

Title: US-10-072-301-27

Perfect score: 1371

Sequence: 1 QVQLQESGPGLVKPSSETLSL.....AWDESLNGVVFEGGTKVTVL 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1371	100.0	258	14	US-10-072-301-27 Sequence 27, Appl
2	1371	100.0	258	14	US-10-071-866-27 Sequence 27, Appl
3	1371	100.0	258	15	US-10-360-828-27 Sequence 27, Appl
4	1340	97.7	254	14	US-10-072-301-19 Sequence 19, Appl
5	1340	97.7	254	14	US-10-071-866-19 Sequence 19, Appl
6	1340	97.7	254	15	US-10-360-828-19 Sequence 19, Appl
7	1031.5	75.2	252	10	US-09-880-748-1223 Sequence 123, Ap
8	1031.5	75.2	252	12	US-10-293-418-1223 Sequence 123, Ap
9	1003.5	73.2	244	13	US-10-039-785-44 Sequence 44, Appl
10	1003.5	73.2	244	14	US-10-139-785-44 Sequence 44, Appl
11	1002	73.1	255	10	US-09-880-748-1642 Sequence 1642, Ap
12	1002	73.1	255	12	US-10-293-418-1642 Sequence 1642, Ap
13	994.5	72.5	252	10	US-09-880-748-1994 Sequence 1994, Ap
14	994.5	72.5	252	12	US-10-293-418-1994 Sequence 1994, Ap
15	987	72.0	251	10	US-09-880-748-1510 Sequence 1510, Ap

16	987	72.0	251	12	US-10-293-418-1510	Sequence 1510, Ap
17	987	72.0	255	10	US-09-880-748-1597	Sequence 1597, Ap
18	987	72.0	255	12	US-10-293-418-1597	Sequence 1597, Ap
19	985.5	71.9	250	13	US-10-039-785-50	Sequence 50, Appl
20	985.5	71.9	250	14	US-10-139-785-50	Sequence 50, Appl
21	982	71.6	251	10	US-09-880-748-1546	Sequence 1546, Ap
22	982	71.6	251	12	US-10-293-418-1546	Sequence 1546, Ap
23	966	70.5	247	10	US-09-880-748-1981	Sequence 1981, Ap
24	966	70.5	247	12	US-10-293-418-1981	Sequence 1981, Ap
25	945	68.9	247	10	US-09-880-748-1993	Sequence 1993, Ap
26	945	68.9	247	12	US-10-293-418-1993	Sequence 1993, Ap
27	939.5	68.5	254	10	US-09-880-748-1659	Sequence 1659, Ap
28	939.5	68.5	254	12	US-10-293-418-1659	Sequence 1659, Ap
29	935	68.2	249	10	US-09-880-748-1962	Sequence 1962, Ap
30	935	68.2	249	12	US-10-293-418-1962	Sequence 1962, Ap
31	929	67.8	251	14	US-10-120-414-75	Sequence 75, Appl
32	927	67.6	247	10	US-09-880-748-1998	Sequence 1998, Ap
33	927	67.6	247	12	US-10-293-418-1998	Sequence 1998, Ap
34	925.5	67.5	256	10	US-09-880-748-1607	Sequence 1607, Ap
35	925.5	67.5	256	12	US-10-293-418-1607	Sequence 1607, Ap
36	921	67.2	251	10	US-09-880-748-1538	Sequence 1538, Ap
37	921	67.2	251	12	US-10-293-418-1538	Sequence 1538, Ap
38	915.5	66.8	258	10	US-09-880-748-2083	Sequence 2083, Ap
39	915.5	66.8	258	12	US-10-293-418-2083	Sequence 2083, Ap
40	905	66.0	251	10	US-09-880-748-990	Sequence 990, App
41	905	66.0	251	12	US-10-293-418-990	Sequence 990, App
42	898	65.5	245	10	US-09-880-748-1864	Sequence 1864, Ap
43	898	65.5	245	12	US-10-293-418-1864	Sequence 1864, Ap
44	896	65.4	253	10	US-09-880-748-1619	Sequence 1619, Ap
45	896	65.4	253	12	US-10-293-418-1619	Sequence 1619, Ap

ALIGNMENTS

RESULT 1  
US-10-072-301-27  
; Sequence 27, Application US/10072301  
; Publication No. US20030152913A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF  
; FILE REFERENCE: 25636-718  
; CURRENT APPLICATION NUMBER: US/10/072,301  
; CURRENT FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 27  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.11  
US-10-072-301-27

Query Match	100.0%	Score 1371;	DB 14;	Length 258;
Best Local Similarity	100.0%	Pred. No. 7.3e-87;		
Matches	258;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1 QVQLQESGPGLVKPSSETLSLTCTVSGSGIGHDYWSWIRDPPEGLEWIGFIFFDGSITNN	60		
DB	1 QVQLQESGPGLVKPSSETLSLTCTVSGSGIGHDYWSWIRDPPEGLEWIGFIFFDGSITNN	60		
QY	61 PSINGRVTISLDTSKNQLSLRLTSVTADTAIVFCARLKGAWLLSEPPYFSSDGMVWGQ	120		
DB	61 PSINGRVTISLDTSKNQLSLRLTSVTADTAIVFCARLKGAWLLSEPPYFSSDGMVWGQ	120		
QY	121 GTTIVTSSGGGSGGGSGGGSGGGSGGNFMTLQPPSAGTPEGQRVISISCGSSSDIGSN	180		
DB	121 GTTIVTSSGGGSGGGSGGGSGGGSGGNFMTLQPPSAGTPEGQRVISISCGSSSDIGSN	180		

QY 181 TVNMYQOLPGTAPKLLIYSNNQRPSPGVPDRFSGFGKSGTSASLVISGLQSEDEADYYCAAW 240  
Db 181 TVNMYQOLPGTAPKLLIYSNNQRPSPGVPDRFSGFGKSGTSASLVISGLQSEDEADYYCAAW 240  
QY 241 DESLNGVVFPGGKTATVL 258  
Db 241 DESLNGVVFPGGKTATVL 258

## RESULT 2

US-10-071-866-27  
; Sequence 27, Application US/10071866  
; Publication No. US20030165988A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST  
; FILE REFERENCE: 25636-717  
; CURRENT APPLICATION NUMBER: US/10/071,866  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 27  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.11  
US-10-071-866-27

Query Match 100.0%; Score 1371; DB 14; Length 258;  
Best Local Similarity 100.0%; Pred. No. 7.3e-87;  
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSSGSGIGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSSGSGIGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
QY 61 PSINGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ 120  
Db 61 PSINGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ 120  
QY 121 GTTIVTSSGGGSGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRVVISCSGSSSDIGSN 180  
Db 121 GTTIVTSSGGGSGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRVVISCSGSSSDIGSN 180  
QY 181 TVNMYQOLPGTAPKLLIYSNNQRPSPGVPDRFSGFGKSGTSASLVISGLQSEDEADYYCAAW 240  
Db 181 TVNMYQOLPGTAPKLLIYSNNQRPSPGVPDRFSGFGKSGTSASLVISGLQSEDEADYYCAAW 240  
QY 241 DESLNGVVFPGGKTATVL 258  
Db 241 DESLNGVVFPGGKTATVL 258

## RESULT 3

US-10-360-828-27  
; Sequence 27, Application US/10360828  
; Publication No. US20030206909A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS  
; FILE REFERENCE: 25636-727  
; CURRENT APPLICATION NUMBER: US/10/360,828  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: US 10/071,866  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/072,301

; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/133,978  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 27  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.11 Variant  
US-10-360-828-27

Query Match 100.0%; Score 1371; DB 15; Length 258;  
Best Local Similarity 100.0%; Pred. No. 7.3e-87;  
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSSGSGIGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSSGSGIGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
QY 61 PSINGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ 120  
Db 61 PSINGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ 120  
QY 121 GTTIVTSSGGGSGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRVVISCSGSSSDIGSN 180  
Db 121 GTTIVTSSGGGSGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRVVISCSGSSSDIGSN 180  
QY 181 TVNMYQOLPGTAPKLLIYSNNQRPSPGVPDRFSGFGKSGTSASLVISGLQSEDEADYYCAAW 240  
Db 181 TVNMYQOLPGTAPKLLIYSNNQRPSPGVPDRFSGFGKSGTSASLVISGLQSEDEADYYCAAW 240  
QY 241 DESLNGVVFPGGKTATVL 258  
Db 241 DESLNGVVFPGGKTATVL 258

## RESULT 4

US-10-072-301-19  
; Sequence 19, Application US/10072301  
; Publication No. US20030152913A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF  
; FILE REFERENCE: 25636-718  
; CURRENT APPLICATION NUMBER: US/10/072,301  
; CURRENT FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.11  
US-10-072-301-19

Query Match 97.7%; Score 1340; DB 14; Length 254;  
Best Local Similarity 98.8%; Pred. No. 9.8e-85;  
Matches 251; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSSGSGIGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSSGSGIGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
QY 61 PSINGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ 120  
Db 61 PSINGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ 120

QY	121 GTTIVVSSGGCGSGGCGSGGCGGSNFMLTQPPSASGTPGQRVSI	SCSGSSSDIGSN	180
Db	121 GTTIVTPS	GCGSGSGCGSGGCGGSNFMLTQPPSASGTPGQRVSI	SCSGSSSDIGSN
			180
QY	181 TVNWVYQQLPGTAPKLLIYSNNORP	SGVDPRFSGFKSGTSASLVI	SGLOSEADYYCAAW
			240
Db	181 TVNWVYQQLPGTAPKLLIYSNNORP	SGVDPRFSGFKSGTSASLVI	SGLOSEADYYCAAW
			240
QY	241 DESLNGVVF	FGGGTK	254
			:
Db	241 DESLNGVVF	FGGGR	254

## RESULT 5

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US-10-071-866-19
; Sequence 19, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST E
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071, 866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.11
US-10-071-866-19

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Query Match	97.7%;	Score 1340;	DB 14;	Length 254;
Best Local Similarity	98.8%;	Pred. No. 9.8e-85;		
Matches 251; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1	QVQLQESGPGGLVKPSETSLTCTVSGGSGIGHDYSWIRQPPGEGLEWIGRIFFPDGSTNYN	60
Db	1	QVQLQESGPGGLVKPSETSLTCTVSGGSGIGHDYSWIRQPPGEGLEWIGRIFFPDGSTNYN	60
QY	61	PSLNGRVTISLDTSKNQSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ	120
Db	61	PSLNGRVTISLDTSKNQSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ	120
QY	121	GTTVTVSSGGGSGGGSGGGSGGGSGGGSNFMLTQPPSASGTPGQRVISICSGSSSDIGSN	180
Db	121	GTTVTVPSSGGGSGGGSGGGSGGGSGGGSNFMLTQPPSASGTPGQRVISICSGSSSDIGSN	180
QY	181	TVNWMYQQLPGTAPKLLIYSNNQRPESGVEDRFSGFKSGTSASLVISGLQSEDEADYYCAAW	240
Db	181	TVNWMYQQLPGTAPKLLIYSNNQRPESGVEDRFSGFKSGTSASLVISGLQSEDEADYYCAAW	240
QY	241	DESLNGVVFVGSGTK 254	
Db	241	DESLNGVVFVGSGGPR 254	

## RESULT 6

US-10-360-828-19  
; Sequence 19, Application US/10360828  
; Publication No. US20030206909A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shaobing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS  
; FILE REFERENCE: 25636-727  
; CURRENT APPLICATION NUMBER: US/10/360, 828  
; CURRENT FILING DATE: 2003-02-07

```

; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1.
; SEQ ID NO 19
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.11
US-10-360-828-19

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OTHER INFORMATION: C10ne 15.150.11  
US-10-360-828-19

Query Match	97.7%;	Score 1340;	DB 15;	Length 254;
Best Local Similarity	98.8%;	Pred. No. 9.8e-85;		
Matches 251; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1	QVQLQESGPGLVKPSERTLSLTCTVSGGSGIGHDYWSMIRQPPGEGLEWIGTFFPDGSTNYN	60
Db	1	QVQLQESGPGLVKPSERTLSLTCTVSGGSGIGHDYWSMIRQPPGEGLEWIGTFFPDGSTNYN	60
QY	61	PSLNGRVTISLDTSKNQLSRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVDWGQ	120
Db	61	PSLNGRVTISLDTSKNQLSRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVDWGQ	120
QY	121	GTTVTVSSGGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRVISICSGSSSDIGSN	180
Db	121	GTTVTVPSGGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRVISICSGSSSDIGSN	180
QY	181	TVMWYQQLPGTAPKLLIYSNNORPSGVPDRFSFGKSGTSASLVISGLQSEDEADYYCAAW	240
Db	181	TVMWYQQLPGTAPKLLIYSNNORPSGVPDRFSFGKSGTSASLVISGLQSEDEADYYCAAW	240

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QY      241 DESLNGVFFGGGTK 254
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Db      241 DESLNGVFFGGGPR 254
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## RESULT 7

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; Sequence 1223, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1223
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1223

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Query Match	75.2%;	Score 1031.5;	DB 10;	Length 252;
Best Local Similarity	78.1%;	Pred. No. 1.7e-63;		
Matches 203; Conservative	15;	Mismatches 31;	Indels 11;	Gaps 3;



QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIQH--DYMSWIRQPPGEGLEWIGFIFPDGSTN 58  
Db 1 QVQLQESGPGVVKPSETLSLTCTVSGGFISSRTSYMGWIRQPPGKLEWIGNITYYTKTY 60  
QY 59 YNPISLNGRVYTIISLDTSKNQSLRLTSVTAADTAVYFCARLKGAWLLSEPPYFSSDGMVW 118  
Db 61 YSPSLKSRVTISADTSKNQSLKLSVTAADTAVYFCARAGYDLITGYPFYF-----DSW 115  
QY 119 GGGTTVTYSSGGGSGGGSGGGSGGGSGGNFMLTQPPSASGTPGQRVISISCGSSSDIG 178  
Db 116 GKGTMTYVSSGGGSGGGSGGGSGGGG-----AQSVLTQPPSASGTPGQRVYISCGSSSNIG 171  
QY 179 SNTVNMVYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCA 238  
Db 172 SNTVNMVYQQLPGTAPKLLMYLNNQRPSPGVDRFSGSKSGTSASLAIISGLQSEDEADYYCL 231  
QY 239 AWDESINGVVFEGGTKVTYL 258  
Db 232 TWDDSLNGPVPFEGGTKVTYL 251

RESULT 8  
US-10-293-418-1223

/ Sequence 1223, Application US/10293418  
/ Publication No. US2003022396A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Ruben et al.  
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
/ FILE REFERENCE: PF523P2  
/ CURRENT APPLICATION NUMBER: US/10/293,418  
/ PRIOR FILING DATE: 2002-11-27  
/ PRIOR APPLICATION NUMBER: 60/331,469  
/ PRIOR FILING DATE: 2001-11-16  
/ PRIOR APPLICATION NUMBER: 60/340,817  
/ PRIOR FILING DATE: 2001-12-19  
/ PRIOR APPLICATION NUMBER: 09/880,748  
/ PRIOR FILING DATE: 2001-06-15  
/ PRIOR APPLICATION NUMBER: 60/293,499  
/ PRIOR FILING DATE: 2001-05-25  
/ PRIOR APPLICATION NUMBER: 60/277,379  
/ PRIOR FILING DATE: 2001-03-21  
/ PRIOR APPLICATION NUMBER: 60/276,248  
/ PRIOR FILING DATE: 2001-03-16  
/ PRIOR APPLICATION NUMBER: 60/240,816  
/ PRIOR FILING DATE: 2000-10-17  
/ PRIOR APPLICATION NUMBER: 60/212,210  
/ PRIOR FILING DATE: 2000-06-16  
/ NUMBER OF SEQ ID NOS: 3247  
/ SEQ ID NO 1223  
/ LENGTH: 252  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-293-418-1223

Query Match 75.2%; Score 1031.5; DB 12; Length 252;  
Best Local Similarity 78.1%; Pred. No. 1.7e-63;  
Matches 203; Conservative 15; Mismatches 31; Indels 11; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIQH--DYMSWIRQPPGEGLEWIGFIFPDGSTN 58  
Db 1 QVQLQESGPGVVKPSETLSLTCTVSGGFISSRTSYMGWIRQPPGKLEWIGNITYYTKTY 60  
QY 59 YNPISLNGRVYTIISLDTSKNQSLRLTSVTAADTAVYFCARLKGAWLLSEPPYFSSDGMVW 118  
Db 61 YSPSLKSRVTISADTSKNQSLKLSVTAADTAVYFCARAGYDLITGYPFYF-----DSW 115  
QY 119 GGGTTVTYSSGGGSGGGSGGGSGGGSGGNFMLTQPPSASGTPGQRVISISCGSSSDIG 178  
Db 116 GKGTMTYVSSGGGSGGGSGGGSGGGG-----AQSVLTQPPSASGTPGQRVYISCGSSSNIG 171  
QY 179 SNTVNMVYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCA 238  
Db 172 SNTVNMVYQQLPGTAPKLLMYLNNQRPSPGVDRFSGSKSGTSASLAIISGLQSEDEADYYCL 231

QY 239 AWDESINGVVFEGGTKVTYL 258  
Db 232 TWDDSLNGPVPFEGGTKVTYL 251

RESULT 9  
US-10-039-785-44

/ Sequence 44, Application US/10039785  
/ Publication No. US20020067646A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Salcedo et al.  
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL  
/ FILE REFERENCE: PF550  
/ CURRENT APPLICATION NUMBER: US/10/039,785  
/ PRIOR FILING DATE: 2002-05-07  
/ PRIOR APPLICATION NUMBER: 60/369,860  
/ PRIOR FILING DATE: 2002-04-05  
/ PRIOR APPLICATION NUMBER: 60/341,237  
/ PRIOR FILING DATE: 2001-12-20  
/ PRIOR APPLICATION NUMBER: 60/331,310  
/ PRIOR FILING DATE: 2001-11-14  
/ PRIOR APPLICATION NUMBER: 60/331,044  
/ PRIOR FILING DATE: 2001-11-07  
/ PRIOR APPLICATION NUMBER: 60/327,364  
/ PRIOR FILING DATE: 2001-10-09  
/ PRIOR APPLICATION NUMBER: 60/323,807  
/ PRIOR FILING DATE: 2001-09-21  
/ PRIOR APPLICATION NUMBER: 60/309,176  
/ PRIOR FILING DATE: 2001-08-02  
/ PRIOR APPLICATION NUMBER: 60/294,981  
/ PRIOR FILING DATE: 2001-06-04  
/ PRIOR APPLICATION NUMBER: 60/293,473  
/ PRIOR FILING DATE: 2001-05-25  
/ NUMBER OF SEQ ID NOS: 66  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 44  
/ LENGTH: 244  
/ TYPE: PRT  
/ ORGANISM: Artificial sequence  
/ FEATURE:  
/ OTHER INFORMATION: T1014A02 BCFV  
US-10-039-785-44

Query Match 73.2%; Score 1003.5; DB 13; Length 244;  
Best Local Similarity 75.2%; Pred. No. 1.4e-61;  
Matches 194; Conservative 18; Mismatches 31; Indels 15; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIQHDYMSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGISIDYMSWVRSQPKGLEWIGSIDYAGSTNYN 60  
QY 61 PSLSNGRVYTIISLDTSKNQSLRLTSVTAADTAVYFCARLKGAWLLSEPPYFSSDGMVWQ 120  
Db 61 PSLSKRVYTIIDSKSKQFPLKIDSVTAADTAVYFCARQLGRI-----SDYWGQ 108  
QY 121 GTTVYSSGGGSGGGSGGGSGGGSGGNFMLTQPPSASGTPGQRVISISCGSSSDIGSN 180  
Db 109 GTLVYSSGGGSGGGSGGGSGGGG-----ALSYLTQPPSASGTPGQRVYISCGSSSNIGN 165  
QY 181 TVNMVYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTSASLVISGLQSEDEADYYCAW 240  
Db 166 TVNMVYQQLPATAPKLLIYSNNQRPSPGVDRFSGSKSGTSASLAIISGLQSEDEADYYCATW 225  
QY 241 DESLNGVVFEGGTKVTYL 258  
Db 226 DDSRGGWVFEGGTKVTYL 243

RESULT 10  
US-10-139-785-44  
/ Sequence 44, Application US/10139785



```
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014A02 scFv
; US-10-139-785-44

Query Match          73.2%; Score 1003.5; DB 14; Length 244;
Best Local Similarity 75.2%; Pred. No. 1.4e-61;
Matches 194; Conservative 18; Mismatches 31; Indels 15; Gaps 2;

QY      1 QVQLQESGPGLVKPSSETLSLTCTVSGSGISGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYN 60
Db      1 QVQLQESGPGLVKPSSETLSLTCTVSGSGISDYMSWVRQSPGKLEWIGSIDYAGSTNYN 60

QY      61 PSLNGRVTISLDTSKNQSLRLTSVTAADTAIVYFCARLKGAWLLEPPYFSSDGMVWGQ 120
Db      61 PSLKSRVTMTIDSKRKQPPKIDSVTAADTAMYYCARQLGRI-----SDYWGQ 108

QY      121 GTTVTVSSGGGGSGGGGGSGGGSGGSGNFMLTQPPSASGTPGQRVSVISCGSSSDIGSN 180
Db      109 GTLVTVSSGGGGSGGGGGSGGGSGG--ALSYVLTQPPSASGTPGQRTVISCAGSSSNIGGN 165

QY      181 TVNMWYQQLPGTAPKLLIYSNNQRPSPGVPDRFSGFKSGTSASLVISGLQSEDEADYYCAAW 240
Db      166 TVNMWYQQLPATAPKLLIYSNNQRPSPGVPDRFSGSKSGTSASLAIISGLQSEDEADYYCATW 225

QY      241 DESLNGVVFEGGTXYTVL 258
Db      226 DDSRGGWVFEGGTXYTVL 243

RESULT 11
US-09-880-748-1642
; Sequence 1642, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
```

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; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1642
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-1642

Query Match          73.1%; Score 1002; DB 10; Length 255;
Best Local Similarity 75.7%; Pred. No. 1.8e-61;
Matches 196; Conservative 23; Mismatches 34; Indels 6; Gaps 2;

QY      1 QVQLQESGPGLVKPSSETLSLTCTVSGSGISGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYN 60
Db      1 QVQLQWAGAGLKPSETLSLTCAVYGGSPSGYMSWIRQSPGKLEWIGEINHGSTNYN 60

QY      61 PSLNGRVTISLDTSKNQSLRLTSVTAADTAIVYFCARLKGAWLLEPPYFSSDGMVWG 119
Db      61 PSLKSRVTISVDASKNQPSLKLSSVTAADTAIVYCARERSYYDILTGYSPPRSKYGMDVWG 120

QY      120 QGTVTVSSGGGGSGGGGGSGGGSGGSGNFMLTQPPSASGTPGQRVSVISCGSSSDIGS 179
Db      121 RGLTVTVS-----SGGGGGSGGGGGSGGGSGQSVLTQPPSASGTPGQRTVISCSSSSNIGS 175

QY      180 NTVMWYQQLPGTAPKLLIYSNNQRPSPGVPDRFSGFKSGTSASLVISGLQSEDEADYYCAA 239
Db      176 NTVMWYQRLPGAAPQLLIYNNQRPSPGIPDRFSGSKSGTSGLVISGLQSEDEADYYCAS 235

QY      240 WDESLNGVVFEGGTXYTVL 258
Db      236 WDDSLNGRVFEGGTXYTVL 254

RESULT 12
US-10-293-418-1642
; Sequence 1642, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1642
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-418-1642
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Query Match 73.1%; Score 1002; DB 12; Length 255;  
Best Local Similarity 75.7%; Pred. No. 1.8e-61;  
Matches 196; Conservative 23; Mismatches 34; Indels 6; Gaps 2;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGISGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGISGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
QY 61 PSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAW-LISEPPYFSSDGMVDWG 119  
DB 61 PSLKSRVTISVDASKNQLSLRLTSVTAADTAVYFCARERSYDILTGYSPRSKYGMVDWG 120  
QY 120 QGTTVTYVSSGGGSGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRVISISCGSSSDIGS 179  
DB 121 RGLTVTVS-----SGGGSGGGGSGGGGSGSVLTQPPSASGTPGQRTVITISCGSSSNIGS 175  
QY 180 NTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTASLVISGLQSEDEADYYCA 239  
DB 176 NTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTASLVISGLQSEDEADYYCA 235  
QY 240 WDESINGVVFGGGTKVTVL 258  
DB 236 WDSLNGRVFVGGETKLTVL 254

RESULT 13

US-09-880-748-1994  
; Sequence 1994, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1994  
; LENGTH: 252  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1994

Query Match 72.5%; Score 994.5; DB 10; Length 252;  
Best Local Similarity 74.6%; Pred. No. 5.9e-61;  
Matches 194; Conservative 21; Mismatches 34; Indels 11; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGI--GHDYMSWIRQPPGEGLEWIGFIFPDGSTN 58  
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGI--GHDYMSWIRQPPGEGLEWIGFIFPDGSTN 58  
QY 59 YNPGLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAW-LISEPPYFSSDGMVDW 118  
DB 61 YNPGLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAW-LISEPPYFSSDGMVDW 114  
QY 119 GGGTTVTYVSSGGGSGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRVISISCGSSSDIG 178  
DB 115 GGGTTVTYVSSGGGSGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRVISISCGSSSDIG 171  
QY 179 SNTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTASLVISGLQSEDEADYYCA 238  
DB 172 SNTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTASLVISGLQSEDEADYYCA 231

QY 239 AWDESINGVVFGGGTKVTVL 258  
DB 232 TWDRLRGLVFGGTKVTVL 251

RESULT 14

US-10-293-418-1994  
; Sequence 1994, Application US/10293418  
; Publication No. US20030223996A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523P2  
; CURRENT APPLICATION NUMBER: US/10/293,418  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1994  
; LENGTH: 252  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-1994

Query Match 72.5%; Score 994.5; DB 12; Length 252;  
Best Local Similarity 74.6%; Pred. No. 5.9e-61;  
Matches 194; Conservative 21; Mismatches 34; Indels 11; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGI--GHDYMSWIRQPPGEGLEWIGFIFPDGSTN 58  
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGI--GHDYMSWIRQPPGEGLEWIGFIFPDGSTN 58  
QY 59 YNPGLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAW-LISEPPYFSSDGMVDW 118  
DB 61 YNPGLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAW-LISEPPYFSSDGMVDW 114  
QY 119 GGGTTVTYVSSGGGSGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRVISISCGSSSDIG 178  
DB 115 GGGTTVTYVSSGGGSGGGGSGGGGSGGSGNFMLTQPPSASGTPGQRVISISCGSSSDIG 171  
QY 179 SNTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTASLVISGLQSEDEADYYCA 238  
DB 172 SNTVMWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGFKSGTASLVISGLQSEDEADYYCA 231  
QY 239 AWDESINGVVFGGGTKVTVL 258  
DB 232 TWDRLRGLVFGGTKVTVL 251

RESULT 15

US-09-880-748-1510  
; Sequence 1510, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748

; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1510  
; LENGTH: 251  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1510

Query Match 72.0%; Score 987; DB 10; Length 251;  
Best Local Similarity 75.8%; Pred. No. 1.9e-60;  
Matches 197; Conservative 20; Mismatches 31; Indels 12; Gaps 4;

QY 1 QVQLQESGPGLVKPSETLSLTCTVSGSGIGH--DYMSWIRQPPGEGLEWIGFIFFDGSTN 58  
Db 1 QVQLQESGPGLVKPSETLSLTCTVSGSGFISRTSYMGWIRQPPGKLEWIGNITYTGKTY 60  
QY 59 YNPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLLSEPPYFSSDGMVW 118  
Db 61 YSPSLKSRVTISADTSKNQLSLKSSVTAADTAVYCCARAGYDILLTGYPFYF-----DSW 115  
QY 119 GQGTITVTVSSGGGGSGGGSGGGSGGGSGNFMLTQPPSASGTPGQRVVISCSGSSSDIG 178  
Db 116 GRGTLTVTVSSGGGGSGGGSGGGSGGGG---AQAVLTQPSASGTPGQRTVISCSGSSSNIG 171  
QY 179 SNTVNWYQQLPGTAPKLLIYSNNQRPSPGVDPDRFSGFKSGTISASLVISGLQSEDEADYYCA 238  
Db 172 STTVAWYQQVPGTAPKLLIYSNDRRPPSGVDPDRFSGSKSGTISASLAIISGLQSEDEADYYCA 231  
QY 239 AWDESLNGVVFEGGKVTVL 258  
Db 232 SWDDSPH-VVFGGKLTIVL 250

Search completed: May 13, 2004, 15:43:33  
Job time : 38.199 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 14:50:27 ; Search time 11.6476 Seconds  
(without alignments)  
2130.694 Million cell updates/sec

Title: US-10-072-301-27

Perfect score: 1371

Sequence: 1 QVQLQESGPGLVKPSSETLSL.....AWDESLNGVVFEGGTKVTVL 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	575.5	42.0	268	2	A56446	Ig heavy chain V r
2	548	40.0	249	2	S41374	single chain Fv an
3	532	38.8	233	2	S25752	Ig lambda chain -
4	513	37.4	112	2	D44151	Ig lambda chain V
5	508.5	37.1	149	2	S23626	Ig lambda chain V
6	506	36.9	234	2	S25757	Ig lambda chain -
7	502	36.6	112	2	B44151	Ig lambda chain V
8	501	36.5	112	2	C44151	Ig lambda chain V
9	501	36.5	129	2	S78058	Ig lambda chain pr
10	498.5	36.4	235	2	S25754	Ig lambda chain -
11	498	36.3	110	2	S57408	Ig lambda chain V-
12	498	36.3	216	2	A42193	Ig lambda chain (B
13	497	36.3	130	2	S78057	Ig lambda chain pr
14	496	36.2	112	2	A44151	Ig lambda chain V
15	492.5	35.9	135	2	S78051	Ig heavy chain pre
16	491.5	35.8	155	2	S31511	Ig heavy chain - h
17	490	35.7	233	2	S25744	Ig lambda chain -
18	489	35.7	235	2	S25750	Ig lambda chain -
19	488.5	35.6	155	2	S31512	Ig heavy chain - h
20	488	35.6	233	2	JC5322	p53 specific singl
21	483.5	35.3	140	2	I37782	Ig variable region
22	481	35.1	117	2	S23627	Ig lambda chain pr
23	481	35.1	137	2	S31676	Ig heavy chain V r
24	479.5	35.0	130	2	S31690	Ig heavy chain V r
25	479.5	35.0	146	2	S09711	Ig heavy chain V r
26	479	34.9	110	2	S57428	Ig light chain V-J
27	478	34.9	98	2	S36047	Ig lambda chain -
28	472	34.4	130	2	S30534	Ig heavy chain V r
29	469	34.2	118	2	S20780	Ig heavy chain V r

30	465	33.9	139	2	S31586	Ig heavy chain V r
31	464	33.8	216	2	S03401	Ig lambda chain (K
32	462.5	33.7	112	1	L1HUMM	Ig lambda chain V-
33	461	33.6	111	1	L1HUV0	Ig lambda chain V-
34	458.5	33.4	147	2	S13519	Ig heavy chain V r
35	452	33.0	130	2	S09712	Ig lambda chain V
36	452	33.0	146	1	G1HUH2	Ig heavy chain pre
37	451.5	32.9	129	1	D2HUWA	Ig heavy chain V-I
38	449.5	32.8	121	2	S44113	Ig heavy chain V r
39	449	32.7	98	2	S36048	Ig lambda chain -
40	449	32.7	220	2	A49444	Ig gamma-1 heavy c
41	449	32.7	231	2	B23746	Ig Fab region IV-J
42	448.5	32.7	143	2	B49028	Ig heavy chain V-I
43	448	32.7	235	2	S05270	Ig lambda chain pr
44	447.5	32.6	146	2	S09710	Ig heavy chain V r
45	447	32.6	109	1	L1HUWA	Ig lambda chain V-

ALIGNMENTS

RESULT 1  
A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996  
C/Accession: A56446  
R/Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.  
J. Biol. Chem. 270, 7829-7835, 1995  
A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally identi  
A/Reference number: A56446; MUID:95229583; PMID:7713873  
A/Accession: A56446  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-268 <TAN>  
A/Cross-references: GB:U20617  
C/Keywords: heterotetramer; immunoglobulin

Query Match 42.0%; Score 575.5; DB 2; Length 268;  
Best Local Similarity 47.9%; Pred. No. 1.8e-30;  
Matches 124; Conservative 36; Mismatches 76; Indels 23; Gaps 6;

QY	1	QVQLQESGPGLVKPSSETLSLCTVSSGSGIGHDYMSWRQPPGEGLEWIGFIF-FDGSITNY	59
DB	3	QVQLQESGAEVLKPGASVKLSCTTSGFNKIDTYMHWKORPEQGLEWIGRIAPANGITKY	62
QY	60	NPSLNGRVTISLDTSKQSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWG	119
DB	63	DPKFGKATIAADTSNTAVYLQSLTSEDTAVYYCA-----SYLTRENYWG	111
QY	120	QGTIVTVSSGGSGGGSGGGSGGGSNFMLTQPPS-ASGTPGQRVISCSGSSSDIG	178
DB	112	QGTIVTVS-----SGGGSGGGSDSGGGSDIELTQSPAIMSASLGEKVTMSCRASSS---	163
QY	179	SNTVNMWYQQLPGTAPKLLIYSNNQRPSPGVPDRFSGFSGTSASLVISGLQSEDEADYYCA	238
DB	164	VNFIWYQKSDASPKLWVYTTSHLPQGVPARFSGSGSGNSYSLTISMEGDAATYYCQ	223
QY	239	AWDESLNGVVFEGGTKVTV	257
DB	224	QFTSS--PFTFGSGTKLEI	240

RESULT 2  
S41374  
single chain Fv antibody - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C/Accession: S41374  
R/Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.  
submitted to the EMBL Data Library, January 1994  
A/Description: Construction and functional characterization of a single chain Fv antibod  
A/Reference number: S41374



Query Match	36.94%	Score 506;	DB 2;	Length 234;
Best Local Similarity	82.54%	Pred. No. 4.9e-26;		
Matches	94;	Conservative	12;	Mismatches 8;
			Indels	0;
			Gaps	0;

```

Oy      145 GGGSNFMLTQPPSASGTPGQRVISCSGSSDDIGSNTVNWYQQLPGTAPKLLIYSNNQRP 204
          |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      15  GSWAQSVLTQPPSASGTPGQRVITISCSGSTNIGSNTVNWYQQLPGTAPKLLIYNNNERP 74

```

```

Oy      205  SGVPRFRSGFKSGTASLVISGLQSEDEADYYCAAMDESINGVFGGGTKTVL  258
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      75  SGVPRFRSGSKSGTASLVISGLQSDDEADYYCAAMDSLNGRLLGGGKTLTVL  128
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

## RESULT 7

ig lambda chain V region (BO-09) - human (Fragment)  
C/Species: Homo sapiens (man)  
C/Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 21-Jan-2000  
C/Accession: B44151  
R/Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caochien, R.H.; Graff, R.; Degraw, J.; Pyat  
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992  
A/Title: Human combinatorial antibody libraries to hepatitis B surface antigen.  
A/Reference number: A44151; MUID:92228746; PMID:1373487  
A/Accession: B44151  
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A/Molecule type: mRNA  
A/Residues: 1-112 <ZEB>  
A/Cross-references: GB:M88310; NID:g183954; PIDN:AAA35968.1; PID:g183955  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;14-90/Domain: immunoglobulin homology <IMM>

Query Match	36.6%	Score 502;	DB 2;	Length 112;
Best Local Similarity	87.9%	Pred. No. 4.2e-26;		
Matches 94; Conservative	7;	Mismatches 6;	Indels 0;	Gaps 0;

Oy	152	LTPPSASGTPGQRVISICSGSSSDIGSNTVNWYQQLPGTAPKLLIYSNNQRPSCGYE	DRF	211
		:           :           :           :		
Db	3	LTPPSASGTPGQRTVTISCSGSSSNCTNTVNWYQQLPGAAPKLLIYSNNERPSCGYE	DRF	62

Oy	212	SGFKSGTSASLVISGLQSEDEADYYCAAMDESINGVFEGGKTVTL	258
		:           :	
Db	63	SGSKSGTSASLAISGLQSEDEADYYCEAWDSDLGGPLFGGKTVTL	109

## RESULT 8

I9:lambda chain V region (BO-10) - human (Fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 21-Jan-2000  
 C:Accession: C44151  
 R:Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caochien, R.H.; Graff, R.; Degraw, J.; Pyatt  
 Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992  
 A>Title: Human combinatorial antibody libraries to hepatitis B surface antigen.  
 A:Reference number: A44151, MUID:92228746; PMID:1373487  
 A:Accession: C44151  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-112 <ZEB>  
 A>Note: nucleotide translation not given  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F;14-90/Domain: immunoglobulin homology <IMM>

Query Match	36.5%	Score 501;	DB 2;	Length 112;
Best Local Similarity	87.9%	Pred. No. 4.8e-26;		
Matches 94; Conservative	8;	Mismatches 5;	Indels 0;	Gaps 0;

```

Oy      152 LTQPPSASGTPGQRVISISCSGSSSDIGSNTVNWYQQLPGTAPKLLIYSNNQRPSCGYPDRF 211
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      3   LTQPPSASGTPGQRVTISCSGSTSNIGNTVNWYQQLPGTAPKLLIYSNSERPSGYPDRF 62

```

QY 212 SGFKSGTSASLVISGLQSEDEADYYCAAMDESLNGVVFGGGTKVTVL 258

Db

63 SGSKSGTSASLAISGLQSEDEAEYCYCEAMWDSLQGPVFGGKTIVL 109

## RESULT 9

Ig lambda chain precursor V-J region (clone mAb 67VL) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
 C/Accession: S78058; S23723  
 R/Harindranath, N.  
 submitted to the EMBL Data Library, August 1990

A;Accession: S78058  
A;Molecule type: mRNA  
A;Residues: 1-129 <HAR>  
A;Cross-references: EMBL:X54446; NID:g37923; PIDN:CAA38313.1; PID:g930121  
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins  
Int. Immunol. 3, 865-875, 1991  
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h  
patient.  
A;Reference number: S23716; MUID:92031262; PMID:1718404  
A;Accession: S23723  
A;Molecule type: mRNA  
A;Residues: 19-129 <HAW>  
A;Cross-references: EMBL:X54446  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;1-18/Domain: signal sequence (fragment) #status predicted <SIG>  
F;19-129/Product: Ig lambda chain (fragment) #status predicted <MAT>  
F;33-109/Domain: immunoglobulin homology <IMM>

Query Match	36.5%;	Score 501;	DB 2;	Length 129;
Best Local Similarity	84.2%;	Pred. No. 5.6e-26;		
Matches	96;	Conservative	8;	Mismatches 10;
			Indels	0;
			Gaps	0;

```
QY      145 GGGSNFMLTOPPSASGTPGQRVISCSGSSSDIGSNTVMWYQQLPGTAPKLLIYNNQRP 204
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      15  GSWAQSVLTQPPSASGTPGQRVITISCSGSSNIGSNVYVWYQQLPGTAPKLLIYNNQRP 74
```

```
QY      205  SGVPDRFSGFKSGTSASLVISGIQSEDEADYCAAMDESINGVFGGGTKVTL 256
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      75  SGVPDRFSGSKSGTSASLVISGLRSEDEADYCAAMDSLSGWFEGGKTLTVL 128
```

## RESULT 10

I; Lambda chain - human (fragment)  
 C; Species: Homo sapiens (man)  
 C; Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C; Accession: S25754  
 R; Combriato, G.; Klobeck, H.G.  
 Eur. J. Immunol. 21, 1513-1522, 1991  
 A; Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam  
 A; Reference number: S16439; MUID:91257162; PMID:1904362  
 A; Accession: S25754  
 A; Status: preliminary; translation not shown  
 A; Molecule type: mRNA  
 A; Residues: 1-235 <COM>  
 A; Cross-references: EMBL:X57819; NID:G33737; PIDN:CAA40956.1; PID:g33738  
 C; Superfamily: immunoglobulin V region; immunoglobulin homology  
 C; Keywords: heterotrimer; immunoglobulin  
 F; 150-218/Domain: immunoglobulin homology <IMM>

Query Match	36.4%;	Score 498.5;	DB 2;	Length 235;
Best Local Similarity	85.2%;	Pred. No. 1.5e-25;		
Matches 98;	Conservative 5;	Mismatches 11;	Indels 1;	Gaps 1;

```
QY      145 GGGSNFMLTQPSPASGTPGQRVYSICSSGSSSDIGSNTVMWYQQLPGTAPKLLIYSNNORP 204
        | : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
DB      15 GSWAQSVLTPPSASGTPGQRVLIISCGSSSSNIGNTVMWYQQLPGRAPKLLIHNNQRP 74
```

QY 205 SGVPDRFSGFKSGTSASLVISGLQSEDEADYYCAAMDESLNG-VFEGGKTIVL 258



Db 75 SGVPDRFSGSKSGTSASLAISGLQSEDEADYCAAWDSLNGRVVFGGTGKLTVL 129

RESULT 11  
S57408  
Ig lambda chain V-J region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 10-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S57408  
R/Paterson, G.; Wilson, G.; Kennedy, P.G.E.; Willison, H.J.  
submitted to the EMBL Data Library, June 1995  
A/Description: Analysis of anti-GM1 ganglioside IgM antibodies cloned from motor neuropathic patients  
A/Reference number: S57408  
A/Accession: S57408  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-110 <PAT>  
A/Cross-references: EMBL:X87888, NID:g871268, PIDN:CAA61140.1, PID:g871269  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
F/15-91/Domain: immunoglobulin homology <IMM>

Query Match  
Best Local Similarity 36.3%; Score 498; DB 2; Length 110;  
Matches 95; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
QY 151 MLTOPPSASGTPGQRVVISCSGSSSDIGSNTVNMWYQQLPGTAPKLLIYSNNQRPSPGVPDR 210  
Db 3 VLTQPPSASGTPGQRTVISCSGSSSNIGTNTVNMWYQQLPGTAPKLLIYSNDQCPSPGVPDR 62  
QY 211 FSGFKSGTSASLVISGLQSEDEADYCAAWDESLNGVFGGKTGKTVL 258  
Db 63 FSGSKSGTSASLAISGLQSEDEADYCAAWDYSLNGVVFGGGTGKLTVL 110

RESULT 12  
A42193  
Ig lambda chain (BJP-DIA) - human  
N/Alternate names: amyloid fibril protein AL-DIA; Bence Jones protein; Ig lambda chain (C)  
C/Species: Homo sapiens (man)  
C/Date: 03-Mar-1994 #sequence\_revision 07-Apr-1994 #text\_change 21-Jan-2000  
C/Accession: A42193; S18297  
R/Klaefki, H.W.; Kratzin, H.D.; Pick, A.I.; Eckart, K.; Karas, M.; Hilschmann, N.  
Biochemistry 31, 3265-3272, 1992  
A/Title: Complete amino acid sequence determinations demonstrate identity of the urinary  
A/Reference number: A42193; MUID:92207944; PMID:1554711  
A/Accession: A42193  
A/Molecule type: protein  
A/Residues: 1-216 <KLA>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin; pyroglutamic acid  
F/131-199/Domain: immunoglobulin homology <IMM>  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
Query Match  
Best Local Similarity 36.3%; Score 498; DB 2; Length 216;  
Matches 93; Conservative 8; Mismatches 7; Indels 0; Gaps 0;  
QY 151 MLTOPPSASGTPGQRVVISCSGSSSDIGSNTVNMWYQQLPGTAPKLLIYSNNQRPSPGVPDR 210  
Db 3 VLTQPPSASGTPGQRTVISCSGSSSNIGSNTVNMWYQQLPGTAPKLLIYSNNQRPSPGVPGR 62  
QY 211 FSGFKSGTSASLVISGLQSEDEADYCAAWDESLNGVFGGKTGKTVL 258  
Db 63 FSGSKSGTSASLAISGLQSEDEADYCATWDSVNGWVFGGTGKLTVL 110

RESULT 13  
S78057  
Ig lambda chain precursor V-J region (clone mAb 61VL) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C/Accession: S78057; S23722

R/Harindranath, N.  
submitted to the EMBL Data Library, August 1990  
A/Reference number: S78051  
A/Accession: S78057  
A/Molecule type: mRNA  
A/Residues: 1-130 <HAR>  
A/Cross-references: EMBL:X54438; NID:g37920; PIDN:CAA38307.1; PID:g37921  
R/Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Butastero, S.E.; Wilder, R.L.; Nocklin  
Int. Immunol. 3, 865-875, 1991  
A/Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and  
patient.  
A/Reference number: S23716; MUID:92031262; PMID:1718404  
A/Accession: S23722  
A/Molecule type: mRNA  
A/Residues: 20-130 <HAW>  
A/Cross-references: EMBL:X54438  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F/1-19/Domain: signal sequence #status predicted <SIG>  
F/20-130/Product: Ig lambda chain (fragment) #status predicted <MAT>  
F/34-110/Domain: immunoglobulin homology <IMM>

Query Match  
Best Local Similarity 36.3%; Score 497; DB 2; Length 130;  
Matches 94; Conservative 9; Mismatches 11; Indels 0; Gaps 0;  
QY 145 GGGSNFMLTOPPSASGTPGQRVVISCSGSSSDIGSNTVNMWYQQLPGTAPKLLIYSNNQRP 204  
Db 16 GSAQSVLTQPPSASGTPGQRTVISCSGSSSNIGSNTVNMWYQQLPGTAPKLLIYSNNQRP 75  
QY 205 SGVPDRFSGSKSGTSASLVISGLQSEDEADYCAAWDESLNGVFGGKTGKTVL 258  
Db 76 SGVPDRFSGSKSGTSASLAISGLQSEDEADYCATWDSLSAVIFGGGTGKLTVL 129

RESULT 14  
A44151  
Ig lambda chain V region (BO-08) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 21-Jan-2000  
C/Accession: A44151  
R/Zebedee, S.L.; Barbash II, C.F.; Hom, Y.L.; Caotchien, R.H.; Graff, R.; Degraw, J.; Pya  
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992  
A/Title: Human combinatorial antibody libraries to hepatitis B surface antigen.  
A/Reference number: A44151; MUID:92228746; PMID:1373487  
A/Accession: A44151  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: protein  
A/Residues: 1-112 <ZEB>  
A/Note: nucleotide translation not given  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/14-90/Domain: immunoglobulin homology <IMM>  
Query Match  
Best Local Similarity 36.2%; Score 496; DB 2; Length 112;  
Matches 92; Conservative 10; Mismatches 5; Indels 0; Gaps 0;  
QY 152 LTQPPSASGTPGQRVVISCSGSSSDIGSNTVNMWYQQLPGTAPKLLIYSNNQRPSPGVPDRF 211  
Db 3 LTQPPSASGTPGQRTVISCSGSSSNIGTNTVNMWYQQLPGTAPKLLIYSNNQRPSPGVPDRF 62  
QY 212 SGFKSGTSASLVISGLQSEDEADYCAAWDESLNGVFGGKTGKTVL 258  
Db 63 SGSKAGTSASLAISGLQSEDEADYCEAWDNLHGPVFGGTGKLTVL 109

RESULT 15  
S78051  
Ig heavy chain precursor V-D-J region (clone mAb 61VH) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C/Accession: S78051; S23716



R;Harindranath, N.  
submitted to the EMBL Data Library, August 1990

A;Reference number: S78051

A;Accession: S78051

A:Molecule type: mRNA

A;Residues: 1-135 <HAR>

A;Cross-references: EMBL:X54437; NID:g37814; PIDN:CAA38306.1; PID:g930117

R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins

Int. Immunol. 3, 865-875, 1991

A/Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and high-affinity anti-CD4 monoclonal antibodies.

A:Reference number: S23716; MUID:92031262; PMID:17184044

A;Accession: S23716

A:Accession: S23116  
A:Molecule type: mRNA

A;Residues: 13-111 <HAW>

A;CROSS-references: EMBL:X54437

C; Superfamily: immunoglobulin V region; immunoglobulin homology

**C; Keywords:** immunoglobulin C; superlativity; immunologic

```
c:\keywoks> runningjobin
F:\1-13\Domain: signal sequence (fragment) #status predicted <SIG>
```

F:14-135/Product: 19 heavy chain (fragment) #status predicted <MAT>  
F:1-13/Domain: signal sequence #status predicted <SIG>

F:27-111/Domains: immunoglobulin homology <IMM>

Query Match	35.98; Score 492.5; DB 2; Length 135;
-------------	---------------------------------------

Best Local Similarity 73.8%; Pred. No. 2.1e-25;  $\Delta$

```

2000 2000a 2000a1 2000a1.1 2000a1.1.1 2000a1.1.1.1 2000a1.1.1.1.1
Matches 96; Conservative 12; Mismatches 13; Indels 9; Gaps 2;

```

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSI--GHDYWSWIRQPPGEGLEWIGIFFDGSTN 58

db 13 OLOESGPGLVKPSSETLSLTCTVSGGSIIRGSHYWGWIROPKGLEWIGSIYSGNTY 72

QY 59 YNPSLNGRVTISLDTSKNQLSLRLTSVTADTAVYFCARLKGAWLLSEPPYSSDGMVW 118

```

Db      73 FNP SLKSRVTISVDTSKNQFSLKLSSVTADTAVYYCARL-----GPD DYTLDGMDVW 125

```

QY 119 GQGTIVTVSS 128

Db 126 GGGTIVTVSS 135

Search completed: May 13, 2004, 15:08:43  
Job time : 11.6476 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:01 ; Search time 7.26408 Seconds  
(without alignments)  
1849.388 Million cell updates/sec

Title: US-10-072-301-27

Perfect score: 1371

Sequence: 1 QVQLQESGPGLVKPSSETLSL.....AMDESLNGVVGSGTKVTVL 258

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462.5	33.7	112	1	LV1H_HUMAN P06887 homo sapien
2	461	33.6	111	1	LV1A_HUMAN P01699 homo sapien
3	452	33.0	146	1	HV2I_HUMAN P06331 homo sapien
4	451.5	32.9	129	1	HV2F_HUMAN P01824 homo sapien
5	447	32.6	109	1	LV1F_HUMAN P04208 homo sapien
6	441	32.2	130	1	LV1G_HUMAN P06316 homo sapien
7	436	31.8	111	1	LV1D_HUMAN P01702 homo sapien
8	433.5	31.6	112	1	LV1B_HUMAN P01700 homo sapien
9	426	31.1	111	1	LV1C_HUMAN P01701 homo sapien
10	413	30.1	109	1	LV1I_HUMAN P06888 homo sapien
11	408.5	29.8	117	1	HV2G_HUMAN P01825 homo sapien
12	382	27.9	111	1	LV2G_HUMAN P01710 homo sapien
13	372	27.1	111	1	LV2F_HUMAN P01709 homo sapien
14	370.5	27.0	137	1	HV46_MOUSE P01822 mus musculu
15	367.5	26.8	113	1	HV47_MOUSE P01823 mus musculu
16	360.5	26.3	112	1	LV2K_HUMAN P04209 homo sapien
17	360	26.3	103	1	LV1E_HUMAN P01703 homo sapien
18	360	26.3	111	1	LV2B_HUMAN P01705 homo sapien
19	358	26.1	111	1	LV2D_HUMAN P01707 homo sapien
20	357	26.0	111	1	LV6D_HUMAN P06318 homo sapien
21	356	26.0	111	1	LV2H_HUMAN P01711 homo sapien
22	352	25.7	111	1	LV2C_HUMAN P01706 homo sapien
23	347.5	25.3	110	1	LV2J_HUMAN P01713 homo sapien
24	347.5	25.3	131	1	LV6E_HUMAN P06319 homo sapien
25	347	25.3	111	1	LV2I_HUMAN P01712 homo sapien
26	346.5	25.3	112	1	LV6A_HUMAN P01721 homo sapien
27	346.5	25.3	144	1	HV43_MOUSE P01819 mus musculu
28	344.5	25.1	116	1	HV60_MOUSE P18531 mus musculu
29	344	25.1	109	1	LV2E_HUMAN P01708 homo sapien
30	342	24.9	111	1	LV3B_HUMAN P80748 homo sapien
31	336	24.5	106	1	LV4A_HUMAN P01715 homo sapien
32	336	24.5	111	1	LV2A_HUMAN P01704 homo sapien
33	335	24.4	106	1	LV4B_HUMAN P01716 homo sapien

34	332	24.2	106	1	LV4E_HUMAN P06889 homo sapien
35	329.5	24.0	116	1	HV6I_MOUSE P18532 mus musculu
36	328	23.9	108	1	LV5A_HUMAN P01719 homo sapien
37	324	23.6	107	1	LV4C_HUMAN P01717 homo sapien
38	324	23.6	111	1	LV6C_HUMAN P06317 homo sapien
39	324	23.6	117	1	HV62_MOUSE P18533 mus musculu
40	321	23.4	135	1	HV02_XENLA P20957 xenopus lae
41	313.5	22.9	112	1	LV6B_HUMAN P01722 homo sapien
42	310	22.6	120	1	HV2B_HUMAN P01815 homo sapien
43	307.5	22.4	125	1	HV2D_HUMAN P01817 homo sapien
44	305	22.2	108	1	LV3A_HUMAN P01714 homo sapien
45	304	22.2	111	1	LV7A_HUMAN P01720 homo sapien

ALIGNMENTS

RESULT 1					
LV1H_HUMAN		STANDARD;	PRT;	112 AA.	
ID	LV1H_HUMAN				
AC	P06887;				
DT	01-JAN-1988 (Rel. 06, Created)				
DT	01-JAN-1988 (Rel. 06, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Ig lambda chain V-I region MEM.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=85257662; PubMed=2410269;				
RA	Mihaesco E., Roy J.P., Congy N., Peran-Rivat L., Mihaesco C.;				
RT	"The amino acid sequence of a lambda light chain presenting abnormal				
RL	physicochemical and antigenic features.";				
RL	Eur. J. Biochem. 150:349-357(1985).				
CC	-I- MISCELLANEOUS: RESIDUES 33-36 AND SOME OF THE SEQUENCED PEPTIDES				
CC	WERE POSITIONED BY HOMOLOGY.				
CC	-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+				
CC	MARKERS.				
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.				
DR	PIR; A25479; LIHUM.				
DR	HSSP; P01703; 7FAB.				
DR	GO; GO:0005576; C:extracellular; NAS.				
DR	GO; GO:0003823; F:antigen binding; NAS.				
DR	GO; GO:0006955; P:immune response; NAS.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig; 1.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS0835; IG LIKE; 1.				
KW	Immunoglobulin V region; Monoclonal antibody;				
KW	Pyroliidone carboxylic acid.				
FT	DOMAIN 1 106 IG-LIKE.				
FT	MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.				
FT	DISULFID 22 90 BY SIMILARITY.				
FT	NON TER 112 112				
FT	SEQUENCE 112 AA; 11789 MW; 748124F079CFFBE4 CRC64;				
Query Match					
Best local Similarity 33.7%; Score 462.5; DB 1; Length 112;					
Matches 90; Conservative 8; Mismatches 10; Indels 1; Gaps 1;					
Oy	151 MLTQPPSASGTPGQRVISICSSSSSDIGSN-TVNWYQQLPGTAPKLLIYSNMQRPSGVPD	209			
Db	3 VLTQPPSASGTPGQRVITISCGSSSNVGSNZPAYWYQQLPGTAPKLLIYNYNQRPSGVPD	62			
Oy	210 RFSGFKSGTSASLVISGLQSEDEADYYCAAMDESLNGVVGSGTKVTVL	258			
Db	63 RFSASRSSTASLAISGLQSEDEADYYCAAMWDSLDGYVFGTGTKTVTVL	111			
RESULT 2					

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LV1A_HUMAN
ID LV1A_HUMAN STANDARD; PRT; 111 AA.
AC P01659;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-I region VOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023790; PubMed=8093332;
RA Engelhard M., Hilschmann N.;
RT "Pattern of antibody structure. The amino acid sequence of a
RT monoclonal immunoglobulin L-chain of lambda-type, subgroup 1
RT (Bence-Jones-protein Vor.). A contribution to the elucidation of the
RT origin of antibody specificity."
RL Hoppe-Seyler's Z. Physiol. Chem. 356:1413-1444(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE OZ+ MARKER.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01962; L1HUV0.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein;
KW Pyrolydione carboxylic acid.
FT DOMAIN 1 105 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 89 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11514 MW; 21D9F64250DFC8E0 CRC64;

Query Match
Best Local Similarity 33.6%; Score 461; DB 1; Length 111;
Matches 87; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 151 MLTQPPSASGTPGQRVVISCSGSSSDISNTVNMVYQQLPGTAPKLLIYSNMORPSGVDPDR 210
Db 3 VLTQPPSASGTPGQRVVISCSGSGNFIDGRNSVNMVYQVHPTAPRLLIYSSDQRSSGVDPDR 62
QY 211 FSGFKSGTSASLVISGLQSEDEADYYCAWDESLNGVVFGGGKTVTL 258
Db 63 FSGSKSGTSASLVISGLQSENEADYFCATWDSLDGPVFGGKTVTL 110

RESULT 3
HV2I_HUMAN STANDARD; PRT; 146 AA.
ID HV2I_HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85205332; PubMed=3922855;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT repeat sequence in 5' flanking region."
RL Gene 33:181-189(1985).
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DR PIR; A02101; G1HUM2.
DR HSSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.
FT DOMAIN 20 117 V SEGMENT.
FT DOMAIN 118 127 D SEGMENT.
FT DOMAIN 128 146 J SEGMENT.
FT DISULFID 42 115 BY SIMILARITY.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Query Match
Best Local Similarity 33.0%; Score 452; DB 1; Length 146;
Matches 93; Conservative 8; Mismatches 23; Indels 6; Gaps 3;

QY 1 QVQLQESGPGLVKPSPTSLTCTVSGSIGHDYMWIRQPPGEGLEWIGFIFDGSTNYN 60
Db 21 QVQLQGWAGLVKPSPTSLTCAVFGSFGYSWIRQPPGRLGLEWIGFIFDGSTNYK 80
QY 61 PSINGRVTISLDTFSKNQLSLRTSVTAADTAVYFCAR--LKGAWLISEPPYFSSDGMVW 118
Db 81 TSLKSRVTISLDTFSKNLFSKLSSVTADTAVYVCARGLRGW--NDVDY--GMDVW 136
QY 119 GQGTVTVSS 128
Db 137 GQGTVTVSS 146

RESULT 4
HV2F_HUMAN STANDARD; PRT; 129 AA.
ID HV2F_HUMAN STANDARD; PRT; 129 AA.
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82222235; PubMed=6806818;
RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
RT immunoglobulin D."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02099; D2HUMA.
DR HSSP; P01825; 7FAB.
DR GlycoSuiteDB; P01824;
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 113 IG-LIKE.
FT NON_TER 129 129
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SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;
Query Match 32.9%; Score 451.5; DB 1; Length 129;
Best Local Similarity 65.9%; Pred. No. 2.4e-25;
Matches 89; Conservative 15; Mismatches 18; Indels 13; Gaps 3;
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHD--YMSWIROPGEGLWIGFIFFDGSTN 58
Db 1 RLQLQESGPGLVKPSSETLSLTCTVSGGPIRRTGYWGWIRPPGKLEWIGGVYTGSIY 60
QY 59 YNPSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLLSEPPYF-----SSD 113
Db 61 YNPSLRGRVTISVDTSRNQFSILNRSMASADTAMYCAR-----GNPPPYDIDGTGSD 114
QY 114 GMDVWGQGTVTVSS 128
Db 115 GIDVWGQGTVTWVSS 129
RESULT 5
LV1F_HUMAN STANDARD; PRT; 109 AA.
ID LV1F_HUMAN
AC P04208;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83221661; PubMed=6407018;
RA Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
RT "Complete covalent structure of a human immunoglobulin D: sequence of
RT the lambda light chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
DR PIR; A01967; L1HUMA.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 97 V SEGMENT.
FT DOMAIN 98 109 J SEGMENT.
FT DISULFID 22 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;
Query Match 32.6%; Score 447; DB 1; Length 109;
Best Local Similarity 81.5%; Pred. No. 4.2e-25;
Matches 88; Conservative 7; Mismatches 11; Indels 2; Gaps 1;
QY 151 MLTQPPSASGTPGQRVISCSGSSSDIGSNTVMWYQQLPGTAPKLLIYSNNORPSGVDR 210
Db 3 VLTQPPSASGTPGQRVITISCFGSSSNIGRYVYVWYQQLPGTAPKLLIYKDNQRPSPGVDR 62
QY 211 FSGFKSGTSASLVISGLQSEDEADYCAAWDESLNGVFGGKTKVTVL 258
Db 63 FSGSKSGTSASLAISGLRSEDEADYCAAWDDSL--WVFGGKTKLTVL 108
RESULT 6
LV1G_HUMAN STANDARD; PRT; 130 AA.
ID LV1G_HUMAN
AC P06316;
DT 01-JAN-1988 (Rel. 06, Created)
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DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region BL2 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85062823; PubMed=6095199;
RA Tsujimoto Y., Croce C.M.;
RT "Molecular cloning of a human immunoglobulin lambda chain variable
RT sequence.";
RL Nucleic Acids Res. 12:8407-8414(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC -----
DR EMBL; X01147; CAA25598.1; .
DR PIR; A01966; L1HUBL.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 130 IG LAMBDA CHAIN V-I REGION BL2.
FT DOMAIN 20 115 V SEGMENT.
FT DOMAIN 116 130 J SEGMENT.
FT DISULFID 41 108 BY SIMILARITY.
FT NON TER 130 130
SQ SEQUENCE 130 AA; 13564 MW; FA44BB17D3A55EBF CRC64;
Query Match 32.2%; Score 441; DB 1; Length 130;
Best Local Similarity 71.1%; Pred. No. 1.3e-24;
Matches 81; Conservative 17; Mismatches 16; Indels 0; Gaps 0;
QY 145 GGSNFMLTQPPSASGTPGQRVISCSGSSSDIGSNTVMWYQQLPGTAPKLLIYSNNORP 204
Db 16 GSMAQSVLTQPPSVSAAPGQKVTISCSGSSSNIGNDYVSWYQVPGTAPKLLIYDNNRPF 75
QY 205 SGVDRFSGFKSGTSASLVISGLQSEDEADYCAAWDESLNGVFGGKTKVTVL 258
Db 76 SGIDRFSGSKSGTSATLGIQTGDEADYCCGTWNNSLSGWVFGGKTKLTVL 129
RESULT 7
LV1D_HUMAN STANDARD; PRT; 111 AA.
ID LV1D_HUMAN
AC P01702;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-I region NIG-64.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83186114; PubMed=6404900;
RA Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA Shimizu A.;
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RT "Comparative studies on the structure of the light chains of human  
immunoglobulins. IV. Assignment of a subgroup.",  
J. Biochem. 93:421-429(1983).  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01965; LIHUNG.  
DR HSSP; P01703; 7FAB.

DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Pyridone carboxylic acid.  
FT DOMAIN 1 105 IG-LIKE.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 89 BY SIMILARITY.  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;

Query Match 31.8%; Score 436; DB 1; Length 111;  
Best Local Similarity 75.0%; Pred. No. 2.5e-24;  
Matches 81; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 151 MLTPPSASGTPGQRVISICSGSSSDIGSNTVNMVYQQLPGTAPKLLIYSNNQRPSPGVDPDR 210  
DB 3 VLTQPPSVSAAPGQKVTISCSGSSNGTGNVYVYQQLPGTAPKLLIYRDKRPSGVDPDR 62  
QY 211 FSGFKSGTSASLVISGLQSEDEADYYCAAMDESLNGVFGGKTIVTL 258  
DB 63 FSGSKSGTSATLGTITGLTGDEADYYCGTWDSLSVGMFGGKTIVTL 110

RESULT 8  
LV1B\_HUMAN STANDARD; PRT; 112 AA.  
ID LV1B\_HUMAN  
AC P01701;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-I region HA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71103824; PubMed=5532227;  
RA Shinoda T., Titani K., Putnam F.W.;  
RT "Amino acid sequence of human lambda chains. II. Chymotryptic  
peptides and sequence of protein Ha.";  
RL J. Biol. Chem. 245:4475-4487(1970).  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01963; LIHUA.  
DR HSSP; P01703; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein;  
KW Pyridone carboxylic acid.  
FT DOMAIN 1 106 IG-LIKE.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 90 BY SIMILARITY.  
FT NON\_TER 112 112  
SQ SEQUENCE 112 AA; 11896 MW; 8D73378F3F5CD039 CRC64;

Query Match 31.6%; Score 433.5; DB 1; Length 112;  
Best Local Similarity 77.1%; Pred. No. 3.8e-24;  
Matches 84; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 151 MLTPPSASGTPGQRVISICSGSSSDIGSNTVNMVYQQLPGTAPKLLIYSNNQRPSPGVDPDR 209  
DB 3 VLTQPPSVSAAPGQKVTISCSGSSNGTGNVYVYQQLPGTAPKLLIYRDKRPSGVDPDR 62  
QY 210 FSGFKSGTSASLVISGLQSEDEADYYCAAMDESLNGVFGGKTIVTL 258  
DB 63 FSGSKSGTSATLGTITGLTGDEADYYCATWDSLSNAVFGGKTIVTL 111

RESULT 9  
LV1C\_HUMAN STANDARD; PRT; 111 AA.  
ID LV1C\_HUMAN  
AC P01701;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-I region NEW.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=69060892; PubMed=4177823;  
RA Langer B., Steinmetz-Kayne M., Hilschmann N.;  
RT "The complete amino acid sequence of Bence Jones protein New (lambda-  
type). Subgroups in the variable part of immunoglobulin L-chains of  
the lambda-type.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 349:945-951(1968).  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01964; LIHUNW.  
DR HSSP; P01703; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein;  
KW Pyridone carboxylic acid.  
FT DOMAIN 1 105 IG-LIKE.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 89 BY SIMILARITY.  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11453 MW; AABCBCA3C49F2AD3 CRC64;

Query Match 31.1%; Score 426; DB 1; Length 111;  
Best Local Similarity 72.2%; Pred. No. 1.3e-23;  
Matches 78; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY 151 MLTPPSASGTPGQRVISICSGSSSDIGSNTVNMVYQQLPGTAPKLLIYSNNQRPSPGVDPDR 210  
DB 3 VLTQPPSVSAAPGQKVTISCSGSSNGTGNVYVYQQLPGTAPKLLIYRDKRPSGVDPDR 62  
QY 211 FSGFKSGTSASLVISGLQSEDEADYYCAAMDESLNGVFGGKTIVTL 258  
DB 63 ISASKSGTSATLGTITGLTGDEADYYCATWDSLSNAVFGGKTIVTL 110

RESULT 10  
LV1I\_HUMAN STANDARD; PRT; 109 AA.  
ID LV1I\_HUMAN  
AC P06888;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ig lambda chain V-I region EPS.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=86000126; PubMed=3929803;  
RA Toft K.G., Sletten K., Husby G.;  
RT "The amino-acid sequence of the variable region of a carbohydrate-  
RT containing amyloid fibril protein EPS (immunoglobulin light chain,  
RT type lambda).";  
RL Biol. Chem. Hoppe-Seyler 366:617-625(1985).  
CC -I- MISCELLANEOUS: RESIDUES 1-2, 56-62, AND 74-78 AND THE SEQUENCED  
CC PEPTIDES WERE POSITIONED BY HOMOLOGY.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A24656; LIHUEP.  
DR HSSP; P01703; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Amyloid; Glycoprotein.  
FT DOMAIN 1 105 IG-LIKE.  
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .).  
FT DISULFID 22 89 BY SIMILARITY.  
FT NON\_TER 109 109  
SQ SEQUENCE 109 AA; 11414 MW; 556A313E24D5AC73 CRC64;  
  
Query Match 30.1%; Score 413; DB 1; Length 109;  
Best Local Similarity 73.1%; Pred. No. 1e-22;  
Matches 79; Conservative 12; Mismatches 15; Indels 2; Gaps 1;  
  
QY 151 MLTQPPSASGTPGQRVISICSGSSSDIGSNTVMYQQLPGTAPKLLIYSNNQRPSPGVDR 210  
Db 3 VLTQPPSLSAAPGQRVISICSGSSSNIGKNYVDWYQQLPGTAPKLLIFNNKRPSPGIPDR 62  
  
QY 211 FSGFKSGTSASLVISGLQSEDEADYCCAWDSESLNGVFGGTVTL 258  
Db 63 FSGSKSGTSATLIGTGLGTGDEAIYCGTWDNRRS--VFGGTVTVV 108  
  
RESULT 11  
HV2G\_HUMAN STANDARD; PRT; 117 AA.  
ID HV2G\_HUMAN  
AC P01825;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-II region NEMW.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=77242302; PubMed=407927;  
RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;  
RT "Amino acid sequence of the VH region of a human myeloma  
RT immunoglobulin (IgG New).";  
RL Biochemistry 16:3412-3420(1977).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.  
RX MEDLINE=78066916; PubMed=618887;  
RA Saul F.A., Amzel L.M., Poljak R.J.;  
RT "Preliminary refinement and structural analysis of the Fab fragment  
RT from human immunoglobulin new at 2.0-A resolution.";  
RL J. Biol. Chem. 253:585-597(1978).  
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA

CC PROTEIN.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A90404; GIHUMN.  
DR PDB; 7FAB; 31-JAN-94.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.  
FT DOMAIN 1 111 IG-LIKE.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT STRAND 3 7  
FT STRAND 11 12  
FT TURN 14 15  
FT STRAND 18 25  
FT TURN 30 31  
FT STRAND 33 39  
FT TURN 41 42  
FT STRAND 46 51  
FT TURN 53 54  
FT STRAND 57 59  
FT HELIX 61 63  
FT TURN 64 66  
FT STRAND 67 72  
FT TURN 73 76  
FT STRAND 77 82  
FT HELIX 87 89  
FT STRAND 91 98  
FT STRAND 104 107  
FT STRAND 111 115  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;  
  
Query Match 29.8%; Score 408.5; DB 1; Length 117;  
Best Local Similarity 59.2%; Pred. No. 2.2e-22;  
Matches 77; Conservative 22; Mismatches 16; Indels 15; Gaps 2;  
  
QY 1 QVQLQESGPGLVKPSSETISLTCTVSGSIGHDYMSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
Db 1 QVQLQSGPGLVLRPSQTLTLCTVSGSTFSNDYYTWVQPPGRGLEWIGVVFYHGTSDDT 60  
  
QY 61 PSINGRVTISLDTSKNQSLRLTSVTAADTAVYFCAR--LKGAWLSEPPYFSSDGMQVW 118  
Db 61 TPLRSRVMTLVDTSKNQPSRLSSVTAAADTAVYVCARNLIAGC-----IDVW 107  
  
QY 119 GQGTVTVSS 128  
Db 108 GQGS LTVSS 117  
  
RESULT 12  
LV2G\_HUMAN STANDARD; PRT; 111 AA.  
ID LV2G\_HUMAN  
AC P01710;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-II region BO.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71103825; PubMed=5532228;  
RA Wikler M., Putnam F.W.;  
RT "Amino acid sequence of human lambda chains. 3. Tryptic peptides,  
RT chymotryptic peptides, and sequence of protein Bo.";  
RL J. Biol. Chem. 245:4488-4507(1970).



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CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01976; L2HUBO.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein;
KW Pyrrolidone carboxylic acid.
FT DOMAIN 1 106 IG-LIKE.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11785 MM; 92F5A1BF72421BAC CRC64;

Query Match
Best Local Similarity 27.9%; Score 382; DB 1; Length 111;
Matches 73; Conservative 19; Mismatches 14; Indels 2; Gaps 2;

QY 152 LTQPPSASGTPGQRVISCSGSSSDIGSNT-VNMYQQLPGTAPKLLIYSNNQRPSPGVPDR 210
DB 4 LTQPPSASGSPGQSVTISCTGTSSDVGDKNKYSWYQHPGRAPKLVIFEVSGRPSGVPDR 63

QY 211 FSGFKSGTSASLVISGLQSEDEADYCYCAMDESLNGVFGGTRKTVL 258
DB 64 FSGSKSGNTASLTVSGLQAEDEADYCYSSYVDN-NNFVFGGTRKTVL 110

RESULT 13
LV2F_HUMAN
ID LV2F_HUMAN STANDARD; PRT; 111 AA.
AC P01709;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region MGC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75013804; PubMed=4415202;
RA Felt J.W., Deutsch H.F.;
RT "Primary structure of the Mcg lambda chain.";
RL Biochemistry 13:4102-4114(1974).
RN [2]
RP LAMBDA CHAIN GENES.
RX MEDLINE=76093781; PubMed=812801;
RA Felt J.W., Deutsch H.F.;
RT "A new lambda-chain gene.";
RL Immunochimistry 12:643-652(1975).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
RA Panagiotopoulos N.;
RT "Rotational allomerism and divergent evolution of domains in
RT immunoglobulin light chains.";
RL Biochemistry 14:3953-3961(1975).
RN [4]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=90133913; PubMed=2515285;
RA Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
RT "Three-dimensional structure of a light chain dimer crystallized in
RT water. Conformational flexibility of a molecule in two crystal
RT forms.";
RL J. Mol. Biol. 210:601-615(1989).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
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CC -1- MISCELLANEOUS: THE MCG-TYPE C REGION APPEARS TO BE CORRELATED WITH
CC A VERY UNUSUAL V-REGION SUBSTITUTION, 103-THR ABOVE FOR GLY,
CC SUGGESTING THAT THE V-C JOINING MECHANISM IS NOT ALWAYS RANDOM.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+
CC MARKERS.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90381; L2HDMC.
DR PDB; 2MCG; 15-JUL-92.
DR PDB; 1A8J; 17-JUN-92.
DR PDB; 1DCL; 15-MAY-97.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure;
KW Pyrrolidone carboxylic acid.
FT DOMAIN 1 108 IG-LIKE.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT STRAND 5 5
FT STRAND 10 12
FT STRAND 18 23
FT TURN 26 32
FT STRAND 36 40
FT TURN 42 43
FT STRAND 50 51
FT TURN 52 54
FT STRAND 55 55
FT TURN 62 63
FT STRAND 66 68
FT STRAND 72 77
FT HELIX 82 84
FT STRAND 86 93
FT STRAND 99 101
FT STRAND 105 109
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11558 MM; 7CC1D6E2FA377BA CRC64;

Query Match
Best Local Similarity 27.1%; Score 372; DB 1; Length 111;
Matches 74; Conservative 16; Mismatches 16; Indels 2; Gaps 2;

QY 152 LTQPPSASGTPGQRVISCSGSSSDIGS-NTVNMWYQQLPGTAPKLLIYSNNQRPSPGVPDR 210
DB 4 LTQPPSASGSLGQSVTISCTGTSSDVGGYVSWYQHPGRAPKLVIFEVNKRPSGVPDR 63

QY 211 FSGFKSGTSASLVISGLQSEDEADYCYCAMDESLNGVFGGTRKTVL 258
DB 64 FSGSKSGNTASLTVSGLQAEDEADYCYSSYEGSDN-FVFGTGTXTVL 110

RESULT 14
HV46_MOUSE
ID HV46_MOUSE STANDARD; PRT; 137 AA.
AC P01822;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig heavy chain V region MOPC 315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89238351; PubMed=2497341;
RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
RT gene segment.";
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Db 40 QVKLQSGGGLVKGPGSLKLSCAASGSDFSRYMWSWVRQAPGKLEWIGETINDSSTINY 99  
QY 60 NPSLNGRVTISLDTSKNQLSLRTSVTAADTAVYFCARLKGAWLSEPPYSSDGMVWG 119  
Db 100 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYICARAS-----YYGHS--YWG 148  
QY 120 QGTTVTVSSGGGSGGGSGGGSGGSGNFMLTQ-PPASGTPGQRVISCSGSSSDIG 178  
Db 149 QGTTVTVS-----SGGGSGGGSGGGSGGSDIELTQSPASLSASVGETVTITCRASGNI-- 201  
QY 179 SNTVNMWYQQLPGTAPKLLIYSNNQRPSPGVDPDRFGSGFKSGTSASLVIISGLQSEDEADYCA 238  
Db 202 HNYLAWYQOKGKSPOLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSIQPEDFGSYTCQ 261  
QY 239 -AMDESLNGVFEGGGTXTV 257  
Db 262 HFW---TTPYTFGGGTXLEI 278

RESULT 2  
Q7QM2  
ID Q7QM2 PRELIMINARY; PRT; 243 AA.  
AC Q7QM2;  
DT 01-OCT-2003 (Tremblrel. 25, Created)  
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE SCFV 6H8 protein (Fragment).  
GN SCFV 6H8.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Balb/C;  
RA Peter J.C., Eftekhari P., Billiard P., Wallukat G.;  
RT "scfv single chain antibody variable fragment as inverse agonist for  
RT the beta-2 adrenergic receptor."  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ574851; CAB00495.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 243 AA; 25976 MW; BEFF64D2DCFAF76 CRC64;

Query Match 38.8%; Score 531.5; DB 11; Length 243;  
Best Local Similarity 45.0%; Pred. No. 8e-34;  
Matches 117; Conservative 40; Mismatches 76; Indels 27; Gaps 8;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGFI-FDGSSTNY 59  
Db 1 QVQLQSGSELVRPGASVKLSCKASGYTFTTYMMHWKQRHGGGLEWIGNITYPGSGITNY 60  
QY 60 NPSLNGRVTISLDTSKNQLSLRTSVTAADTAVYFCARLKGAWLSEPPYSSDGMVWG 119  
Db 61 DEKFKNKGILTVDTSSSTAYMHLSSLASDSAVYYCAR-----GGRGLDVG 107  
QY 120 QGTTVTVSSGGGSGGGSGGGSGGSGNFMLTQPPSA-SGTPGQRVISCSGSSSDIG 178  
Db 108 AGTTLTVS-----SGGGSGGGSGGGSGGSDIQMTQSSSSFSVSLGDRVITITCK-ASEDI- 160  
QY 179 SNTVNMWYQQLPGTAPKLLIYSNNQRPSPGVDPDRFGSGFKSGTSASLVIISGLQSEDEADYCA 238  
Db 161 YNRLAWYQOKPGNAPRLILSGATSLTGVPSRFSGSGSGKDYTLISLTQTEDEVATYYCQ 220  
QY 239 A-WDESLNGVFEGGGTXTV 257  
Db 221 QYWSIR---TFGGGTXLEI 236

RESULT 3  
Q921A6 PRELIMINARY; PRT; 241 AA.  
ID Q921A6  
AC Q921A6;  
DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Anti-CEA 79 single chain Fv fragment (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98170165; Pubmed=9509426;  
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,  
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;  
RT "Cloning and characterization of cDNAs encoding VH and VL of a  
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and  
RT generation of a single-chain Fv molecule (scfv).";  
RL Mol. Cells 7:816-819(1997).  
DR EMBL; U88067; AAB48044.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_2.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

Query Match 37.1%; Score 508.5; DB 11; Length 241;  
Best Local Similarity 46.0%; Pred. No. 5e-32;  
Matches 120; Conservative 34; Mismatches 76; Indels 31; Gaps 11;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYMSWIRQPPGEGLEWIGFI-FDGSSTNY 59  
Db 1 QVKLQSGPELKKPGETVTKISCKASGYTFTDYGMNWKQAPGKLGKMGWINTYTGEPY 60  
QY 60 NPSLNGRVTISLDTSKNQLSLRTSVTAADTAVYFCARLKGAWLSEPPYSSDGMVWG 119  
Db 61 ADDEKGFAPFSLFETASSTAYLQINNKNEDTATYFCARKD---LLR---YF-----DYWG 109  
QY 120 QGTTVTVSSGGGSGGGSGGGSGGSGNFMLTQPPSA-SGTPGQRVISCSGSSSDIG 178  
Db 110 QGTTVTVS-----SGGGSGGGSGGGSGGSDIELTQSPSSLASISLGKVTITCK-ASQDI- 162  
QY 179 SNTVNMWYQQLPGTAPK---LLIYSNNQRPSPGVDPDRFGSGFKSGTSASLVIISGLQSEDEAD 234  
Db 163 NKYLAWYQHKPKGPRSAHTLHIYIQ---PGTPSRFSGSGSGGRDYSFSSINLEPEDIAT 218  
QY 235 YYCAAMDESLNGVFEGGTKV 255  
Db 219 YYCLHYD---NLHTFEGGTXL 236

RESULT 4  
Q96EYO PRELIMINARY; PRT; 613 AA.  
ID Q96EYO  
AC Q96EYO;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011857; AAH11857.1; -.  
DR PIR; S15590; S15590.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.



DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match 36.2%; Score 496; DB 4; Length 613;  
Best Local Similarity 47.9%; Pred. No. 1.4e-30;  
Matches 115; Conservative 20; Mismatches 61; Indels 44; Gaps 5;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYWSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGSGSISYYSWIRQPPGKLEWIGRIYTSGSTNYN 79  
QY 61 PSINGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLLSEPPYFSSDGMVWGQ 120  
Db 80 PSLKSRVTMSVDTSKNQFSLKLSVTAADTAVYCA-----SQPWELPTVGLFYWGQ 131  
QY 121 GTTVTVSSGGGGSGGGSGGGSGGSGNFMLTQPPSASGTPGQRVVISCSGSSSDIGSN 180  
Db 132 GTLVTVSSG-----SASAPTLFPLVSCENSPSDTSSV 163  
QY 181 TVNMYQQ--LPGTAPKLLIYSNNQRP--GVPDRFSGFKSGTSASLVISG--LQSEDE 232  
Db 164 AVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGKTAATSQVLLPSKDVWGQTDE 223

RESULT 5

Q9UL73 PRELIMINARY; PRT; 119 AA.

AC Q9UL73;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; Pubmed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035041; AAD56277.1; -.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 119  
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;

Query Match 35.4%; Score 485.5; DB 4; Length 119;  
Best Local Similarity 75.0%; Pred. No. 1.4e-30;  
Matches 96; Conservative 8; Mismatches 15; Indels 9; Gaps 3;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIGHDYWSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYSWIRQPPGKLEWIGRIYTSGSTNYT 60  
QY 61 PSINGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLLSEPPYFSSDGMVWGQ 120  
Db 61 PSLKSRVTISVDRSKNQFSLKLSLTAADTAVYFCARLSN-W----GPYY----FDYWGQ 111  
QY 121 GTTVTVSS 128

Db 112 GTLVTVSS 119

RESULT 6

Q8WUX4 PRELIMINARY; PRT; 588 AA.

AC Q8WUX4;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC019235; AAH19235.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;

Query Match 34.6%; Score 474.5; DB 4; Length 588;  
Best Local Similarity 47.1%; Pred. No. 6.5e-29;  
Matches 113; Conservative 19; Mismatches 69; Indels 39; Gaps 5;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSIGHDYWSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
Db 20 QVQLQWAGAGLKPSETLSLTCTGVYGGSFSGYWSWIRQPPGKLEWIGBINHSGSTNYN 79  
QY 61 PSINGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLLSEPPYFSSDGMVWGQ 120  
Db 80 PSLKSRVTISVDTSKKQLSLKLSVNAADTAVYCAV---ITRASPTDGRYGMVWGQ 136  
QY 121 GTTVTVSSGGGGSGGGSGGGSGGSGNFMLTQPPSASGTPGQRVVISCSGSSSDIGSN 180  
Db 137 GTTVTVSSG-----SASAPTLFPLVSCENSPSDTSSV 168  
QY 181 TVNMYQQ--LPGTAPKLLIYSNNQRP--GVPDRFSGFKSGTSASLVISG--LQSEDE 232  
Db 169 AVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGKTAATSQVLLPSKDVWGQTDE 228

RESULT 7

Q9BU10 PRELIMINARY; PRT; 597 AA.

AC Q9BU10;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC002963; AAH02963.1; -.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match 34.6%; Score 474.5; DB 4; Length 597;  
Best Local Similarity 47.1%; Pred. No. 6.6e-29;  
Matches 113; Conservative 19; Mismatches 69; Indels 39; Gaps 5;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGISGHYWSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
Db 20 QVQLQQWGAGLKPSETLSLTCTGVYSGSFGYWSWIRQPPGKLEWIGELINHSGSTNYN 79  
QY 61 PSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ 120  
Db 80 PSLKSRVTISVDTSKKQLSLKLSVNAADTAVYCARV--ITRASPGTDGRYGMVWGQ 136  
QY 121 GTTVTVSSGGGGGGGGGGGGGGGSGSNFMLTQPPSASGTPGQRVSTISGSSSDIGSN 180  
Db 137 GTTVTVSSG-----SASAPTLFPLVSCENSPSDTSSV 168  
QY 181 TVNMYQQ--LPGTAPKLLIYSNNQRP---GVPDFRFSFGKSGTSASLVISG---LQSEDE 232  
Db 169 AVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGKKAATSGVLLPSKDVWGCTDE 228

RESULT 8

Q96AA6 PRELIMINARY; PRT; 618 AA.  
AC Q96AA6;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BC017356; AAH17356.1; -  
DR PIR; S15590; S15590.  
DR InterPro; IPR007110; Ig\_Like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;

Query Match 34.6%; Score 474.5; DB 4; Length 618;  
Best Local Similarity 47.1%; Pred. No. 6.9e-29;  
Matches 113; Conservative 19; Mismatches 69; Indels 39; Gaps 5;  
QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGISGHYWSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
Db 20 QVQLQQWGAGLKPSETLSLTCTGVYSGSFGYWSWIRQPPGKLEWIGELINHSGSTNYN 79  
QY 61 PSLNGRVTISLDTSKNQLSLRLTSVTAADTAVYFCARLKGAWLSEPPYFSSDGMVWGQ 120  
Db 80 PSLKSRVTISVDTSKKQLSLKLSVNAADTAVYCARV--ITRASPGTDGRYGMVWGQ 136  
QY 121 GTTVTVSSGGGGGGGGGGGGGGGSGSNFMLTQPPSASGTPGQRVSTISGSSSDIGSN 180

Db 137 GTTVTVSSG-----SASAPTLFPLVSCENSPSDTSSV 168  
QY 181 TVNMYQQ--LPGTAPKLLIYSNNQRP---GVPDFRFSFGKSGTSASLVISG---LQSEDE 232  
Db 169 AVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGKKAATSGVLLPSKDVWGCTDE 228

RESULT 9

Q8NEJ1 PRELIMINARY; PRT; 236 AA.  
AC Q8NEJ1;  
DT 01-OCT-2002 (Tremblrel. 22, Created)  
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BC030984; AAH30984.1; -  
DR InterPro; IPR003599; Ig\_Like.  
DR InterPro; IPR007110; Ig\_Like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25024 MW; 1703B77942630E08 CRC64;

Query Match 34.5%; Score 472.5; DB 4; Length 236;  
Best Local Similarity 80.0%; Pred. No. 3.2e-29;  
Matches 92; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 145 GGSNFMLTQPPSASGTPGQRVSTISGSSSDIGSNVYMYQQLPGTAPKLLIYSNNQRP 204  
Db 16 GSWAQSVLTQPPSASGSPGQRVSTISGSSRSNIGSNVYMYQQVPGTAPKLLIYRNDQRP 75  
QY 205 SGVPDRFSFGKSGTSASLVISGLQSEDEADYCAAMDESLN-GVVFSGGTRVTVL 258  
Db 76 SGVPDRFSFGKSGTSASLVISGLRSEDEADYCAAMDSLVSHVFGGTRVTVL 130

RESULT 10

Q9BQB8 PRELIMINARY; PRT; 597 AA.  
AC Q9BQB8;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Muscle, and lymph;  
RA Strausberg R.;  
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BC006180; AAH06180.1; -  
DR EMBL; BC001872; AAH01872.1; -  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig\_Like.

DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KM Hypothetical protein-  
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 34.2%; Score 468.5; DB 4; Length 597;  
Best Local Similarity 46.7%; Pred. No. 1.9e-28;  
Matches 112; Conservative 19; Mismatches 70; Indels 39; Gaps 5;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYWSWIRQPPGEGLEWIGFIFPDGSTNYN 60  
Db 20 QVQLQGWAGLKPSETLSLTCTGVYGGSPSGYWSWIRQPPGKLEWIGEINHSGITNYN 79  
QY 61 PSLNGRVTISLDTSKNQSLRLTSVTAADTAVYFCARLKGAWLLSEPPYFSSDGMVWGQ 120  
Db 80 PSLKSRVTISVDTSKQLSLKSSVNAADTAVYICARV---ITRASPGTDGRYGMVWGQ 136  
QY 121 GTTVTVSSGGGGGGGGGGGGGSGNSFMLTQPPSASGTPGQRVISCSGSSSDIGSN 180  
Db 137 GTTVTVSSG-----SASAPTLFPLV6CENSPSDTSSV 168  
QY 181 TVNWMYQQ--LPGTAPKLLIYSNNQRPSS--GVPDRFSGFKSGTSASLVISG---LQSEDE 232  
Db 169 AVGCLAQDFLPDSITFSWKYKNSDISSTRGFSVLRGKXAATQVLLPSKDVWGQTD 228

RESULT 11

Q925S1 PRELIMINARY; PRT; 218 AA.

AC Q925S1;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE MRP5 (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX PubMed=11819679;  
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,  
RA Su C.;  
RT "Mechanism of exogenous nucleic acids and their precursors improving  
RT the repair of intestinal epithelium after irradiation in mice.";  
RL World J. Gastroenterol. 6:709-717(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Cui D., Zeng G., Yan X., Li X., Su C.;  
RT "Cloning of mouse genes related to repairing of intestinal epithelium  
RT of the irradiated mice by treatment with the intestinal RNA of mice of  
RT the same strain.";  
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
DR EMBL; AF240168; AAK43733.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 218  
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 33.6%; Score 460; DB 11; Length 218;  
Best Local Similarity 45.2%; Pred. No. 2.7e-28;  
Matches 103; Conservative 33; Mismatches 72; Indels 20; Gaps 5;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGHDYWSWIRQPPGEGLEWIGFI-FPDGSTNY 59

Db 3 QVQLQSGPELKKPGETVTRISCKASGYTFTTAGMGMWQKMPGKGLKMWIGINTHSQVPRKY 62  
QY 60 NPSLNGRVTISLDTSKNQSLRLTSVTAADTAVYFCARLKGAWLLSEPPYFSSDGMVWG 119  
Db 63 ABEFKGRFAFSLETASATYAIQISNLKNEIDATYFCNR-----WDYDGFAYWG 111  
QY 120 QGTTVTSSGGGGGGGGGGGGGSGNSFMLTQ-PPSASGTPGQRVISCSGSSS--D 176  
Db 112 QGTTVTSS-----SGGGGGGGGGSGGSDIVLTQSPASLAVSLGQRATISCRASESVDN 166  
QY 177 IGSNTVMYQQLPGTAPKLLIYSNNQRPSPGVPPDRFSGFKSGTSASLVY 224  
Db 167 IGISFMNWFQKPGQPKLLIYAASKQSGSVPAGLLASGSGTDPSLNI 214

RESULT 12

Q72379 PRELIMINARY; PRT; 478 AA.

AC Q72379;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein DKFZp686K04218 (Fragment).  
GN DKFZp686K04218.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RI Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BX538066; CAD97996.1; -.  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match 33.5%; Score 459; DB 4; Length 478;  
Best Local Similarity 45.0%; Pred. No. 8.3e-28;  
Matches 113; Conservative 18; Mismatches 60; Indels 60; Gaps 8;

QY 1 QVQLQESGPGLVKPSSETLSLTCTVSGSGSIGH-DY-MSWIRQPPGEGLEWIGFIFPDGSTN 58  
Db 19 QVQLQESGPGLVKPSQTLSTLTCTVSGSGSIGSDYFWSWIRQAPRGLEWMGYIYSGSTY 78  
QY 59 YNPSLNGRVTISLDTSKNQSLRLTSVTAADTAVYFCARLKGAWLLSEPPYFSSDGMVW 118  
Db 79 YNPSLESRLSISIDTSKQPSLRNLSTAADTAVYFCARVGL-----GTAFDIW 128  
QY 119 GGGTTVTSSGGGGGGGGGGGGGSGNSFMLTQPPSASGTPGQ-RVISISC----- 170  
Db 129 GGGTTVTSSASPTS-----PKVPLSLDSTPDGNNVAVCLVQGFFP 171  
QY 171 -----SGSSSDIGSNTVMYQQLPGTAPKLLIYSNNQRPSPGVPPDRFSGFKSGTSASLVISG 226  
Db 172 QEPLSVTWSBSGN-----VTARNPPPS---QDASGDLVYTTSSQLTLP 212  
QY 227 LQSEDEADYYC 237  
Db 213 TQCPDGKSVTC 223

RESULT 13

Q96SB0 PRELIMINARY; PRT; 108 AA.

AC Q96SB0;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Anti-streptococcal/anti-myoelin immunoglobulin lambda light chain



DE variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98375893; PubMed=9712075;  
 RA Adderson E.B., Shikhan A.R., Ward K.E., Cunningham M.W.;  
 RT "Molecular analysis of polyclonal antibodies from  
 RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin  
 RT antibody V region genes.";  
 RL J. Immunol. 161:2020-2031(1998).  
 DR EMBL; U96394; AAB68783.1; -.  
 DR PDB; 1KU4; 29-MAY-02.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON TER 1  
 SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;  
 Query Match 32.5%; Score 445; DB 4; Length 108;  
 Best Local Similarity 84.8%; Pred. No. 1.8e-27;  
 Matches 84; Conservative 8; Mismatches 7; Indels 0; Gaps 0;  
 QY 151 MLTOPPSASGTPGQRVISICSGSSSDIGSNTVNMVYQQLPGTAPKLLIYSNNQPSGVPDR 210  
 Db 3 VLTQPPSASGTPGQRVITISCGSSSNIGSNVYVYQQLPGTAPKLLIYRNQPSGVPDR 62  
 QY 211 FSGFKSGTSASLVISGLQSEDEADYCAAWDESLNGVF 249  
 Db 63 FSGSKSGTSASLAISGLRSEDEADYCAAWDDLISGFMM 101  
 RESULT 14  
 Q86SX2 PRELIMINARY; PRT; 139 AA.  
 AC Q86SX2;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Human full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line)  
 DE of Homo sapiens (Human) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=B-cell;  
 RA Genoscope;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=B-cell;  
 RA Li W.B., Gruber C., Jesse J., Polayes D.;  
 RT "Full-length cDNA libraries and normalization";  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX248300; CAD62627.1; -.  
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00409; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Plasmid.  
 FT NON TER 1  
 SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 32.3%; Score 443; DB 4; Length 139;  
 Best Local Similarity 84.5%; Pred. No. 3.4e-27;  
 Matches 82; Conservative 8; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 QVOIQESGPGLVKPSSETLSTCTVSGSIGHDYMSWIRQPEGLEWIGIFFDGSTNN 60  
 Db 33 QVOIQESGPGLVKPSSETLSTCTVSGSIGSYMSWIRQPEGLEWIGIYSGSTNN 92  
 QY 61 PSINGRVTISLDTSKNQLSLRTSVTAADTAVYFCAR 97  
 Db 93 PSLSRVTISVDTSKNQFSLKLSVTADTAVYFCAR 129  
 RESULT 15  
 Q8WUK4 PRELIMINARY; PRT; 237 AA.  
 ID Q8WUK4;  
 AC Q8WUK4;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 DE Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Tonsil;  
 RA Strauberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC020233; AAH20233.1; -.  
 DR PIR; S12441; S12441.  
 DR PIR; S12627; S12627.  
 DR PIR; S29258; S29258.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 237 AA; 24897 MW; 73C7D70B8039D186 CRC64;  
 Query Match 32.1%; Score 440; DB 4; Length 237;  
 Best Local Similarity 74.1%; Pred. No. 1.1e-26;  
 Matches 86; Conservative 14; Mismatches 14; Indels 2; Gaps 2;  
 QY 145 GGSNFMLTQPPSASGTPGQRVISICSGSSSDIGSN-TVMYQQLPGTAPKLLIYSNNQ 203  
 Db 16 GSWAQSVLTQPPSVSGAPGQRTVITISCTGSSSNIGAGYDVHMYQQLPGTAPKLLIYNSNR 75  
 QY 204 PSGVPPDRFSGFKSGTSASLVISGLQSEDEADYCAAWDESLNG-VFEGGKTAVL 258  
 Db 76 PSGVPPDRFSGFKSGTSASLAITGLQAEDEADYCCSYDSSLGFFVFGGKTAVL 131

Search completed: May 13, 2004, 15:06:59  
 Job time : 34.6922 secs



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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:48:56 ; Search time 51.4563 Seconds  
(without alignments)  
1372.754 Million cell updates/sec

Title: US-10-072-301-29

Perfect score: 1336  
Sequence: 1 QVQLQQWGAGLTKSWGTLTL.....CLQHDNFPPLTFGGTKVEIK 250

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp19808:\*  
2: geneseqp19908:\*  
3: geneseqp20008:\*  
4: geneseqp20018:\*  
5: geneseqp20028:\*  
6: geneseqp20038a:\*  
7: geneseqp20038b:\*  
8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	838	62.7	249	5	ABP45310	Abp45310 Human Bly
2	820.5	61.4	249	5	AAU75150	Aau75150 Amino aci
3	774.5	58.0	256	3	AAV55072	Aay55072 Interleuk
4	774.5	58.0	260	3	AAV55075	Aay55075 Single ch
5	774.5	58.0	367	3	AAV55078	Aay55078 Single ch
6	774.5	58.0	381	3	AAV55079	Aay55079 Single ch
7	774.5	58.0	519	3	AAV55080	Aay55080 Single ch
8	774.5	58.0	546	3	AAV55074	Aay55074 Single ch
9	774.5	58.0	626	3	AAV55081	Aay55081 Single ch
10	774.5	58.0	640	3	AAV55082	Aay55082 Single ch
11	760	56.9	251	5	ABP45038	Abp45038 Human Bly
12	741.5	55.5	248	5	ABP45349	Abp45349 Human Bly
13	741.5	55.5	252	5	ABP45315	Abp45315 Human Bly
14	739.5	55.4	250	5	ABP45402	Abp45402 Human Bly
15	736	55.1	255	5	ABP45631	Abp45631 Human Bly
16	734.5	55.0	250	5	ABP45634	Abp45634 Human Bly
17	734.5	55.0	253	5	AAU72867	Aau72867 P5-9 sing
18	731	54.7	253	5	ABP45322	Abp45322 Human Bly
19	730.5	54.6	254	5	ABP45648	Abp45648 Human Bly
20	729.5	54.6	244	2	AAV21883	Aay21883 Amino aci
21	719	53.8	241	4	AAAB46061	Aab46061 Human TF
22	719	53.8	909	2	AAAB50092	Aar50092 Humanised
23	717.5	53.7	240	4	AAAB46020	Aab46020 Human MUC
24	716	53.6	253	5	ABP44943	Abp44943 Human Bly
25	715.5	53.6	241	7	ADCG4791	Adc64791 Hu-B-A5 c

26	714.5	53.5	241	7	ADCG4785	Adc64785 Hu-E4-1 c
27	713	53.4	249	5	ABP44946	Abp44946 Human Bly
28	711.5	53.3	240	4	AAAB45992	Aab45992 Human MUC
29	710	53.1	255	5	ABP45586	Abp45586 Human Bly
30	709.5	53.1	242	3	AAV58236	Aay58236 Internall
31	705	52.8	253	5	ABP45591	Abp45591 Human Bly
32	703.5	52.7	240	4	AAAB46039	Aab46039 Human TF
33	702.5	52.6	240	4	AAAB46021	Aab46021 Human MUC
34	702	52.5	239	5	ABP45871	Abp45871 Human Bly
35	702	52.5	245	2	AAV06714	Aay06714 Antibody
36	701	52.5	237	5	ABP45895	Abp45895 Human Bly
37	699.5	52.4	240	4	AAAB46018	Aab46018 Human MUC
38	699.5	52.4	251	5	AAU72868	Aau72868 P5-10 sin
39	699	52.3	239	5	ABP45911	Abp45911 Human Bly
40	698.5	52.3	241	7	ADCG4788	Adc64788 Hu-A-E5 c
41	698	52.2	255	5	ABP45615	Abp45615 Human Bly
42	697.5	52.2	240	4	AAAB45993	Aab45993 Human MUC
43	697.5	52.2	240	4	AAAB45991	Aab45991 Human MUC
44	696.5	52.1	241	7	ADCG4787	Adc64787 Hu-A-D2 c
45	696	52.1	255	5	ABP45592	Abp45592 Human Bly

ALIGNMENTS

RESULT 1	ABP45310	ABP45310 standard; protein; 249 AA.
XX	AC	ABP45310;
XX	DT	19-AUG-2002 (first entry)
XX	DE	Human Blys binding bcfv SEQ ID 1321.
XX	KW	Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX	KW	tumour necrosis factor; B cell proliferation; B cell differentiation;
XX	KW	immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX	KW	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX	KW	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX	OS	common variable immunodeficiency; acquired immunodeficiency syndrome.
XX	PN	Homo sapiens.
XX	PD	WO200202641-A1.
XX	PD	10-JAN-2002.
XX	PF	15-JUN-2001; 2001WO-US019110.
XX	PR	16-JUN-2000; 2000US-0212210P.
XX	PR	17-OCT-2000; 2000US-0240816P.
XX	PR	16-MAR-2001; 2001US-0276248P.
XX	PR	21-MAR-2001; 2001US-0277379P.
XX	PR	25-MAY-2001; 2001US-0293499P.
XX	PA	(HUMA-) HUMAN GENOME SCI INC.
XX	PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX	PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX	PI	WPI; 2002-114799/15.
XX	PT	Antibodies against B lymphocyte stimulating polypeptides, useful for the
XX	PT	diagnosis and treatment of cancers and immune disorders.
XX	PS	Claim 1; Page 1979-1980; 3148pp; English.
XX	CC	This invention describes novel antibodies that immunospecifically bind to
XX	CC	B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
XX	CC	tumour necrosis factor (TNF) super family and induces B cell
XX	CC	proliferation and differentiation. The antibodies of the invention have
XX	CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 249 AA;

Query Match 62.7%; Score 838; DB 5; Length 249;  
Best Local Similarity 63.8%; Pred. No. 7.6e-45;  
Matches 166; Conservative 27; Mismatches 45; Indels 22; Gaps 3;

QY 1 QVQLQQMGAGLLKSWGTLSTCAVSGASFSGYWMSWIRPPGKGLEWIGETINHRGSTTYN 60  
Db 1 QVQLQQMGAGLLKPSSETLSLTCAVYGSFSGYWSWIRPPGKGLEWIGETINHRGSTTYN 60  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTAADTAVVYCAR-----TVAGTS---DYWGQGT 110  
Db 61 PSLKSRVTISVDTSKNQFSLKLSVTAAADTAVVYCARGPRTYDILTGRRYWFDPWGRGT 120  
QY 111 LVTVSSGSASAPTGGGGSGGGSGGGGGSETTLTQSPAFMSATPDKVISISCKASR 170  
Db 121 LVTVS-----SGGGSGGGSGGGSGGGSDIVMTQSPSTLSASVGDRTVITCRASQ 168  
QY 171 DVDDVNWYQORPGEAPFIIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAAYYF 230  
Db 169 GISSWLAWYQOKPGRAPKVLILYKASTLESQVPSRFSFGSGSGTDFTLTISLQPEDFATYY 228  
QY 231 CLQHDNFPPLTFGGGTKEYEIK 250  
Db 229 CQQSYSTPMTFGQGTKEYEIK 248

RESULT 2

AAU75150  
ID AAU75150 standard; protein; 249 AA.  
XX

AAU75150;

DT 23-APR-2002 (first entry)

DE Amino acid sequence of human anti-IL8 scFv clone 123-57.

KW Human antibody; immunoglobulin; Ig; variable heavy-chain; VH;  
XX variable light-chain; VL; anti-IL8; interleukin-8; scFv clone.

OS Homo sapiens.  
OS Synthetic.

PN WO200200729-A2.

PD 03-JAN-2002.

PF 25-JUN-2001; 2001WO-US020542.

XX 23-JUN-2000; 2000US-00602373.  
PR 23-JUN-2000; 2000US-00602972.  
PR 23-JUN-2000; 2000US-00603658.  
PR 23-JUN-2000; 2000US-00603663.

PA (GENE-) GENETASTIX CORP.

PI Zhu L, Hua SB;

DR WPI; 2002-090521/12.  
N-PSDB; ABK32984.

XX  
PT Screening libraries of tester proteins against protein, peptide or  
PT nucleic acid target(s) using a two-hybrid method in yeast, useful for  
PT generating recombinant human antibodies and screening for their affinity  
PT binding with target antigens.

PS Example 8; Fig 16; 251pp; English.

XX  
CC The present invention relates to compositions and methods for high  
CC throughput generation and screening of a human antibody or immunoglobulin  
CC (Ig) library in yeast. The method comprises expressing a library of  
CC tester fusion proteins in yeast cells, each tester fusion protein  
CC comprising either an activation domain or a DNA binding domain of a  
CC transcription activator and a tester protein having a large diversity  
CC within the library. The tester protein comprises a first polypeptide  
CC subunit (e.g. human variable heavy-chain, VH) whose sequence varies  
CC within the library, a second polypeptide subunit (e.g. human variable  
CC light-chain, VL) whose sequence varies within the library independently  
CC of the first polypeptide, and a linker peptide which links the first and  
CC second polypeptide subunits. The method is useful for generating  
CC recombinant human antibodies and screening for their affinity binding  
CC with target antigens. The present sequence represents the amino acid  
CC sequence for an anti-IL8 scFv clone as described in the methods of the  
CC present invention  
XX  
SQ Sequence 249 AA;

Query Match 61.4%; Score 820.5; DB 5; Length 249;  
Best Local Similarity 62.8%; Pred. No. 9.4e-44;  
Matches 157; Conservative 32; Mismatches 60; Indels 1; Gaps 1;

QY 1 QVQLQQMGAGLLKSWGTLSTCAVSGASFSGYWMSWIRPPGKGLEWIGETINHRGSTTYN 60  
Db 1 QVQLQESGPGLVTPSETLSLFCNVSGASISSYCWSWLRQPAKRLIEWIGRVCTSGKTYYN 60  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTAADTAVVYCARVAGTSVDYWGQGTLYTVSSGSAS 120  
Db 61 PSLKSRVTISLDTSTNQISLKLTSMTAADTAVVYCARVAGTSVDYWGQGTLYTVSSGSAS 119  
QY 121 APTGGGGSGGGSGGGSGGGGGSETTLTQSPAFMSATPDKVISISCKASRPVDDVNWYQ 180  
Db 120 GPSGGGGSGGGSGGGSGGGGGSETTLTQSPSSLSASVGDRTVITCQASEDIGNQYLNWYQ 179  
QY 181 QRPGEAPFIIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAAYYFCLQHDNFPPLT 240  
Db 180 QKPGKAPTLILYDASNLTGTVPSRFSRSGTGVTDFTFTITSLQPEDIATYYCQQYNNLPIT 239  
QY 241 FGGGTKEYEIK 250  
Db 240 FGQGTKEYEIK 249

RESULT 3

AAV55072  
ID AAV55072 standard; protein; 256 AA.  
XX

AAV55072;

DT 25-FEB-2000 (first entry)

DE Interleukin-6 specific ScFv protein sequence.

KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretable functional protein; antigenic protein;  
KW protein isolation; diagnosis; interleukin-6; scFv.

OS Synthetic.

OS Homo sapiens.

PN WO9960113-A1.

PD 25-NOV-1999.

PF 30-APR-1999; 99WO-JP002341.  
XX  
PR 20-MAY-1998; 98JP-00138652.  
PR 01-OCT-1998; 98JP-00279876.  
XX  
PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Tsuchiya M, Saito M, Ohtomo T;  
XX  
DR WPI; 2000-039382/03.  
DR N-PSDB; AAZ40291.  
XX  
PT Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
PT production of drugs treating abnormal functions of the protein.  
XX  
PS Example 1; Page 54-56; 120pp; Japanese.  
XX  
CC This sequence represents a ScFv specific for human interleukin-6. The  
CC invention relates to a method for isolating a gene encoding a membrane-  
CC bound protein, comprising introducing a vector into a cell, contacting an  
CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the cDNA.  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for  
CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein  
XX  
SQ Sequence 256 AA;

Query Match 58.0%; Score 774.5; DB 3; Length 256;  
Best Local Similarity 59.7%; Pred. No. 7.1e-41;  
Matches 151; Conservative 38; Mismatches 49; Indels 15; Gaps 3;

QY 1 QVQLQQWAGALLKSWGTLSTCAVSGASF-SGYWWSWIRQPPGKLEWIGEINHRGTTY 59  
Db 1 QVQLQESGPGLVPRPSQTLSTCTVSGYSITSDHAWSWVRQPPGRLIEWIGYISGITYY 60  
QY 60 NPSLDGRVTISLDTSTNQISLKLTSMTAADTAVYYCARTVAGTS--DYWGQGLVTVSSG 117  
Db 61 NPSLSKRVMTLRDTSKNQPSLRSLSSVTAADTAVYYCARSLARTTAMDYWGQSLVTVS-- 118  
QY 118 SASAPRTGGGSGGGSGGGSGGGSETTLTQSPAFMSATPGDKVISISCKASRDVDDVN 177  
Db 119 -----SGGGSGGGSGGGSGGGSDIQMTQSPSSLASVGDRTVITCRASQDISSYLN 168  
QY 178 WYQQRPGEAPIFIIEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAYFCLQHDNF 237  
Db 169 WYQQKPKGAPKLLIYYSRLHSGVPSRFSGSGSDTFTFTISSLPEDIATYYCCQGNTL 228  
QY 238 PLTFGGGTKEIK 250  
Db 229 PYTFGGGTKEIK 241

RESULT 4  
AAY55075  
ID AAY55075 standard; protein; 260 AA.  
XX  
AC AAY55075;  
XX  
DT 25-FEB-2000 (first entry)  
XX  
DE Single chain Fv protein sequence shPM1(deltaEL).  
XX  
KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretable functional protein; antigenic protein;  
KW protein isolation; diagnosis; ScFv.  
XX

OS Synthetic.  
XX  
PN W09960113-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 30-APR-1999; 99WO-JP002341.  
XX  
PR 20-MAY-1998; 98JP-00138652.  
PR 01-OCT-1998; 98JP-00279876.  
XX  
PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Tsuchiya M, Saito M, Ohtomo T;  
XX  
DR WPI; 2000-039382/03.  
DR N-PSDB; AAZ40305.  
XX  
PT Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
PT production of drugs treating abnormal functions of the protein.  
XX  
PS Example 7; Page 80-82; 120pp; Japanese.  
XX  
CC This sequence represents a single chain Fv (ScFv) sequence. The invention  
CC relates to a method for isolating a gene encoding a membrane-bound  
CC protein, comprising introducing a vector into a cell, contacting an  
CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the cDNA.  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for  
CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein  
XX  
SQ Sequence 260 AA;

Query Match 58.0%; Score 774.5; DB 3; Length 260;  
Best Local Similarity 59.7%; Pred. No. 7.2e-41;  
Matches 151; Conservative 38; Mismatches 49; Indels 15; Gaps 3;

QY 1 QVQLQQWAGALLKSWGTLSTCAVSGASF-SGYWWSWIRQPPGKLEWIGEINHRGTTY 59  
Db 20 QVQLQESGPGLVPRPSQTLSTCTVSGYSITSDHAWSWVRQPPGRLIEWIGYISGITYY 79  
QY 60 NPSLDGRVTISLDTSTNQISLKLTSMTAADTAVYYCARTVAGTS--DYWGQGLVTVSSG 117  
Db 80 NPSLSKRVMTLRDTSKNQPSLRSLSSVTAADTAVYYCARSLARTTAMDYWGQSLVTVS-- 137  
QY 118 SASAPRTGGGSGGGSGGGSGGGSETTLTQSPAFMSATPGDKVISISCKASRDVDDVN 177  
Db 138 -----SGGGSGGGSGGGSGGGSDIQMTQSPSSLASVGDRTVITCRASQDISSYLN 187  
QY 178 WYQQRPGEAPIFIIEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAYFCLQHDNF 237  
Db 188 WYQQKPKGAPKLLIYYSRLHSGVPSRFSGSGSDTFTFTISSLPEDIATYYCCQGNTL 247  
QY 238 PLTFGGGTKEIK 250  
Db 248 PYTFGGGTKEIK 260

RESULT 5  
AAY55078  
ID AAY55078 standard; protein; 367 AA.  
XX  
AC AAY55078;  
XX  
DT 25-FEB-2000 (first entry)  
XX







```
Db      248 PYTFGGTKVEIK 260
      |||||
RESULT 7
ID      AAY55080 standard; protein; 519 AA.
XX
AC      AAY55080;
XX
DT      25-FEB-2000 (first entry)
XX
DE      Single chain Fv protein sequence shPM1(deltaEL)-BVGS3.
XX
KW      Gene isolation; membrane-bound protein; fusion protein; drug production;
KW      antigen-binding cell; secretable functional protein; antigenic protein;
KW      protein isolation; diagnosis; ScFv.
XX
OS      Synthetic.
XX
PN      WO9960113-A1.
XX
PD      25-NOV-1999.
XX
PF      30-APR-1999; 99WO-JP002341.
XX
PR      20-MAY-1998; 98JP-00138652.
PR      01-OCT-1998; 98JP-00279876.
XX
PA      (CHUS ) CHUGAI SEIYAKU KK.
XX
PI      Tsuchiya M, Saito M, Ohmoto T;
XX
DR      WPI; 2000-039382/03.
DR      N-PSDB; AAZ40312.
XX
PT      Efficient and selective isolation of a gene encoding membrane protein
PT      with low or no antigenic binding activity, for diagnosis, study of, and
PT      production of drugs treating abnormal functions of the protein.
XX
PS      Example 7; Page 95-100; 120pp; Japanese.
XX
CC      This sequence represents a single chain Fv (ScFv) sequence. The invention
CC      relates to a method for isolating a gene encoding a membrane-bound
CC      protein, comprising introducing a vector into a cell, contacting an
CC      antigen with the cell expressing the fused protein encoded by the vector
CC      on its surface to select an antigen-binding cell, and isolating the cDNA.
CC      The vector contains DNA encoding a secretable functional protein with
CC      antigenicity and binding affinity, and a cDNA ligated to DNA downstream
CC      of the 3' end of the coding sequence. The method can be used to isolate a
CC      membrane-bound protein for diagnosis and study. It can also be used for
CC      producing drugs treating abnormal functions of the protein. Such a
CC      technique is efficient and selective, which is different from the prior-
CC      art transmembrane trap (TMT) method wherein an epitope recognised by an
CC      antibody is carried in a fused protein
XX
SQ      Sequence 519 AA;
OY      Query Match 58.0%; Score 774.5; DB 3; Length 519;
Db      Best Local Similarity 59.7%; Pred. No. 1.4e-40;
Matches 151; Conservative 38; Mismatches 49; Indels 15; Gaps 3;
OY      1 QVQLQOWGAGLTKSWGTSLTCAVSGASF-SGYWYMWIRPPGKLEWIGEINHRGTTY 59
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      20 QVQLQESGPGLVKPSQTLSTLCTVSGYSITSDHAWSWVRQPPGRLIEWIGISYSGITTY 79
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY      60 NPSLDGRVTISLDTSTNQISLKLTSMTAADTAVVYCCARTVAGTS--DYWGQGLTVTVSSG 117
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      80 NPSLKSRTVMTLRDTSKNQFSLRLSSVTAAADTAVVYCARSLARTTAMDYWGQSLTVYS-- 137
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY      118 SASAPFTGGGGSGGGSGGGSGGGSETTLTQSPAFMSATPBDKVISICKASRDVDDVN 177
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      138 -----SGGGSGGGGGSGGGSDIQMTQSPSSLSASVGDRTVITTCRASQDISSYLN 187
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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OY      178 WYQORPGEAPIFILEDATTLVPGISPRPSGSGYGTDTLTINNIDSEDAAYFCLQHDNF 237
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      188 WYQKPKGAKPKLLIYTSRLHSGVPSRFGSGSGGTDTFTTISLSLOPEDIATYYCCQGNLT 247
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY      238 PLTFGGGTKEIK 250
      |||||
Db      248 PYTFGGTKVEIK 260
      |||||
RESULT 8
ID      AAY55074 standard; protein; 546 AA.
XX
AC      AAY55074;
XX
DT      25-FEB-2000 (first entry)
XX
DE      Single chain Fv protein sequence hPM1-BVGS3.
XX
KW      Gene isolation; membrane-bound protein; fusion protein; drug production;
KW      antigen-binding cell; secretable functional protein; antigenic protein;
KW      protein isolation; diagnosis; ScFv.
XX
OS      Synthetic.
XX
PN      WO9960113-A1.
XX
PD      25-NOV-1999.
XX
PF      30-APR-1999; 99WO-JP002341.
XX
PR      20-MAY-1998; 98JP-00138652.
PR      01-OCT-1998; 98JP-00279876.
XX
PA      (CHUS ) CHUGAI SEIYAKU KK.
XX
PI      Tsuchiya M, Saito M, Ohmoto T;
XX
DR      WPI; 2000-039382/03.
DR      N-PSDB; AAZ40303.
XX
PT      Efficient and selective isolation of a gene encoding membrane protein
PT      with low or no antigenic binding activity, for diagnosis, study of, and
PT      production of drugs treating abnormal functions of the protein.
XX
PS      Example 5; Page 73-78; 120pp; Japanese.
XX
CC      This sequence represents a single chain Fv (ScFv) sequence. The invention
CC      relates to a method for isolating a gene encoding a membrane-bound
CC      protein, comprising introducing a vector into a cell, contacting an
CC      antigen with the cell expressing the fused protein encoded by the vector
CC      on its surface to select an antigen-binding cell, and isolating the cDNA.
CC      The vector contains DNA encoding a secretable functional protein with
CC      antigenicity and binding affinity, and a cDNA ligated to DNA downstream
CC      of the 3' end of the coding sequence. The method can be used to isolate a
CC      membrane-bound protein for diagnosis and study. It can also be used for
CC      producing drugs treating abnormal functions of the protein. Such a
CC      technique is efficient and selective, which is different from the prior-
CC      art transmembrane trap (TMT) method wherein an epitope recognised by an
CC      antibody is carried in a fused protein
XX
SQ      Sequence 546 AA;
OY      Query Match 58.0%; Score 774.5; DB 3; Length 546;
Db      Best Local Similarity 59.7%; Pred. No. 1.5e-40;
Matches 151; Conservative 38; Mismatches 49; Indels 15; Gaps 3;
OY      1 QVQLQOWGAGLTKSWGTSLTCAVSGASF-SGYWYMWIRPPGKLEWIGEINHRGTTY 59
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      20 QVQLQESGPGLVKPSQTLSTLCTVSGYSITSDHAWSWVRQPPGRLIEWIGISYSGITTY 79
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY      60 NPSLDGRVTISLDTSTNQISLKLTSMTAADTAVVYCCARTVAGTS--DYWGQGLTVTVSSG 117
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

Db 80 NPSLSKSRVTMLRDTSKNOFSLRLSSVTAADTAVVYCARSLARTTAMDYWGQSLTVS-- 137  
QY 118 SASAPITGGGSGGGSGGGSGGGSETTLTQSPAFMSATPGDKVISICKASRDVDDVN 177  
Db 138 -----SGGGSGGGSGGGSGGSDIQMTQSPSSLASVGDRTVITCRASQDISSYLN 187  
QY 178 WYQORPGEAPIFIIEDATTLVPGISPRFSGSGYGTDTLTINNIDSEDAAYFCLQHDNF 237  
Db 188 WYQOKPGKAPKLLIYTSRLHSGVPSRFSGSGGTDFTFTTISLQPEDIAFYCCQGGNTL 247  
QY 238 PLTFGGGTKEIK 250  
Db 248 PYTFGGGTKEIK 260

RESULT 9  
AAY55081  
ID AAY55081 standard; protein; 626 AA.

AC AAY55081;

DT 25-FEB-2000 (first entry)

DE Single chain Fv protein sequence shPM1-kappa-BvGS3.

KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretable functional protein; antigenic protein;  
KW protein isolation; diagnosis; ScFv.

OS Synthetic.

PN WO9960113-A1.

PD 25-NOV-1999.

PF 30-APR-1999; 99WO-JP002341.

PR 20-MAY-1998; 98JP-00138652.

PR 01-OCT-1998; 98JP-00279876.

PA (CHUS ) CHUGAI SEIYAKU KK.

PI Tsuchiya M, Saito M, Ohtomo T;

DR WPI; 2000-039382/03.

DR N-PSDB; AAZ40316.

PT Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
PT production of drugs treating abnormal functions of the protein.

PS Example 7; Page 103-109; 120pp; Japanese.

CC This sequence represents a single chain Fv (ScFv) sequence. The invention  
CC relates to a method for isolating a gene encoding a membrane-bound  
CC protein, comprising introducing a vector into a cell, contacting an  
CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the cDNA.  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for  
CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein

XX Sequence 626 AA;

Query Match 58.0%; Score 774.5; DB 3; Length 626;  
Best Local Similarity 59.7%; Pred. No. 1.7e-40;  
Matches 151; Conservative 38; Mismatches 49; Indels 15; Gaps 3;

QY 1 QVQLQWAGLILKSWGTLITCAVSGASF-SGYWSWIRQPPGKLEWIGELNHRGTTY 59  
Db 20 QVQLQESGPGLVPRPSQTLISLTCTVSGYSITSDHAWSWVRQPPGRGLEWIGYISGITTY 79  
QY 60 NPSLDGRVTISLDTSTNQISLKLTSMTAADTAVVYCARVAGTS--DYWGQGLTVVSSG 117  
Db 80 NPSLSKSRVTMLRDTSKNOFSLRLSSVTAADTAVVYCARSLARTTAMDYWGQSLTVS-- 137  
QY 118 SASAPITGGGSGGGSGGGSGGGSETTLTQSPAFMSATPGDKVISICKASRDVDDVN 177  
Db 138 -----SGGGSGGGSGGGSGGSDIQMTQSPSSLASVGDRTVITCRASQDISSYLN 187  
QY 178 WYQORPGEAPIFIIEDATTLVPGISPRFSGSGYGTDTLTINNIDSEDAAYFCLQHDNF 237  
Db 188 WYQOKPGKAPKLLIYTSRLHSGVPSRFSGSGGTDFTFTTISLQPEDIAFYCCQGGNTL 247  
QY 238 PLTFGGGTKEIK 250  
Db 248 PYTFGGGTKEIK 260

RESULT 10  
AAY55082  
ID AAY55082 standard; protein; 640 AA.

AC AAY55082;

DT 25-FEB-2000 (first entry)

DE Single chain Fv protein sequence shPM1-MCH4-BvGS3.

KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretable functional protein; antigenic protein;  
KW protein isolation; diagnosis; ScFv.

OS Synthetic.

PN WO9960113-A1.

PD 25-NOV-1999.

PF 30-APR-1999; 99WO-JP002341.

PR 20-MAY-1998; 98JP-00138652.

PR 01-OCT-1998; 98JP-00279876.

PA (CHUS ) CHUGAI SEIYAKU KK.

PI Tsuchiya M, Saito M, Ohtomo T;

DR WPI; 2000-039382/03.

DR N-PSDB; AAZ40321.

PT Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
PT production of drugs treating abnormal functions of the protein.

PS Example 7; Page 111-117; 120pp; Japanese.

CC This sequence represents a single chain Fv (ScFv) sequence. The invention  
CC relates to a method for isolating a gene encoding a membrane-bound  
CC protein, comprising introducing a vector into a cell, contacting an  
CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the cDNA.  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for  
CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein

Query Match	58.0%;	Score 774.5;	DB 3;	Length 640;
Best Local Similarity	59.7%;	Pred. No. 1.7e-40;		
Matches 151;	Conservative 38;	Mismatches 49;	Indels 15;	Gaps 3
QY	1 QVQLQQGAGLLKSWGTLSTCAVSGASF-SGYYSWIRQPPGKGLIEWIGEINHRGSTTY 59			
Db	20 QVQLQESGPGLVPRPSQTLSTLTCTVSGYSITSDHAWSWVRQPPGRLGLEWIGYISYGITTY 79			
QY	60 NPSLDGRVTISLDTSTNQISLKTSMTPADTAIVYVCARTVAGTS--DYWGCGTLVTSSG 117			
Db	80 NPSLKSRTVMTLRDTSKNQFSLRLSSVTPADTAIVYCARSLARTTAMDYWGCGSLTVTS-- 137			
QY	118 SASAPFTGGGGSGGGSGGGSGGGSETTLTQSPAFMSATPGDKVVISCKASRDVDDVN 177			
Db	138 -----SGGGSGGGSGGGSGGGSGDIQMTQSPSSLSASVGDRTYITCRASQDISSYLN 187			
QY	178 WYQRPGEAPIFIIEDATTLVPGISPRSGSGYGTDTFTLTINNIDSEDAVYFCLQHDNF 237			
Db	188 WYQKPKGAPKLLIYTSRLHSGVPSRPSGSGGTDTFTTISLQPEDIAITYYQQGNTL 247			
QY	238 PLTEGGGTKEIK 250			
Db	248 PYTFGGGTKEIK 260			
RESULT 11				
ABP45038				
ID	ABP45038 standard; protein; 251 AA.			
XX	ABP45038;			
AC				
XX	19-AUG-2002 (first entry)			
DT				
XX	Human Blys binding scFv SEQ ID 1049.			
DE				
XX	Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;			
KW	tumour necrosis factor; B cell proliferation; B cell differentiation;			
KW	immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;			
KW	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;			
KW	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;			
KW	common variable immunodeficiency; acquired immunodeficiency syndrome.			
XX	Homo sapiens.			
OS				
XX	WO200202641-A1.			
PN				
XX	10-JAN-2002.			
PD				
XX	15-JUN-2001; 2001WO-US019110.			
PF				
XX	16-JUN-2000; 2000US-0212210P.			
PR	17-OCT-2000; 2000US-0240816P.			
PR	16-MAR-2001; 2001US-0276248P.			
PR	21-MAR-2001; 2001US-0277379P.			
PR	25-MAY-2001; 2001US-0293499P.			
XX				
PA	(HUMA-) HUMAN GENOME SCI INC.			
PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.			
XX				
PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;			
XX				
DR	WPI; 2002-114799/15.			
XX				
PT	Antibodies against B lymphocyte Stimulating polypeptides, useful for the			
PT	diagnosis and treatment of cancers and immune disorders.			
XX				
PS	Claim 1, Page 1654-1655; 3148pp; English.			
XX				
CC	This invention describes novel antibodies that immunospecifically bind to			
CC	B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the			

CC	tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of Blys. The antibodies bind to Blys and so may be used to detect and quantitate the presence of Blys in biological samples and may be used in this way to diagnose disease associated with aberrant expression of Blys. They may also be administered to treat diseases associated with aberrant Blys expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention
XX	Sequence 251 AA;
SQ	
	Query Match                  56.9%; Score 760; DB 5; Length 251; Best Local Similarity    59.9%; Pred. No. 5.6e-40; Matches 157; Conservative    28; Mismatches 53; Indels 24; Gaps 6
QY	1 QVQLQQWAGLLKSWGTLSTLCAVSCASFSG--YYMSWIRPPPKGLEWIGEINHRGSTT 58   :       :   1 QLQLQESGPGLVKPSETLSLTCTVSGGFISRTSYMGWIRQPKGPBWIGNIYYTGKTY 60
Db	
QY	59 YNPSLDGRVTISLDTSTNQISLKLTSMTAADTAVYYCARTVAGTS-----DYWGQG 109   :   61 YSPSLKSRVTISVDTSKNQLSLKLNSVTAADTAVYYCAR--AGYDLLTGYPFPYDWSWKG 118
Db	
QY	110 TLTVSSGSASAPTTGGGGSGGGSGGGSGGGSEITLTQS PAFMSATPGDKVISCKAS 169   119 TLTVTSS-----GGGGSGGGSGGGGS---ALEIVLTQSPATLSLSPGERATLSCRAS 168 
Db	
QY	170 RDVDDDVNWYQQRPEAPIFIETDATTLVPGISPRFGSGYGTDFTLTINNIDSEDAAAY 229 :   :   169 QSVS SYLA WYQOKPGQAPRLLYDASNRA TGIPARFSGSGGTDTLTISSLEPEDFAVY 228   :   229 YCQQRSNMPFLTFFGGGTKEIK 250
Db	
RESULT 12	
ID	ABP45349 standard; protein; 248 AA.
XX	ABP45349;
AC	.
XX	
DT	19-AUG-2002 (first entry)
XX	
DE	Human Blys binding scFv SEQ ID 1360.
XX	
KM	Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
KW	
OS	Homo sapiens.
PN	WO200202641-A1.
PD	
PJ	10-JAN-2002.
PF	
PL	15-JUN-2001; 2001WO-US019110.
PM	
PO	16-JUN-2000; 2000US-0212210P.
PP	17-OCT-2000; 2000US-0240816P.
PR	16-MAR-2001; 2001US-0276248P.
PT	21-MAR-2001; 2001US-0277379P.
PU	25-MAY-2001; 2001US-0293499P.



XX (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
DR  
XX  
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.  
XX  
XX  
PS Claim 1, Page 2025-2026; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiaids activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 248 AA;  
Query Match 55.5%; Score 741.5; DB 5; Length 248;  
Best Local Similarity 58.9%; Pred. No. 7.9e-39;  
Matches 152; Conservative 31; Mismatches 56; Indels 19; Gaps 5;  
QY 1 QVQLQWAGALLKSWGTLSTLCAVSGASFSGYYMSWIRQPGKLEWIGEINHRGTTYN 60  
DB 1 QVQLQESGPGELVKPSETLSLSTCAVSGSFSIRSYMSWIRQSPGRLEWIGHIYHSGSTDYN 60  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAVYYCAR---TVAGT---SDYWGQGLTV 112  
DB 61 PSLRSRYTMSIDTSKNQFSLNLTSTYADTAVYYCARDHYDVLTGSLYLAQAFDVGQGLTV 120  
QY 113 TVSSGSASAPPTGGSGSGSGSGSGSGSETTLTQSPAFMSATPGDKVISICKARQV 172  
DB 121 TVSS-----GGGSGSGSGSGSGSGS---ALDIQLTQSPSSLSASVGDRTTITCRASQSI 170  
QY 173 DDDVNMVYQQRPGEAPFIIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAVYFCL 232  
DB 171 GRYLNMVYQOKPGRAPRLLIFFVTSLSHSDVPSRFSGSGGTDFTSLTISNLQPEDFATYYCQ 230  
QY 233 QHDFPLTFGGGTKVEIK 250  
DB 231 QSYTDP-TFGQGTRLLEIK 247  
RESULT 13  
ABP45315  
ID ABP45315 standard; protein; 252 AA.  
XX  
AC ABP45315;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scFv SEQ ID 1326.  
XX  
KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KM antiaids; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

KM common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200202641-A1.  
PN  
XX  
XX 10-JAN-2002.  
PD  
XX  
XX 15-JUN-2001; 2001WO-US019110.  
PF  
XX  
XX 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-027379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
DR  
XX  
XX  
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.  
XX  
PS Claim 1, Page 1985-1986; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiaids activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 252 AA;  
Query Match 55.5%; Score 741.5; DB 5; Length 252;  
Best Local Similarity 58.6%; Pred. No. 8e-39;  
Matches 154; Conservative 26; Mismatches 56; Indels 27; Gaps 6;  
QY 1 QVQLQWAGALLKSWGTLSTLCAVSGASFSGYYMSWIRQPGKLEWIGEINHRGTTYN 60  
DB 1 QVQLQWAGALLKPSSETLSLSTCAVYGSFSGYYMSWIRQPGKPEWIKITHSGTTYN 60  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAVYYCARTVAGTS-----DYWGQGT 110  
DB 61 PSLKSRVTMSVDTSTNQFSLKLSYTAADTAVYYCARERADYDILGYFYGMVWGQGT 120  
QY 111 LVTSSGSASAPPTGGSGSGSGSGSGSETTLTQSPAFMSATPGDKVISICK-AS 169  
DB 121 MVTVS-----SGGSGSGSGSGSGSGSVLTQ-PASVSGSPGQSITISCTGS 167  
QY 170 RDVD--DDVNMVYQQRPGEAPFIIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDA 227  
DB 168 SDVGYNVYVSWYQHPKAPKLMYEGSKRPSGVSNNRFGSGSGNTASLTISGLQADEDA 227  
QY 228 YVFCLQH-DNFPPLTFGGGTKVEI 249  
DB 228 DYYCSSYTRSTRVFGGGLTV 250



[illegible]

```

Db      61 PSLKSRVTISVDTSKNQFSLKLXSVTAADTAVYYCARGERDILTGYYLDGMDVMGRGTMV 120
Oy      113 TVSSGSASAPTGGGSGGGGSGGGGSETTLTQSPAFMSATPGDXVISCK-ASRD 171
Db      121 TVS-----SGGGSGGGGSGGGGSGSVLTQPPS-VSAAPGQKVTISCTGTSSD 167
Oy      172 VD--DDVNMWYQQRPGEAFFIATEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAY 229
Db      168 VGGYNVSWYQQHPGKAPKLMITYBSKRP SGVSNRFSGSKSGNTASLTISGLQAEDEADY 227
Oy      230 FCLQH-DNFPPLTFGGGTKEI 249
Db      228 YCSSYTRSTRVFGGGLTV 248

RESULT 15
ABP45631
ID      ABP45631 standard; protein; 255 AA.
XX
AC      ABP45631;
XX
XX      19-AUG-2002 (first entry)
DE      Human Blys binding scFv SEQ ID 1642.
XX
XX      Blys; B lymphocyte stimulator; TNF superfamily; human; cyostatic;
XX      tumour necrosis factor; B cell proliferation; B cell differentiation;
XX      immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX      antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX      systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX      common variable immunodeficiency; acquired immunodeficiency syndrome.
OS      Homo sapiens.
XX
XX      WO200202641-A1.
PN      10-JAN-2002.
XX
XX      15-JUN-2001; 2001WO-US019110.
PF      16-JUN-2000; 2000US-0212210P.
XX      17-OCT-2000; 2000US-0240816P.
PR      16-MAR-2001; 2001US-0276248P.
PR      21-MAR-2001; 2001US-0277379P.
PR      25-MAY-2001; 2001US-0293499P.
XX
XX      (HUMA-) HUMAN GENOME SCI INC.
PA      (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI      Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
XX      WPI; 2002-114799/15.
DR
XX
XX      Claim 1; Page 2362-2363; 3148pp; English.
XX
XX      This invention describes novel antibodies that immunospecifically bind to
XX      B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX      tumour necrosis factor (TNF) super family and induces B cell
XX      proliferation and differentiation. The antibodies of the invention have
XX      cyostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX      antirheumatic and antiAIDS activity and can be used in vaccines to
XX      inhibit the expression and activity of Blys. The antibodies bind to Blys
XX      and so may be used to detect and quantitate the presence of Blys in
XX      biological samples and may be used in this way to diagnose disease
XX      associated with aberrant expression of Blys. They may also be
XX      administered to treat diseases associated with aberrant Blys expression
XX      and activity such as cancer, immune, and autoimmune disorders and
XX      diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX      immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX      acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent

```

CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 255 AA;

Query Match 55.1%; Score 736; DB 5; length 255;  
Best Local Similarity 58.6%; Pred No. 1.8e-38;  
Matches 156; Conservative 21; Mismatches 59; Indels 30; Gaps 6;  
QY 1 QVQLQOMGAGLLKSWGTLSTCAVSGASFSGYWSWIRQPPGKLEWIGETINHGSTTNN 60  
Db 1 QVQLQOMGAGLLKPSSETLSLTCVYGSFSGYWSWIRQSPGKLEWIGETINHGSTNN 60  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAVYYCAR-----TVAGTS-----DYWG 107  
Db 61 PSLSKRVTVISVDASKNQPSLKLSSVTADTAVYYCARERSYYDILTGYSPRSKYGMVWG 120  
QY 108 QGTLVTSSGSASAPITGGSGSGSGSGSGSGSTTLTQSPAFMSATPDKVISCK 167  
Db 121 RGTIVTVS-----SGGGSGSGSGSGSGSGSVLTQPS-ASGTPGQRTVISCS 167  
QY 168 ASRD--VDDVNMYQORPGEAFIFIIDATTLVPGISPRFSGSGYGTDFTLINNIDSED 225  
Db 168 GSSSNIGSNTVNMYQRLPGAAPQLLIYNNDQRPSCIPDRFSGSKSGTSGSLVISGLQSED 227  
QY 226 AAYVECLQHDNF--PLTFGGGTKVEI 249  
Db 228 EADYYCASWDDSLNGRVFGGKLTIV 253

Search completed: May 13, 2004, 15:01:00  
Job time : 51.4563 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:53:42 ; Search time 13.7136 Seconds  
(without alignments)  
941.146 Million cell updates/sec

Title: US-10-072-301-29

Perfect score: 1336

Sequence: 1 QVQLQOWGAGLTKSWGTLTL.....CLQHDNFPPLTFGGGKVEIK 250

Scoring table: BLOSUM62

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfile1.pep.\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	702	52.5	245	4	US-08-918-148-75 Sequence 75, Appl
2	691.5	51.8	248	2	US-08-887-352B-22 Sequence 22, Appl
3	691.5	51.8	248	3	US-09-109-207C-22 Sequence 22, Appl
4	691.5	51.8	248	3	US-09-296-005-22 Sequence 22, Appl
5	691.5	51.8	248	4	US-09-920-171-22 Sequence 22, Appl
6	687.5	51.5	248	2	US-08-887-352B-23 Sequence 23, Appl
7	687.5	51.5	248	3	US-09-109-207C-23 Sequence 23, Appl
8	687.5	51.5	248	3	US-09-296-005-23 Sequence 23, Appl
9	687.5	51.5	244	4	US-08-918-148-79 Sequence 79, Appl
10	681.5	51.0	244	4	US-08-918-148-77 Sequence 77, Appl
11	680.5	50.9	244	4	US-09-509-031-16 Sequence 16, Appl
12	678	50.7	482	4	US-10-092-246-36 Sequence 36, Appl
13	677.5	50.7	240	4	US-10-092-246-37 Sequence 37, Appl
14	677.5	50.7	240	4	US-08-918-148-78 Sequence 78, Appl
15	675	50.5	245	4	US-08-488-113B-148 Sequence 148, App
16	672	50.3	240	1	US-08-477-484B-148 Sequence 148, App
17	672	50.3	240	2	US-08-646-360-148 Sequence 148, App
18	672	50.3	240	3	US-08-839-765-148 Sequence 148, App
19	672	50.3	240	3	US-09-136-389-148 Sequence 148, App
20	672	50.3	240	4	US-09-610-838-148 Sequence 148, App
21	672	50.3	240	4	US-09-711-485-148 Sequence 148, App
22	672	50.3	281	4	US-09-025-769B-178 Sequence 178, App
23	672	50.3	240	4	US-10-092-246-35 Sequence 35, Appl
24	671.5	50.3	244	4	US-10-039-785-44 Sequence 44, Appl
25	668.5	50.0	359	4	US-09-646-028-16 Sequence 16, Appl
26	668.5	50.0	361	4	US-09-646-028-13 Sequence 13, Appl
27	668.5	50.0	361	4	US-09-646-028-13 Sequence 13, Appl

28	664	49.7	245	4	US-08-918-148-76 Sequence 76, Appl
29	664	49.7	249	2	US-08-797-689-18 Sequence 18, Appl
30	664	49.7	249	4	US-09-984-186-18 Sequence 18, Appl
31	659.5	49.4	243	1	US-07-958-140-2 Sequence 2, Appl
32	659.5	49.4	243	5	PCT-US93-09166-2 Sequence 2, Appl
33	658	49.3	235	2	US-08-190-199A-61 Sequence 61, Appl
34	653.5	48.9	269	3	US-08-646-265A-109 Sequence 109, App
35	652.5	48.8	270	2	US-08-652-507-2 Sequence 2, Appl
36	652	48.8	239	4	US-10-092-246-33 Sequence 33, Appl
37	647.5	48.5	239	3	US-08-279-772A-8 Sequence 8, Appl
38	647.5	48.5	239	3	US-08-902-486-11 Sequence 11, Appl
39	647.5	48.5	599	1	US-08-463-163-3 Sequence 3, Appl
40	646.5	48.4	553	2	US-08-661-052-16 Sequence 16, Appl
41	646.5	48.4	553	3	US-09-188-082-16 Sequence 16, Appl
42	646.5	48.4	553	4	US-09-364-088-16 Sequence 16, Appl
43	646.5	48.4	553	4	US-09-102-716-16 Sequence 16, Appl
44	643.5	48.2	256	4	US-09-526-738A-2 Sequence 2, Appl
45	643.5	48.2	258	4	US-09-526-738A-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1  
US-08-918-148-75  
; Sequence 75, Application US/08918148A  
; Patent No. 6342220  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camellia  
; APPLICANT: W.  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Rendly, Brian M.  
; APPLICANT: Gurney, Austin L.  
; TITLE OF INVENTION: Agonist Antibodies  
; FILE REFERENCE: P0979  
; CURRENT APPLICATION NUMBER: US/08/918, 148A  
; CURRENT FILING DATE: 1997-08-25  
; NUMBER OF SEQ ID NOS: 79  
; SEQ ID NO 75  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: artificial  
US-08-918-148-75

Query Match 52.5%; Score 702; DB 4; Length 245;

Best Local Similarity 54.8%; Pred. No. 3.2e-47;  
Matches 138; Conservative 39; Mismatches 61; Indels 14; Gaps 3;

QY 1 QVQLQOWGAGLTKSWGTLTLCAVSGASFGYYWWSWIRQPPGKLEWIGELNHRGTT-y 59  
Db 3 EQVLVQSGGLVKKPGSLRLSCAASGFTFSDYVMSWIRQAPGKLEWVSYSSGSTRYY 62  
QY 60 NPSLDGRVTISLDSTNQISLKLTSMTAADTAVYCAR-TVAGTSDYWGQGLTVYSSGS 118  
Db 63 ADSVKGRFTISRDNSTKTLVQLQMSLRADTAVYCARWSGEDAFDIWGQGTWTVS--- 119  
QY 119 ASAPTGGGSGGGSGGGSGGGSETTLTQSPAFMSATPGDKVISCKASRDVDDVNW 178  
Db 120 -----SGGGSGGGSGGGSGGGSDIVMTQSPSTUSASVGDRAITCRASEGIYHLAW 170  
QY 179 YQRPGEAPFIIEATTLVPGISPRFSGSGYGTFTLTINNIDSEDAAYFCLQHDNFP 238  
Db 171 YQKPKGAPKLLIYKASSLASGAPSRFSGSGGADFTLTISLQPDFAITYYCOQYSNYP 230  
QY 239 LTFGGGKVEIK 250  
Db 231 LTFGGGKLEVK 242  
RESULT 2  
US-08-887-352B-22  
; Sequence 22, Application US/08887352B  
; Patent No. 5994511

```

; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-887-352B-22

Query Match          51.8%; Score 691.5; DB 2; Length 248;
Best Local Similarity 54.4%; Pred. No. 2.1e-46;
Matches 143; Conservative 34; Mismatches 57; Indels 29; Gaps 5;

QY      1 QVQLQWGAAGLLKSWGTLSTCAVSGASF-SGYVSWIRQPPGKLEWIGEINHRGTTY 59
      :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNMWIRQAPGKLEWVASITYDGSINY 60
QY      60 NPSLDGRVTISLDTSTNQISLKTSMTADTAIVYVCARTVAGTSDY-----WGQGTLL 111
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 NPSVKGRITISRDDSKNTFYLQMSLRAEDTAIVYCAR---GSHYFGHWHFAVWGQGTLL 116
QY      112 VTVSSGSASAPITGGGSGGGGSGGGSETTLTQSPAFMSATPGDKVISICKASRD 171
      |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      117 VTVS-----SEGGSGEGGSEGGSDIQLTQSPSSLSASVGDRTVITCRASKP 164
QY      172 VDDD-----VNWYQQRPEAFIFIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDA 227
      ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      165 VDGEGLSYLWYQKPKAPKLLIYAASYLESVPSRFSGSGSGTDFTLTISLQPEDFA 224
QY      228 YVFCLQHDNFPPLTFGGGTKEIK 250
      |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      225 TYCCQSHEDPYTFGGGTKEIK 247

RESULT 3
US-09-109-207C-22
; Sequence 22, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
```

```

; SEQ ID NO 22
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-248
; OTHER INFORMATION: sfv sequence derived from MAE11
;
US-09-109-207C-22

Query Match          51.8%; Score 691.5; DB 3; Length 248;
Best Local Similarity 54.4%; Pred. No. 2.1e-46;
Matches 143; Conservative 34; Mismatches 57; Indels 29; Gaps 5;

QY      1 QVQLQWGAAGLLKSWGTLSTCAVSGASF-SGYVSWIRQPPGKLEWIGEINHRGTTY 59
      :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNMWIRQAPGKLEWVASITYDGSINY 60
QY      60 NPSLDGRVTISLDTSTNQISLKTSMTADTAIVYVCARTVAGTSDY-----WGQGTLL 111
      |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 NPSVKGRITISRDDSKNTFYLQMSLRAEDTAIVYCAR---GSHYFGHWHFAVWGQGTLL 116
QY      112 VTVSSGSASAPITGGGSGGGGSGGGSETTLTQSPAFMSATPGDKVISICKASRD 171
      |||||:|:|:|:~|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      117 VTVS-----SEGGSGEGGSEGGSDIQLTQSPSSLSASVGDRTVITCRASKP 164
QY      172 VDDD-----VNWYQQRPEAFIFIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDA 227
      ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      165 VDGEGLSYLWYQKPKAPKLLIYAASYLESVPSRFSGSGSGTDFTLTISLQPEDFA 224
QY      228 YVFCLQHDNFPPLTFGGGTKEIK 250
      |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      225 TYCCQSHEDPYTFGGGTKEIK 247

RESULT 4
US-09-296-005-22
; Sequence 22, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 22
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-248
; OTHER INFORMATION: sfv sequence derived from MAE11
;
US-09-296-005-22

Query Match          51.8%; Score 691.5; DB 3; Length 248;
Best Local Similarity 54.4%; Pred. No. 2.1e-46;
Matches 143; Conservative 34; Mismatches 57; Indels 29; Gaps 5;

QY      1 QVQLQWGAAGLLKSWGTLSTCAVSGASF-SGYVSWIRQPPGKLEWIGEINHRGTTY 59
      :|||:|:|:|:~|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNMWIRQAPGKLEWVASITYDGSINY 60
QY      60 NPSLDGRVTISLDTSTNQISLKTSMTADTAIVYVCARTVAGTSDY-----WGQGTLL 111
      |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 NPSVKGRITISRDDSKNTFYLQMSLRAEDTAIVYCAR---GSHYFGHWHFAVWGQGTLL 116
QY      112 VTVSSGSASAPITGGGSGGGGSGGGSETTLTQSPAFMSATPGDKVISICKASRD 171
      |||||:|:|:|:~|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      117 VTVS-----SEGGSGEGGSEGGSDIQLTQSPSSLSASVGDRTVITCRASKP 164
```



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QY 172 VDDD---VNWYQQRPGEAPFIPIEDATTLVPGISPRFSGSGYGTDFLTLTINNIDSEDA 227
      ||:|||||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 165 VDGEGDSYLNWYQQRKPKAPKLLIYAASYLESGVPSRFSGSGSTDFLTLTISLQPEDFA 224
      ||:|||||:||||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 228 YFCLQHDNFPLTFGGGKVEIK 250
      ||:|||||:||||:||||:||||:|||||:|||||:|||||:|||||:|||||
Db 225 TYYCQOSHEDPYTFGGGKVEIK 247

```

RESULT 5  
US-09-92

US-09-920-171-22  
; Sequence 22, Application US/099201711

```

; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 22
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sfv sequence derived from MAE11
US-09-920-171-22

```

Query Match	51.8%;	Score 691.5;	DB 4;	Length 248;
Best Local Similarity	54.4%;	Pred. No. 2.1e-46;		
Matches 143;	Conservative 34;	Mismatches 57;	Indels 29;	Gaps 5;

[illegible]

RESULT 6  
US-08-88

US-08-887-352B-23  
; Sequence 23, Application US/08887352B

```

: GENERAL INFORMATION:
: APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
: TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
: TITLE OF INVENTION: Improving Polypeptides
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
:

```

```

: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/887,352B
: FILING DATE: 03-Jul-1997
:
: CLASSIFICATION: 530
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Svoboda, Craig G.
: REGISTRATION NUMBER: 39,044
: REFERENCE/DOCKET NUMBER: P1123
:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-1489
: TELEFAX: 650/952-9881
:
: INFORMATION FOR SEQ ID NO: 23:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 248 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
:
:
US-08-887-352B-23

```

Query Match	51.5%;	Score 687.5;	DB 2;	Length 248;
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Best Local Similarity 54.0%; Pred. No. 4.3e-46;  
Matches 142; Conservative 34; Mismatches 58; Indels 29; Gaps 5;

[illegible]

## RESULT 7

US-09-109-207C-23

```

; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 23

```

```

;
; LENGTH: 248
;
; TYPE: PRT
;
; ORGANISM: Artificial
;
; FEATURE:
;
; NAME/KEY: Artificial
;
; LOCATION: 1-248
;
; OTHER INFORMATION: sPV sequence derived from MAE11
;

```

US-09-109-207C-23

Query Match	51.5%	Score 687.5;	DB 3;	Length 248;
Best Local Similarity	54.0%;	Pred. No. 4.3e-46;		
Matches 142;	Conservative 34;	Mismatches 58;	Indels 29;	Gaps 5.

Qy		1 QVQLQQWAGLGLKSWGTLISLTCAVSGASF-SGYYSWIRQRPFGKLEWIGELINRGSTTY	59
Dd		1 EVQLVESGGGLVQPFGSLRLSCAVSGYSTTSGYSMNWIRQAIFGKLEWVASIKYSGETKY	60
Qy		60 NPSLDGRVTISLDTSTNQISLKLTSMTADTAIVYYCARTVAGTSDY-----WGQGTL	111
Dd		61 NPSSVKGRITISRDSKNTFYLNMSLRAREDIAVYYCAR----GSHYFGHMFVAWVGQGTLL	116
Qy		112 VTVSSGSASAPTTGGSGSGGGSGGGSGSETTLTQSFAFMSATPGDKVSIISCKASRD	171
Dd		117 VTVS-----SEGGSSEGGSGEGGSDIQLTQSPSSLASAVGDRTVITCRASKP	164
Qy		172 VDDD-----VNMYQQRPEGAFFIEDATTLPGISPRFSGSGYGTDFTLTINNIDSEDAA	227
Dd		165 VDGEGLSYLNMVYQOKPKAKPLLIYAASYLESQVPSRFSGSGTDFTLTISLQPEDFA	224
Qy		228 YVFCLQHDFNFPPLTFGGGTKEYEIK	250
Dd		225 TYYCCQSHEDPYTFGGGTKEYEIK	247

RESULT 8  
US-09-296-005-23

Query Match	51.5%;	Score 687.5;	DB 3;	Length 248;
Best Local Similarity	54.0%;	Pred. NO. 4.3e-46;		
Matches 142;	Conservative 34;	Mismatches 58;	Indels 29;	Gaps 5;

[illegible]

RESULT 9  
US-09-920-171-23  
; Sequence 23, Application US/099201711

Query Match	51.5%;	Score 687.5;	DB 4;	length 248;
Best Local Similarity	54.0%;	Pred. No. 4.3e-46;		
Matches 142;	Conservative 34;	Mismatches 58;	Indels 29;	Gaps 5

[illegible]

```

RESULT 10
US-08-918-148-79
; Sequence 79, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 79
; LENGTH: 244
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-79

```

Query Match	51.0%;	Score 681.5;	DB 4;	length 244;
Best Local Similarity	56.9%;	Pred. No. 1.2e-45;		
Matches 144;	Conservative 28;	Mismatches 62;	Indels 19;	Gaps 6;

QY	1	QVQLQQMGAGLLKSWGTLSTLCAVSGA	SFGYYWSMIR	QPPGKLEWIGETINHRG	STTYN	60
			: :			: :
Db	3	QVQLQQSGPGLVKPSETSLTCTVSGDS	ISSYYWSMIR	QPPGKLEWIGETI	YSGSTNYN	62
			: :			: :
QY	61	PSLDGRVTISLDTSTNQISLKLTSMTA	ADTA	VYCCARTVAGTSDYWGQGLTV	VSSGSAS	120
			: :			: :
Db	63	PSLSRVTISVDTSKSKQFSLKLSVTA	ADTA	VYCCAR--GRYFDVMGRGTMTV	VS-----	115
			: :			: :
QY	121	APTGGSGSGSGSGSGSGSEKTLTQSP	AFMSATPGDKV	SISCK-ASRPVD--DDVN		177
			: :			: :
Db	116	-----SGGGSGSGSGSGSGSSYL	TPPS-VSGSPGQSITISCTGTSSD	VGGYVS		167
			: :			: :
QY	178	WYQORPGEAFIFIIEDATLVPGISPR	SGSGYCTDFTLTINNIDSEDA	YFCLQH-DN		236
			: :			: :
Db	168	WYQQHPGAKPLMTYEGSKRPSGVSN	RFSGSKGN	TASLTISGLQAEDEADY	CSSYTT	227
			: :			: :
QY	237	FPLTFGGGTV	VEI	249		
			: :			: :
Db	228	STRVFGGCTKLTV	240			

```

US-08-918-148-77
RESULT 11
US-08-918-148-77
; Sequence 77, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 77
; LENGTH: 244
; TYPE: PR1
; ORGANISM: artificial
US-08-918-148-77

```

Query Match	50.9%;	Score 680.5;	DB 4;	Length 244;
Best Local Similarity	53.4%;	Pred. No. 1.5e-45;		
Matches 134;	Conservative 41;	Mismatches 63;	Indels 13;	Gaps 2;

OY	1 QVQLQQMGAGLLKSWGTLSTLCAVSGASFSGYYWSMIRQPPGKGLWEIGETINHRG-STTY	59
Db	3 QVQLVQSGGGLVRPGSLSLSCAVSGITLTFTYGMHWVRQAPEGKLEWVAGISFDGRSEYY	62
OY	60 NPSLDGRVTISLDTSTNQISLKLTSMTADTAVYYCARTVAGTSDYWGQGLTVVSSGA	119
Db	63 ADSVGRFITISRDSKNTLYLQMNSLRABDTAVYYCARGAHYGFDIWGQTWTYVS----	118
OY	120 SAPTGGGSGGGSGGGSGGGSETTLTQSAPFMSATPGDKVISICKASRDVDVNWY	179
Db	119 -----SGGGGTGGGGSGGGSGDIDMQTQSPSTLSASIGDRVITTCRASEGIVHMLAWY	170
OY	180 QORPGEAFIFIIEDATTLVPGISPRFGSGYGTDFTLTINNIDSEDAAYFCLOHDNFPL	239
Db	171 QOKPGAKPLLIIYKASSLASGAPSRFSGSGCTDFTLTISSLPDDPATYYCCQOYSNYPL	230
OY	240 TFGGGTKVEIK 250	
Db	231 TFGGGTELEIK 241	

## RESULT 12

```

US-09-509-031-16
; Sequence 16, Application US/09509031
; Patent No. 6590080
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/09/509, 031
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cmwlgL protein
; US-09-509-031-16

```

Query Match	50.7%;	Score 678;	DB 4;	Length 482;
Best Local Similarity	49.2%;	Pred. No. 5.1e-45;		
Matches 129;	Conservative 53;	Mismatches 62;	Indels 18;	Gaps 4;

[illegible]

```

RESULT 13
US-10-092-246-36
; Sequence 36, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Md
; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/092,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-36

```

Query Match	50.7%;	Score 677.5;	DB 4;	length 240;
Best Local Similarity	51.6%;	Pred. No. 2.5e-45;		
Matches 130; Conservative	49;	Mismatches 56;	Indels 17;	Gaps 4;

QY 1 QVQLQOMGAGLLKSWGTLTLTCAVSGASFSGYWWSWIRQPPGKGLEWIGEINHRG--STT 58  
Db 3 QVQLQESGPELVKPGASVKISCKASGYTFDYHVMWVKKPGQGLEWIG-MTYPGFNDTN 61  
QY 59 YNPSLDGRVTISLDTSTNQISLKLTSMTADTAIVYVCARTVAGTSYWGQGLVTVSSGS 118  
Db 62 YSETFKGKATLTVDTSNTVMQLSLTSEDTAIVFCARGVG--LDYWGQGTITVVS--- 116  
QY 119 ASAPTGGGGSGGGSGGGSGGSETTLTQSPAFMSATPGDKVISCKASRDVDDVNW 178  
Db 117 -----SGGGSGGGSGGGSGGSDIELTQSPNSLSTISGDRIRITCKASQDVTAVGW 167  
QY 179 YQORPGEAPFIIEDATTLVPGISPRFSGGYGTDFTLTINNIDSEDAAYFCLQHDNFP 238  
Db 168 YQORPGQSPKLLIFWSSSTRHTGVPDRFTSGSGTDFTLTISNVQSEDLADYFCHQYSSYP 227  
QY 239 LTFGGGTKEIK 250  
Db 228 FTFGSGTKLEIK 239

RESULT 14  
US-10-092-246-37  
; Sequence 37, Application US/10092246  
; Patent No. 6501314  
; GENERAL INFORMATION:  
; APPLICANT: The Minister of National Defence, Government of Canada  
; APPLICANT: Fulton, R E  
; APPLICANT: Alvi, Azhar E  
; APPLICANT: Nagata, Leslie  
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of M  
; TITLE OF INVENTION: scfv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)  
; FILE REFERENCE: NEL-0007  
; CURRENT APPLICATION NUMBER: US/10/092,246  
; CURRENT FILING DATE: 2002-03-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Mouse hybridoma cell line 1A4A1  
; US-10-092-246-37

Query Match 50.7%; Score 677.5; DB 4; Length 240;  
Best Local Similarity 51.6%; Pred. No. 2.5e-45;  
Matches 130; Conservative 49; Mismatches 56; Indels 17; Gaps 4;  
QY 1 QVQLQOMGAGLLKSWGTLTLTCAVSGASFSGYWWSWIRQPPGKGLEWIGEINHRG--STT 58  
Db 3 QVQLQESGPELVKPGASVKISCKASGYTFDYHVMWVKKPGQGLEWIG-MTYPGFNDTN 61  
QY 59 YNPSLDGRVTISLDTSTNQISLKLTSMTADTAIVYVCARTVAGTSYWGQGLVTVSSGS 118  
Db 62 YSETFKGKATLTVDTSNTVMQLSLTSEDTAIVFCARGVG--LDYWGQGTITVVS--- 116  
QY 119 ASAPTGGGGSGGGSGGGSGGSETTLTQSPAFMSATPGDKVISCKASRDVDDVNW 178  
Db 117 -----SGGGSGGGSGGGSGGSDIELTQSPNSLSTISGDRIRITCKASQDVTAVGW 167  
QY 179 YQORPGEAPFIIEDATTLVPGISPRFSGGYGTDFTLTINNIDSEDAAYFCLQHDNFP 238  
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QY 239 LTFGGGTKEIK 250  
Db 228 FTFGSGTKLEIK 239

RESULT 15  
US-08-918-148-78  
; Sequence 78, Application US/08918148A  
; Patent No. 6342220

; GENERAL INFORMATION:  
; APPLICANT: Adams, Camellia  
; APPLICANT: W.  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Fendly, Brian M.  
; APPLICANT: Gurney, Austin L.  
; TITLE OF INVENTION: Agonist Antibodies  
; FILE REFERENCE: P0979  
; CURRENT APPLICATION NUMBER: US/08/918,148A  
; CURRENT FILING DATE: 1997-08-25  
; NUMBER OF SEQ ID NOS: 79  
; SEQ ID NO 78  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; NAME/KEY: unknown  
; LOCATION: 208  
; OTHER INFORMATION: unknown amino acid  
US-08-918-148-78

Query Match 50.5%; Score 675; DB 4; Length 245;  
Best Local Similarity 52.8%; Pred. No. 4e-45;  
Matches 133; Conservative 41; Mismatches 64; Indels 14; Gaps 3;  
QY 1 QVQLQOMGAGLLKSWGTLTLTCAVSGASFSGYWWSWIRQPPGKGLEWIGEINHRG--TTY 59  
Db 3 QVQLVESGGGLVKGSLRLSCAASGFTFSHNMNWMVROAPGKGLEWYSSISSSYIY 62  
QY 60 NPSLDGRVTISLDTSTNQISLKLTSMTADTAIVYVCARTVAGTS-DYWGQGLVTVSSGS 118  
Db 63 ADSVKGRFTISRDNKNSLYLQMSLRADPTAVYYCARDRGSTGMVWGRGLTVVS--- 119  
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QY 179 YQORPGEAPFIIEDATTLVPGISPRFSGGYGTDFTLTINNIDSEDAAYFCLQHDNFP 238  
Db 171 YQKPKAKPKLLIYKASSLASGAPSRFSGSGTDFTXTTISLQPDPAFYCCQOYSNP 230  
QY 239 LTFGGGTKEIK 250  
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Search completed: May 13, 2004, 15:10:50  
Job time : 14.7136 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 15:07:07 ; Search time 37.0146 Seconds  
(without alignments)  
1879.405 Million cell updates/sec

Title: US-10-072-301-29

Perfect score: 1336

Sequence: 1 QVQLQQWGAGLLKSWGTSL.....CLQHDNPEPLTFGGTKVEIK 250

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
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- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
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- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1336	100.0	250	14	US-10-072-301-29	Sequence 29, Appl
2	1336	100.0	250	14	US-10-071-866-29	Sequence 29, Appl
3	1336	100.0	250	15	US-10-360-828-29	Sequence 29, Appl
4	1332	99.7	250	14	US-10-072-301-21	Sequence 21, Appl
5	1332	99.7	250	14	US-10-071-866-21	Sequence 21, Appl
6	1332	99.7	250	15	US-10-360-828-21	Sequence 21, Appl
7	838	62.7	249	10	US-09-880-748-1321	Sequence 1321, Ap
8	838	62.7	249	12	US-10-293-418-1321	Sequence 1321, Ap
9	808	60.5	286	12	US-10-406-830-8	Sequence 8, Appl1
10	760	56.9	251	10	US-09-880-748-1049	Sequence 1049, Ap
11	760	56.9	251	12	US-10-293-418-1049	Sequence 1049, Ap
12	741.5	55.5	248	10	US-09-880-748-1360	Sequence 1360, Ap
13	741.5	55.5	248	12	US-10-293-418-1360	Sequence 1360, Ap
14	741.5	55.5	252	10	US-09-880-748-1326	Sequence 1326, Ap
15	741.5	55.5	252	12	US-10-293-418-1326	Sequence 1326, Ap

16	739.5	55.4	250	10	US-09-880-748-1413	Sequence 1413, Ap
17	739.5	55.4	250	12	US-10-293-418-1413	Sequence 1413, Ap
18	736	55.1	255	10	US-09-880-748-1642	Sequence 1642, Ap
19	736	55.1	255	12	US-10-293-418-1642	Sequence 1642, Ap
20	734.5	55.0	250	10	US-09-880-748-1645	Sequence 1645, Ap
21	734.5	55.0	250	12	US-10-293-418-1645	Sequence 1645, Ap
22	734.5	55.0	253	12	US-10-239-656-63	Sequence 63, Appl
23	731	54.7	253	10	US-09-880-748-1333	Sequence 1333, Ap
24	731	54.7	253	12	US-10-293-418-1333	Sequence 1333, Ap
25	730.5	54.7	254	10	US-09-880-748-1659	Sequence 1659, Ap
26	730.5	54.7	254	12	US-10-293-418-1659	Sequence 1659, Ap
27	716	53.6	253	10	US-09-880-748-954	Sequence 954, App
28	716	53.6	253	12	US-10-293-418-954	Sequence 954, App
29	713	53.4	249	10	US-09-880-748-957	Sequence 957, App
30	713	53.4	249	12	US-10-293-418-957	Sequence 957, App
31	710	53.1	255	10	US-09-880-748-1597	Sequence 1597, Ap
32	710	53.1	255	12	US-10-293-418-1597	Sequence 1597, Ap
33	706	52.8	258	14	US-10-072-301-27	Sequence 27, Appl
34	706	52.8	258	14	US-10-071-866-27	Sequence 27, Appl
35	706	52.8	258	15	US-10-360-828-27	Sequence 27, Appl
36	705	52.8	253	10	US-09-880-748-1602	Sequence 1602, Ap
37	705	52.8	253	12	US-10-293-418-1602	Sequence 1602, Ap
38	702	52.5	239	10	US-09-880-748-1882	Sequence 1882, Ap
39	702	52.5	239	12	US-10-293-418-1882	Sequence 1882, Ap
40	701	52.5	237	10	US-09-880-748-1906	Sequence 1906, Ap
41	701	52.5	237	12	US-10-293-418-1906	Sequence 1906, Ap
42	699.5	52.4	251	12	US-10-239-656-65	Sequence 65, Appl
43	699	52.3	239	10	US-09-880-748-1922	Sequence 1922, Ap
44	699	52.3	239	12	US-10-293-418-1922	Sequence 1922, Ap
45	698	52.2	255	10	US-09-880-748-1626	Sequence 1626, Ap

ALIGNMENTS

RESULT 1  
US-10-072-301-29  
; Sequence 29, Application US/10072301  
; Publication No. US20030152913A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF  
; FILE REFERENCE: 25636-718  
; CURRENT APPLICATION NUMBER: US/10/072,301  
; CURRENT FILING DATE: 2002-02-08  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 29  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Clone 15.150.12 Variant  
US-10-072-301-29

Query Match	Score	100.0%	DB 14	Length	250
Best Local Similarity	100.0%	Pred. No. 2.5e-84			
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				Indels	0
				Gaps	0
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Db	1	QVQLQQWGAGLLKSWGTSLTCAVSGASFSGYWWSWITROPKGLWIGELINHRGSTTYN	60		
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QY 181 QRPGEAPIFIIEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAYYFCLQHDNFPPLT 240  
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Db 181 QRPGEAPIFIIEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAYYFCLQHDNFPPLT 240  
QY 241 FGGGTKEIK 250  
| | | | |  
Db 241 FGGGTKEIK 250

RESULT 2  
US-10-071-866-29

; Sequence 29, Application US/10071866  
; Publication No. US20030165988A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST F  
; TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS  
; FILE REFERENCE: 25636-717  
; CURRENT APPLICATION NUMBER: US/10/071,866  
; CURRENT FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 29  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.12 Variant  
US-10-071-866-29

Query Match 100.0%; Score 1336; DB 14; Length 250;  
Best Local Similarity 100.0%; Pred. No. 2.5e-84;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QVQLQQWAGLLKSWGTLISLTCAVSGASFSGYYWMIROPKGLIEWIGELINHRGSTTYN 60  
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| | | | |  
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Db 241 FGGGTKEIK 250

RESULT 3

US-10-360-828-29  
; Sequence 29, Application US/10360828  
; Publication No. US20030206909A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shaobing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS  
; FILE REFERENCE: 25636-727  
; CURRENT APPLICATION NUMBER: US/10/360,828  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: US 10/071,866  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/072,301

; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/133,978  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 29  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.12 Variant  
US-10-360-828-29

Query Match 100.0%; Score 1336; DB 15; Length 250;  
Best Local Similarity 100.0%; Pred. No. 2.5e-84;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 181 QRPGEAPIFIIEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAYYFCLQHDNFPPLT 240  
QY 241 FGGGTKEIK 250  
| | | | |  
Db 241 FGGGTKEIK 250

RESULT 4

US-10-072-301-21  
; Sequence 21, Application US/10072301  
; Publication No. US20030152913A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF  
; TITLE OF INVENTION: VIRUS  
; FILE REFERENCE: 25636-718  
; CURRENT APPLICATION NUMBER: US/10/072,301  
; CURRENT FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.12  
US-10-072-301-21

Query Match 99.7%; Score 1332; DB 14; Length 250;  
Best Local Similarity 99.6%; Pred. No. 4.8e-84;  
Matches 249; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      241 FGGGTKEIK 250
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RESULT 5  
US-10-071-866-21

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; Sequence 21, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST F
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Clone 15.150.12
US-10-071-866-21
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Query Match 99.7%; Score 1332; DB 14; Length 250;  
Best Local Similarity 99.6%; Pred. No. 4.8e-84;  
Matches 249; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      121 APTGGGGGGGGGGGGGGGGGGSETTLTQSPAFMSATPGDKVISISCKASRDVDDVNWYQ 180
      |||||||
Db      121 APTGGGGGGGGGGGGGGGGGGSKTTLTQSPAFMSATPGDKVISISCKASRDVDDVNWYQ 180
QY      181 QRPGEAPFIIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAAYFCLQHDNFPPLT 240
      |||||||
Db      181 QRPGEAPFIIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAAYFCLQHDNFPPLT 240
QY      241 FGGGTKEIK 250
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Db      241 FGGGTKEIK 250
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RESULT 6  
US-10-360-828-21

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; Sequence 21, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07
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; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.12
US-10-360-828-21
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Query Match 99.7%; Score 1332; DB 15; Length 250;  
Best Local Similarity 99.6%; Pred. No. 4.8e-84;  
Matches 249; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      1 QVQLQWAGLGLKSWGTLSLTCAVSGASFSGYYWMTIRPPGKLEWIGEINHRGTTYN 60
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      |||||||
Db      61 PSIDGRVTISLDTSTNQISLKLTSMTAADTAIVYVCARTVAGTSDYWGQGLVTVSSGSAS 120
QY      121 APTGGGGGGGGGGGGGGGGGGSETTLTQSPAFMSATPGDKVISISCKASRDVDDVNWYQ 180
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Db      121 APTGGGGGGGGGGGGGGGGGGSKTTLTQSPAFMSATPGDKVISISCKASRDVDDVNWYQ 180
QY      181 QRPGEAPFIIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAAYFCLQHDNFPPLT 240
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Db      181 QRPGEAPFIIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAAYFCLQHDNFPPLT 240
QY      241 FGGGTKEIK 250
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Db      241 FGGGTKEIK 250
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RESULT 7  
US-09-880-748-1321

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; Sequence 1321, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1321
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1321
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Query Match 62.7%; Score 838; DB 10; Length 249;  
Best Local Similarity 63.8%; Pred. No. 4.2e-50;  
Matches 166; Conservative 27; Mismatches 45; Indels 22; Gaps 3;



[illegible]

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RESULT 8
US-10-293-418-1321
; Sequence 1321, Application US/10293418
; Publication No. US20030223996A1
;
GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1321
;
LENGTH: 249
;
TYPE: PRT
;
ORGANISM: Homo sapiens
;
US-10-293-418-1321

```

Query Match	62.7%	Score 838;	DB 12;	Length 249;
Best Local Similarity	63.8%	Pred. No. 4.2e-50;		
Matches 166;	Conservative 27;	Mismatches 45;	Indels 22;	Gaps 3;

[illegible]

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QY      231 CLQHDNFP LTFGGGKVEIK 250
          | | | | | | | |
Db      229 CQGSYSTP WTFGGGKLEIK 248

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RESULT 9
US-10-406-830-8
; Sequence 8, Application US/10406830
; Publication No. US20040071696A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHA
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 407T-000410US
; CURRENT APPLICATION NUMBER: US/10/406,830
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic antibody.
US-10-406-830-8

```

Query Match	60.5%;	Score 808;	DB 12;	Length 286;
Best Local Similarity	62.8%;	Pred. No. 5.5e-48;		
Matches 159;	Conservative 32;	Mismatches 46;	Indels 16;	Gaps 3;

[illegible]

RESULT 10  
US-09-880-748-1049  
; Sequence 1049, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16



; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1049  
; LENGTH: 251  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1049

Query Match 56.9%; Score 760; DB 10; Length 251;  
Best Local Similarity 59.9%; Pred. No. 9.6e-45;  
Matches 157; Conservative 28; Mismatches 53; Indels 24; Gaps 6;

QY 1 QVQLQWAGLGLKSWGTSLTCAVSGASFSG--YYWSWIRQPPGKLEWIGEINHRGTT 58  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGFISRTSYMGWIRQPPGKPEWIGNIYYTGKTY 60  
QY 59 YNPISLDGRVTISLDTSTNQISLKLTSMTAADTAVYYCARTVAGTS-----DYWGQG 109  
Db 61 YSPSLKSRVTISVDTSKNQSLKLSVTAADTAVYYCAR--AGYDLITGYPFPYFDSWKG 118  
QY 110 TLVTVSSGSASAPITGGGSGGGSGGGSGGGSETTLTQSPAFMSATPGDKVISCKAS 169  
Db 119 TLVTVSS-----GGGSGGGSGGGSGGGSG--ALEIVLTQSPATLSLSPGERATLSCRAS 168  
QY 170 RDVDDVNMWYQORPGEAPFIPIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAAYY 229  
Db 169 QSVSSYLAWYQOKPGQAPRLIYDASNRATGIPARFSGSGSGTDFTLTISLLEPEDFAVY 228  
QY 230 FCLQHDNFP-LTFGGGTKEIK 250  
Db 229 YCQQRSNMPFLTFGGKTVEIK 250

RESULT 11  
US-10-293-418-1049  
; Sequence 1049, Application US/10293418  
; Publication No. US20030223996A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523P2  
; CURRENT APPLICATION NUMBER: US/10/293,418  
; PRIOR FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1049  
; LENGTH: 251  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-1049

Query Match 56.9%; Score 760; DB 12; Length 251;  
Best Local Similarity 59.9%; Pred. No. 9.6e-45;  
Matches 157; Conservative 28; Mismatches 53; Indels 24; Gaps 6;

QY 1 QVQLQWAGLGLKSWGTSLTCAVSGASFSG--YYWSWIRQPPGKLEWIGEINHRGTT 58  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGFISRTSYMGWIRQPPGKPEWIGNIYYTGKTY 60  
QY 59 YNPISLDGRVTISLDTSTNQISLKLTSMTAADTAVYYCARTVAGTS-----DYWGQG 109  
Db 61 YSPSLKSRVTISVDTSKNQSLKLSVTAADTAVYYCAR--AGYDLITGYPFPYFDSWKG 118  
QY 110 TLVTVSSGSASAPITGGGSGGGSGGGSGGGSETTLTQSPAFMSATPGDKVISCKAS 169  
Db 119 TLVTVSS-----GGGSGGGSGGGSGGGSG--ALEIVLTQSPATLSLSPGERATLSCRAS 168  
QY 170 RDVDDVNMWYQORPGEAPFIPIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAAYY 229  
Db 169 QSVSSYLAWYQOKPGQAPRLIYDASNRATGIPARFSGSGSGTDFTLTISLLEPEDFAVY 228  
QY 230 FCLQHDNFP-LTFGGGTKEIK 250  
Db 229 YCQQRSNMPFLTFGGKTVEIK 250

RESULT 12  
US-09-880-748-1360  
; Sequence 1360, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1360  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1360

Query Match 55.5%; Score 741.5; DB 10; Length 248;  
Best Local Similarity 58.9%; Pred. No. 1.8e-43;  
Matches 152; Conservative 31; Mismatches 56; Indels 19; Gaps 5;

QY 1 QVQLQWAGLGLKSWGTSLTCAVSGASFSGYYWSWIRQPPGKLEWIGEINHRGTTYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSIRSYWSWIRQPPGKLEWIGHIYHSGSTDYN 60  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTAADTAVYYCAR---TVAGT---SDYWGQGLV 112  
Db 61 PSLSRRTVMSIDTSKNQSLNLTSVTAADTAVYYCARDHYDVLTGSYLQAFDVGQGLV 120  
QY 113 TVSSGSASAPITGGGSGGGSGGGSGGGSETTLTQSPAFMSATPGDKVISCKASRDV 172  
Db 121 TVSS-----GGGSGGGSGGGSGGGSG--ALDIQLTQSPSSLSASVGDRVITTCRASQSI 170  
QY 173 DDDVNMWYQORPGEAPFIPIEDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAAYYFCL 232  
Db 171 GRYLWYQOKPGRAPRLIYFTSSLSHSDVPSRFSGSGSGTDFTLTISNLPEDFAVYCO 230  
QY 233 QHDNFP-LTFGGGTKEIK 250  
Db 231 QSYTDP-TFGGTRLEIK 247

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RESULT 13
US-10-293-418-1360
; Sequence 1360, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIORITY FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1360
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1360

Query Match
Best Local Similarity 55.5%; Score 741.5; DB 12; Length 248;
Matches 152; Conservative 31; Mismatches 56; Indels 19; Gaps 5;

QY 1 QVQLQOWGAGLTKSWGTLTLTCAVSGASFSGYWYMWIRPPGKGLWIGIINHRGSTTNN 60
DB 1 QVQLQESGPGLVKPSSETLSLSTCTVSGGSIRSYWYMWIRQSPGKLEWIGHIYHSGSTTNN 60
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAVYYCAR---TVAGT---SDYWGQGTLY 112
DB 61 PSLRSRVMTSIDTSKNQFSLNLTSTVTAADTAVYYCARDHYDVLTSYLQAFDVMGQGTLY 120
QY 113 TVSSGSASAPRTGGGSGGGGSGGGGSETTLTQSPAFMSATPGDKVISICKASRDV 172
DB 121 TVSS-----GGGGSGGGGSGGGG---ALDIQLTQSPSSLSASVGDRTVITCRASQSI 170
QY 173 DDDVNMWYQQRPGEPAPFIIEIDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDAAYFCL 232
DB 171 GRYLNMWYQQRPGEPAPRLLIFVTSSLHSDVPSRFSGSGGTDFSLTISNLQPEDFATYYCQ 230
QY 233 QHDFPLTFGGGTKEIK 250
DB 231 QSYTDP-TFGQGTREIK 247

RESULT 14
US-09-880-748-1326
; Sequence 1326, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIORITY FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
```

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; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1326
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1326

Query Match
Best Local Similarity 55.5%; Score 741.5; DB 10; Length 252;
Matches 154; Conservative 26; Mismatches 56; Indels 27; Gaps 6;

QY 1 QVQLQOWGAGLTKSWGTLTLTCAVSGASFSGYWYMWIRPPGKGLWIGIINHRGSTTNN 60
DB 1 QVQLQOWGAGLTKPSSETLSLTCVYSGSFSGYWYMWIRPPGKLEWIGHIYHSGSTTNN 60
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAVYYCARVAGTS-----DYWGQGT 110
DB 61 PSLRSRVMTSVDTSTNQFSLKLNSTVTAADTAVYYCARERADYDILGYFYGMQDVMGQGT 120
QY 111 LTVSSGSASAPRTGGGSGGGGSGGGGSETTLTQSPAFMSATPGDKVISICK-AS 169
DB 121 MVTVS-----SGGGSGGGGSGGGGSGSVLTQ-PASVSGSPQOSITISCTGTS 167
QY 170 RDVD--DDVNMWYQQRPGEPAPFIIEIDATTLVPGISPRFSGSGYGTDFTLTINNIDSEDA 227
DB 168 SDVGNYVSWYQQRPGKAPKLMYEGSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEA 227
QY 228 YVFCLQH-DNFPPLTFGGGTKEI 249
DB 228 DYYCSSYTRSTRVFGGKTLY 250

RESULT 15
US-10-293-418-1326
; Sequence 1326, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIORITY FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1326
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1326
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:50:27 ; Search time 11.2864 Seconds  
(without alignments)  
2130.694 Million cell updates/sec

Title: US-10-072-301-29  
Perfect score: 1336  
Sequence: 1 QVQLQQWGAGLTKSWGTLST.....CLQHDNFPPLTFGGGTKVEIK 250

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	614	46.0	249	2	S41374	single chain Fv an
2	604.5	45.2	268	2	A56446	Ig heavy chain V r
3	535	40.0	233	2	JC5322,	p53 specific singl
4	506	37.9	231	2	B23746	Ig Fab region IV-J
5	502.5	37.6	140	2	A49045	Ig heavy chain V r
6	498.5	37.3	143	2	B49028	Ig heavy chain V-I
7	490	36.7	140	2	S78052	Ig heavy chain pre
8	478	35.8	126	2	S47010	Ig heavy chain V4.
9	472	35.3	115	1	K3HU15	Ig kappa chain pre
10	452	33.8	146	1	GIH0H2	Ig heavy chain pre
11	442.5	33.1	122	2	JI0047	Ig heavy chain V r
12	439	32.9	97	2	S26898	Ig heavy chain V r
13	436.5	32.7	140	2	I37782	Ig variable region
14	431.5	32.3	130	2	S31690	Ig heavy chain V r
15	431	32.3	129	2	S44114	Ig heavy chain V r
16	430	32.2	97	2	S14474	Ig heavy chain V r
17	429	32.1	97	2	G34964	Ig heavy chain V-I
18	429	32.1	145	2	S78055	Ig heavy chain pre
19	425.5	31.8	114	2	I72667	cold agglutinin FS
20	420	31.4	118	2	S24443	Ig heavy chain V r
21	419.5	31.4	147	2	S13519	Ig heavy chain V r
22	418	31.3	139	2	S31586	Ig heavy chain V r
23	416	31.1	220	2	A49444	Ig gamma-1 heavy c
24	415.5	31.1	155	2	S31511	Ig heavy chain - h
25	414	31.0	97	2	S26805	Ig heavy chain V r
26	413.5	30.8	155	2	S31512	Ig heavy chain - h
27	411.5	30.7	123	2	S30530	Ig heavy chain V r
28	410	30.7	137	2	S31676	Ig heavy chain V r
29	409.5	30.7	134	2	S54906	Ig heavy chain V r

30	409	30.6	97	2	JH0428	Ig gamma chain V r
31	408	30.5	130	2	S30534	Ig heavy chain V r
32	406	30.4	118	2	S20780	Ig heavy chain V r
33	405.5	30.4	121	2	S44113	Ig heavy chain V r
34	404	30.2	97	2	S26806	Ig heavy chain V r
35	401.5	30.1	139	2	S31696	Ig heavy chain V r
36	400.5	30.0	127	2	S19668	Ig heavy chain V r
37	398.5	29.8	135	2	S78051	Ig heavy chain pre
38	396.5	29.7	146	2	S09711	Ig heavy chain V r
39	393	29.4	97	2	S26808	Ig heavy chain V r
40	391.5	29.3	123	2	S30529	Ig heavy chain V r
41	385.5	28.9	146	2	S09710	Ig heavy chain V r
42	385	28.8	106	2	S37454	Ig mu chain - huma
43	385	28.8	139	2	A41287	Ig heavy chain pre
44	384	28.7	97	2	S12416	Ig heavy chain V r
45	383.5	28.7	140	2	A24770	hypothetical hybrl

ALIGNMENTS

RESULT 1  
S41374  
single chain Fv antibody - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C;Accession: S41374  
R;Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.  
submitted to the EMBL Data Library, January 1994  
A;Description: Construction and functional characterization of a single chain Fv antiboc  
A;Reference number: S41374  
A;Accession: S41374  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-249 <ART>  
A;Cross-references: EMBL:Z29480

Query Match 46.0%; Score 614; DB 2; Length 249;  
Best Local Similarity 48.1%; Pred. No. 1.6e-32;  
Matches 124; Conservative 40; Mismatches 74; Indels 20; Gaps 4;

QY	1	QVQLQQWGAGLTKSWGTLSTLCVSGASFSGYWSWIRQPPKGLEWIGEI-NHRGSTTY 59
DB	1	QVQLQQSGABLVPRPGASVXLSTASGFNFKDDYIHWVQRPEKGLEWIAIAPASGVNKY 60
QY	60	NPSLDGRVTISLDSTNQISLKLTSMTADTAVVYCAR--TWAGTSDYWGQGLTVVSSG 117
DB	61	VERFDKATITADTSSNTAVYLLSSLTSEDTAVVYCARDTLYTSLGYWGQGSTVTVS-- 118
QY	118	SASAPTGGGSGGGSGGGSGGGSETTLTQSPAFMSATPGDKVISISCKASR-----DV 172
DB	119	-----SRGGSGGGSGGGSGGGSDIELTQSPSPVAVIPGESVSISCRSSKSLYSDG 168
QY	173	DDVNWYQQRPEAFPIEDATTLVPGISPRFSGSGYGTDTTLTINNIDSEDAVYFCL 232
DB	169	DSYLFWFLQRPQSPQLLIYRMSNLASGVPPDRFSGSGGTSFTLRISRVEAEDVGYTCM 228
QY	233	QHDNFPPLTFGGGTKVEIK 250
DB	229	QHREYPLTFGAGTKLELK 246

RESULT 2  
A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996  
C;Accession: A56446  
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.  
J. Biol. Chem. 270, 7829-7835, 1995  
A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally identifi  
A;Reference number: A56446; MUID:95229583; PMID:7713873  
A;Accession: A56446

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-268 <TAN>  
A:Cross-references: GB:U20617  
C:Keywords: heterotetramer; immunoglobulin

Query Match	45.2%;	Score 604.5;	DB 2;	Length 268;
Best Local Similarity	48.8%;	Pred. No. 6.9e-32;		
Matches 123;	Conservative 42;	Mismatches 72;	Indels 15;	Gaps 4;

```

QY      1 QVQLQWQWAGLLKSWGTLSTLTCAVSGSFSGYYSWIRQPPGKGLEWIGEL-NHRGSTTY 59
Db      3 QVKLQESGAEVLKPGASVKLSCTTSGFNIKDTYMHMWKQRPQGLIEWIGRIAPANGITKY 62
QY      60 NPSLDGRVTISLDTSTNQISLKLSTMTAADTAVYYCAR-TVAGTSDYWGQGLVTVSSGS 118
Db      63 DPKFQKATITADTSSNTAYLQLSLSTSEDTAVYYCASYYLTRYENYWGQTTTVTS--- 119
QY      119 ASAPFTGGSGSGSGSGSGGSEETLTQSPAFMSATPGDKVISISCKASRDVDDDVNW 178
Db      120 -----SGGGSGGSDSGGGSDIELTQSPALMSASLGEKVTMSCRASSV-NFIYW 169
QY      179 YQQRPGEAPIFIIEDATTLVPGISPRFSGSYGTDFTLTINNIDSEDAAYYFCLQHDNFP 238
Db      170 YQOKSDASPKLMVYYTSHLPGVPA RFSGSGSGNSYSLTISMEGEDAATYYCQGFSSP 229
QY      239 LTFGGGGTKVEIK 250
Db      230 FTFGSGTKLEIK 241

```

RESULT 3

UC5322

p53 specific single-chain antibody Pab421 - human

C:Species: Homo sapiens (man)

C:Date: 15-May-1997 #sequence\_revision 15-May-1997 #text\_change 18-Jul-1997

C:Accession: UC5322

R:Jannot, C.B.; Hynes, N.E.  
Biochem. Biophys. Res. Commun. 230, 242-246, 1997

A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.

A:Reference number: UC5322; MUID:97168950; PMID:9016757

A:Accession: UC5322

A:Molecule type: mRNA

A:Residues: 1-233 <JAN>

A:Experimental source: hybridoma cell

C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match	40.0%;	Score 535;	DB 2;	length 233;
Best Local Similarity	45.6%;	Pred. No. 1.6e-27;		
Matches 114;	Conservative 41;	Mismatches 73;	Indels 22;	Gaps 6;
QY	5	QQWAGGLKSKWGTSLTC	AVSGASPSGYWMSWIRQPPKGL	EWIGEIN-HRGSTTYNPSL 63
Db	1	QESGAELVRS	GSASVKLSCTTSGFNINDYMHWYKRP	EQGLEWIGRIDPENGDADMTRSS 60
QY	64	DGRVTISLDTSTNQISL	KLTSMTADTAVYYCARTVAGTSDYWGQ	TLVTVSSGSASAPT 123
Db	61	GVKATMTADTSSNTAYL	QLSLTSEDTAVYYCN--AG-MDYWGQ	TTVTVS----- 108
QY	124	GGGSGGGSGGGSGGGSE	TTLTQSPAFMSATPPDKVISISCKASRD	VDDD---VNMY 179
Db	109	-----SGGGSGGGRAS	GGGGSDIELTQSPASLAVSLGQRATISCR	ASKSVSTSGYSYMHWN 164
QY	180	QQRPGEAPFI	IEDATTLVPGISPRFSGSGYGTDTLLTINN	IDSEDAYYFCLQHDNFPL 239
Db	165	QQKPGQPPRL	LIYLVNLSGCVPARFSGSGGTDTFLNIHP	VEEDATYYC-QHIRELT 223
QY	240	TFGGGTKEI	249	
Db	224	RSEGGTKLEI	233	

B23746  
Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
C/Accession: B23746  
R/Leonl, J.; Ghiso, J.; Goni, F.; Frangione, B.  
J. Biol. Chem. 266, 2836-2842, 1991  
A/Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin  
A/Reference number: A23746; MUID:91131575; PMID:1993660  
A/Accession: B23746  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-231 <LEO>  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
F;140-209/Domains: immunoglobulin homology <IMM>

```

Query Match          37.9%; Score 506; DB 2; Length 231;
Best Local Similarity 80.2%; Pred. No. 1,2e-25;
Matches 101; Conservative 4; Mismatches 17; Indels 4; Gaps 1;

QY      2 VQLQQMGAGLILKSWGTLSLTCAVSGASFSGYYSWIRQPPGKGLWEIGELNHRSITTYNP 61
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB       1 VQLQQMGAGLILKPSETLSLTGAVYGGSFSDYYWSWIRQPPGKGLWEIGELNHSGSTNYNP 60
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      62 SLDGRVTISLDSTNQISLKLTSMTAADTAAYVCARTVAGTS---DYWGQGTLYTVSSG 117
        || | ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
DB       61 SLKSRTVISVDTSKNQFSLKLSSVTADTAAYVCARPHDTSGHYWNMYWGQGTLYTVSSG 120
        || | ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY      118 SASAPT 123
        ||||| |||||
DB       121 SASAPT 126

```

RESULT 5  
A49045  
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999  
C/Accession: A49045  
R/Grillot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rassetti, L.Z.; Labaume, S.; Silverman  
Eur. J. Immunol. 22, 1781-1788, 1992  
A/Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes 1 bl  
A/Reference number: A49045; MUID:92324290; PMID:1623923  
A/Accession: A49045  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-140 <GRI>  
A/Cross-references: GB:S39381; NID:g250899; PIDN:AAB22441.1; PID:g250900  
A/Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBI:P:108089)  
C/Superfamily: immunoglobulin V region, immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;34-116/Domain: immunoglobulin homology <IMM>

```
Query Match      37.6%; Score 502.5; DB 2; Length 140;  
Best Local Similarity 80.2%; Pred. No. 1.1e-25;  
Matches 97; Conservative 5; Mismatches 14; Indels 5; Gaps 1;
```

QY           1 QVQLQQWAGALLKSWGTLSTLTCAVSGASFGSYIYMSWIRQPPKGLEWIGEINHRGSTTYN 60  
             ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db          20 QVQLQQWAGALLKPSETLSLTCAVYGGSFSGYYMSWIRQPPKGLEWIGEINHSGSTNYN 79  
  
QY           61 PSLDGRVTISLDTSTNQISLKLTSMATAADTAIVYCAR-----TVAGTSIDYWGQGTLTVS 115  
             ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
Db           80 PSLSRVRTISVDTSKNQFSKLSSVTAADTAIVYCARCGFAATIVESFDYWGGSTLVTS 139  
  
QY           116 S 116  
             -  
Db          140 S 140

## RESULT 4

RESULT 6  
B49028  
Ig heavy chain V-IV region - human (fragment)





F;44-54/Region: complementarity-determining 1  
F;55-69/Region: framework 2  
F;70-76/Region: complementarity-determining 2  
F;77-108/Region: framework 3  
F;109-115/Region: complementarity-determining 3  
F;43-108/Disulfide bonds: #status predicted

Query Match 35.3%; Score 472; DB 1; Length 115;  
Best Local Similarity 88.5%; Pred. No. 8.3e-24;  
Matches 85; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 143 SETLTQSPAFMSATPGDKVSIKASRDVDDVNWYQORPGEAIFILEDATTLVPGIS 202  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 20 AETLTQSPAFMSATPGDKVNISCKASQDIDDDMNWYQORPGEAIFILEDATTLVPGIP 79

QY 203 PRFSGSGYGTDFLTINNIDSEDAAYYFCLQHDNFP 238  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 80 PRFSGSGYGTDFLTINNIESEDAAYYFCLQHDNFP 115

RESULT 10  
GIHUH2

Ig heavy chain precursor V-II region (ARH-77) - human  
C/Species: Homo sapiens (man)  
C/Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 02-Sep-1997  
C/Accession: A02101  
R;Kudo, A.; Ishihara, T.; Nishimura, Y.; Watanabe, T.  
Gene 33, 181-189, 1985  
A/Title: A cloned human immunoglobulin heavy chain gene with a novel direct-repeat seque  
A/Reference number: A02101, MUID:85205332; PMID:3922855  
A/Accession: A02101  
A/Molecule type: mRNA  
A/Residues: 1-146 <KUD>  
A/Note: the sequence was determined from the differentiated gene  
A/Note: the authors translated the codon GGG for residue 17 as Arg  
C/Genetics:  
A/Gene: GDB:IGHV@  
A/Cross-references: GDB:128528; OMIM:147070  
A/Map position: 14q32.33-14q32.33  
A/Introns: 16/3  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-146/Product: Ig heavy chain V-II region (ARH-77) #status predicted <MAT>  
F;20-117/Region: V segment  
F;35-117/Domain: immunoglobulin homology <IMM>  
F;118-127/Region: D segment  
F;128-146/Region: J segment  
F;42-115/Disulfide bonds: #status predicted

Query Match 33.8%; Score 452; DB 1; Length 146;  
Best Local Similarity 72.2%; Pred. No. 2e-22;  
Matches 91; Conservative 6; Mismatches 19; Indels 10; Gaps 2;

QY 1 QVQLQWGAAGLLKSWGTLSTCAVSGASFSGYWSWIRQPPGKGLEWIGETINRGSTTYN 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 21 QVQLQWGAAGLVKPSSETLSLTCAVFGSGFSGYWSWIRQPPGKLEWIGETINRGSTNYK 80  
QY 61 PSLDGRVTISLDTSTNQISLKTSMTAADTAAYYCARV--AGTS-----DYGQGT 110  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 81 TSLKSRVTISLDTSKNLSLKLSSVTAADTAAYYCARGLRGWMDVDVYGGMDVWGQGT 140  
QY 111 LVTYSS 116  
:|||||  
Db 141 TTVYSS 146

RESULT 11  
JL0047

Ig heavy chain V region precursor (clone CR18) - human  
C/Species: Homo sapiens (man)  
C/Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 16-Aug-1996  
C/Accession: JL0047

R;Baer, R.; Forster, A.; Lavenir, I.; Rabbits, T.H.  
J. Exp. Med. 167, 2011-2016, 1988  
A/Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new  
A/Reference number: JL0047; MUID:88258392; PMID:3133445  
A/Accession: JL0047  
A/Molecule type: mRNA  
A/Residues: 1-122 <BAE>  
A/Experimental source: T-cell line RPMI 8402  
A/Note: the authors translated the reading frame which extends to the stop codon; the s  
A/Note: this sequence belongs to the VH II subgroup  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;23-105/Domain: immunoglobulin homology <IMM>

Query Match 33.1%; Score 442.5; DB 2; Length 122;  
Best Local Similarity 84.3%; Pred. No. 6.8e-22;  
Matches 86; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 1 QVQLQWGAAGLLKSWGTLSTCAVSGASFSGYWSWIRQPPGKGLEWIGETINRGSTTYN 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 9 QVQLQWGAAGLLKPSSETLSLTCAVYGGSGFSGYWSWIRQPPGKLEWIGETINRGSTNYN 68

QY 61 PSLDGRVTISLDTSTNQISLKTSMTAADTAAYYCAR-TVAG 101  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 69 PSLKSRVTISVDTSKNQFSKLSSVTAADTAAYYCARGTVRG 110

RESULT 12  
S26898

Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S26898; S12420  
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V  
A/Reference number: S26885, MUID:93021117; PMID:1404388  
A/Accession: S26898  
A/Molecule type: DNA  
A/Residues: 1-97 <TOM>  
A/Cross-references: EMBL:Z12363; NID:932944; PIDN:CAA78233.1; PID:g32945  
A/Experimental source: clone DP-63  
R;Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.  
EMBO J. 8, 3741-3748, 1989  
A/Title: The smaller human V(H) gene families display remarkably little polymorphism.  
A/Reference number: S09421, MUID:90059975; PMID:2511001  
A/Accession: S12420  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-97 <SAN>  
A/Cross-references: EMBL:X56364  
A/Experimental source: V(H)4.2  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 32.9%; Score 439; DB 2; Length 97;  
Best Local Similarity 85.6%; Pred. No. 8.9e-22;  
Matches 83; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 QVQLQWGAAGLLKSWGTLSTCAVSGASFSGYWSWIRQPPGKGLEWIGETINRGSTTYN 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVQLQWGAAGLLKPSSETLSLTCAVYGGSGFSGYWSWIRQPPGKLEWIGETINRGSTNYN 60  
QY 61 PSLDGRVTISLDTSTNQISLKTSMTAADTAAYYCAR 97  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 PSLKSRVTISVDTSKNQFSKLSSVTAADTAAYYCAR 97

RESULT 13

Ig variable region (VDJ) (clone T23-9) - human (fragment)  
I37782  
C/Species: Homo sapiens (man)



C;Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
C;Accession: I37782; S25476  
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A;Title: Somatic diversification in the heavy chain variable region genes expressed by h  
A;Reference number: A36876; MUID:94119917; PMID:8290556  
A;Accession: I37782  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-140 <RES>  
A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;46-128/Domain: immunoglobulin homology <IMM>

Query Match 32.7%; Score 436.5; DB 2; Length 140;  
Best Local Similarity 71.9%; Pred. No. 1.9e-21;  
Matches 87; Conservative 8; Mismatches 21; Indels 5; Gaps 1;  
QY 1 QVQLQOWGAGLLKSWGTLSTCAVSGASFSGYYWSWIRQPPGKGLEWIGELINHRGSTTYN 60  
| | | | : | | | | | | | | | | | | | | | | | | : | | | |  
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIRQPPGKGLEWIGIYVSGSTYTN 79  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTAADTA VYVCARTVAGT-----SDYWGQGTLVTVS 115  
| | | | | | | | | | | | | | | | | | | | | | : | | | | | | | |  
Db 80 PSLSKRVTVISVDTSKNQFSLKLSVTAADTA VYVCARHNSSSWYGRYFDYWGQGTLVTVS 139  
QY 116 S 116  
|  
Db 140 S 140

RESULT 14  
S31690  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31690  
R;Cuisinier, A.M.; Gauthier, L.; Boudit, L.; Fougereau, M.; Tonnelie, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31690  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-130 <CUI>  
A;Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 32.3%; Score 431.5; DB 2; Length 130;  
Best Local Similarity 68.8%; Pred. No. 3.6e-21;  
Matches 88; Conservative 7; Mismatches 18; Indels 15; Gaps 2;  
QY 1 QVQLQOWGAGLLKSWGTLSTCAVSGASFSGYYWSWIRQPPGKGLEWIGELINHRGSTTYN 60  
| | | | : | | | | | | | | | | | | | | | | | | : | | | |  
Db 6 QVQLQESGPGLVKPSSETLSLTCTVSGSISYYWSWIRQPPGKGLEWIGIYVSGSTYTN 65  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTAADTA VYVCARTVAGT-----DYWGQ 108  
| | | | | | | | | | | | | | | | | | | | | | : | | | | | | | |  
Db 66 PSLSKRVTVISVDTSKNQFSLKLSVTAADTA VYVCAR--GSSVLLWFGELLYFDYWGQ 122  
QY 109 GTLVTVSS 116  
| | | | | | | | | | | | | | | | | | | | | | : | | | | | | | |  
Db 123 GTLVTVSS 130

RESULT 15  
S44114  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C;Accession: S44114

R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r  
A;Reference number: S44105  
A;Accession: S44114  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-129 <HAW>  
A;Cross-references: EMBL:Z31579; NID:g472968; PIDN:CAA83451.1; PID:g940525  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 32.3%; Score 431; DB 2; Length 129;  
Best Local Similarity 69.8%; Pred. No. 3.9e-21;  
Matches 88; Conservative 6; Mismatches 24; Indels 8; Gaps 2;  
QY 1 QVQLQOWGAGLLKSWGTLSTCAVSGASF-SGYWSWIRQPPGKGLEWIGELINHRGSTTY 59  
| | | | : | | | | | | | | | | | | | | | | | | : | | | |  
Db 1 QVQLQESGPGLVKPSGTLSTCAVSGSISSSNMWSWIRQPPGKGLEWIGELIYHSGSTNY 60  
QY 60 NPSLDGRVTISLDTSTNQISLKLTSMTAADTA VYVCART-----VAGTSDYWGQTLV 112  
| | | | | | | | | | | | | | | | | | | | | | : | | | | | | | |  
Db 61 NPSFKSRVTISADTSKNQPSLKVNSVTAADTA VYVCARRNYDFWSGGDPFDYWGQTLV 120  
QY 113 TVSSGS 118  
| | | | | | | | | | | | | | | | | | | | | | : | | | | | | | |  
Db 121 TVSSAS 126

Search completed: May 13, 2004, 15:08:44  
Job time : 12.2864 secs

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Db 20 AETTLTQSPAFMSATPGDKVNISCKASQDIDDMMWYQOKPGFAAIFIIQEATTLVPGIP 79  
Qy 203 PRFSGSGYGTDFLTINNIDSEDAAYVFCIQHDNFP 238  
Db 80 PRFSGSGYGTDFLTINNIESEDAAYVFCIQHDNFP 115

RESULT 2  
HV2I\_HUMAN  
ID HV2I\_HUMAN STANDARD; PRT; 146 AA.  
AC P06331;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V-II region ARH-77 precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85205332; PubMed=3922855;  
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;  
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-  
RT repeat sequence in 5' flanking region.";  
RL Gene 33:181-189(1985).  
DR PIR; A02101; GIH0H2.  
DR HSSP; P01825; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; signal.  
FT SIGNAL 1 19  
FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.  
FT DOMAIN 20 117 V SEGMENT.  
FT DOMAIN 118 127 D SEGMENT.  
FT DOMAIN 128 146 J SEGMENT.  
FT DISULFID 42 115 BY SIMILARITY.  
FT NON TER 146 146  
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Query Match 33.8%; Score 452; DB 1; Length 146;  
Best Local Similarity 72.2%; Pred. No. 1.6e-26;  
Matches 91; Conservative 6; Mismatches 19; Indels 10; Gaps 2;

Qy 1 QVQLQQWGAGLTKSWGTLSTLCVAVSGASFSGYWSWIRPPGKGLWIGELNHRGTTYN 60  
Db 21 QVQLQQWGAGLVKPSFTLSLTCAVFGSGFSGYWSWIRPPGKGLWIGELNHRGTTYN 80  
Qy 61 PSLDGRVTISLDTSTNQISLKLTSMTAADTAVYYCARV--AGTS-----DYWGQGT 110  
Db 81 TSLKSRVTISLDTSKNLFSLKLSVTAADTAVYYCARGLRGWMDVDYYGMDVWGQGT 140  
Qy 111 LVTYSS 116  
Db 141 TVTVSS 146

RESULT 3  
HV2F\_HUMAN  
ID HV2F\_HUMAN STANDARD; PRT; 129 AA.  
AC P01824;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-II region WAH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=82222235; PubMed=6806818;  
RA Takahashi N., Tetaert D., Debire B., Lin L.-C., Putnam F.W.;  
RT "Complete amino acid sequence of the delta heavy chain of human  
RT immunoglobulin D.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).  
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA  
CC PROTEIN.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A02099; D2HWA.  
DR HSSP; P01825; 7FAB.  
DR GLYCOSITEDB; P01824; -.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 113 IG-LIKE.  
FT NON TER 129 129  
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 28.0%; Score 374.5; DB 1; Length 129;  
Best Local Similarity 61.2%; Pred. No. 6.3e-21;  
Matches 79; Conservative 10; Mismatches 27; Indels 13; Gaps 3;

Qy 1 QVQLQQWGAGLTKSWGTLSTLCVAVSGASF--SGYWSWIRPPGKGLWIGELNHRGTT 58  
Db 1 RLQLQESGPGLVKPSFTLSLTCTVSGGPIRRTGYWGIRPPGKGLWIGGYTGSIT 60  
Qy 59 YNPSLDGRVTISLDTSTNQISLKLTSMTAADTAVYYCAR-----TVAGTS-----DYWG 107  
Db 61 YNPSLRGRVTISVDSRNQFSLNLRSMASADTAMYYCARGNPPYYDIGTSGDDGIDVWG 120  
Qy 108 QGTLVTVSS 116  
Db 121 QGTVTVSS 129

RESULT 4  
HV2G\_HUMAN  
ID HV2G\_HUMAN STANDARD; PRT; 117 AA.  
AC P01825;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-II region NEWM.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=77242302; PubMed=407927;  
RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;  
RT "Amino acid sequence of the VH region of a human myeloma  
RT immunoglobulin (IgG New).";  
RL Biochemistry 16:3412-3420(1977).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.  
RX MEDLINE=78066916; PubMed=618887;  
RA Saul F.A., Amzel L.M., Poljak R.J.;  
RT "Preliminary refinement and structural analysis of the Fab fragment  
RT from human immunoglobulin new at 2.0-A resolution.";  
RL J. Biol. Chem. 253:585-597(1978).  
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA  
CC PROTEIN.



CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A90404; G1HUM.  
DR PDB; 7FAB; 31-JAN-94.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KM Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.  
FT DOMAIN 1 111 IG-LIKE.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT STRAND 3 7  
FT STRAND 11 12  
FT TURN 14 15  
FT STRAND 18 25  
FT TURN 30 31  
FT STRAND 33 39  
FT TURN 41 42  
FT STRAND 46 51  
FT TURN 53 54  
FT STRAND 57 59  
FT HELIX 61 63  
FT TURN 64 66  
FT STRAND 72 76  
FT TURN 73 76  
FT STRAND 77 82  
FT HELIX 87 89  
FT STRAND 91 98  
FT STRAND 104 107  
FT STRAND 111 115  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;  
  
Query Match 27.4%; Score 365.5; DB 1; Length 117;  
Best Local Similarity 60.7%; Pred. No. 2.6e-20;  
Matches 71; Conservative 20; Mismatches 25; Indels 1; Gaps 1;  
  
QY 1 QVQLQQWAGLLKSWGTLSTCAVSGASFSGYYWSWIRQPPGKGLWIGINHRGTTYN 60  
Db 1 QVQLQQSGPGLVPSQTLSTCTVSGSTFSNDYTWVRQPPGKGLWIGYVFYHGTSDT 60  
  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAVYYCART-VAGTSDYWGQGLTVTVSS 116  
Db 61 TPILRSRVTLVDTSKNQFSRLSSVTAAVTAVYYCARNLIAICIDVWGQGLTVTVSS 117  
  
RESULT 5  
HV46\_MOUSE STANDARD; PRT; 137 AA.  
ID HV46\_MOUSE  
AC P01822;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ig heavy chain V region MOPC 315 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89238351; PubMed=2497341;  
RA Rinfret A., Horne C., Dorrington K.J., Klein M.;  
RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH  
RT gene segment.";  
RL Mol. Immunol. 26:431-434(1989).  
RN [2]  
RP SEQUENCE OF 1-31.  
RX MEDLINE=78094475; PubMed=414225;  
RA Jilka R.L., Pechtka S.;  
RT "Amino acid sequence of the precursor region of MOPC-315 mouse

RT immunoglobulin heavy chain.";  
RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).  
RN [3]  
RP SEQUENCE OF 1-21.  
RX MEDLINE=79148758; PubMed=428562;  
RA Schechter I., Wolf O., Zemel R., Burstein Y.;  
RT "Structure and function of immunoglobulin genes and precursors.";  
RL Fed. Proc. 38:1839-1845(1979).  
RN [4]  
RP SEQUENCE OF 19-136.  
RX MEDLINE=74170779; PubMed=4524622;  
RA Francis S.H., Leslie R.G.O., Hood L., Eisen H.N.;  
RT "Amino-acid sequence of the variable region of the heavy (alpha)  
RT chain of a mouse myeloma protein with anti-hapten activity.";  
RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).  
RN [5]  
RP REVISION TO 53.  
RX MEDLINE=77244979; PubMed=268248;  
RA Hood L., Margolies M.N., Givol D., Zakut R.;  
RL Unpublished results, cited by:  
RL Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;  
RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).  
CC -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA  
CC PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.  
-----  
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-----  
CC EMBL; M27638; AAA61337.1; -;  
CC EMBL; X07880; CAA30727.1; -;  
CC PIR; P0102; AVMS35.  
CC HSSP; P01825; 7FAB.  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR003596; Ig\_v.  
CC Pfam; PF00047; Ig; 1.  
CC SMART; SM00406; IGV; 1.  
CC PROSITE; PS50835; IG LIKE; 1.  
CC Immunoglobulin V region; Signal.  
CC SIGNAL 18  
FT CHAIN 19 137 IG HEAVY CHAIN V REGION MOPC 315.  
FT DOMAIN 19 48 FRAMEWORK-1.  
FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 85 116 FRAMEWORK-3.  
FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 127 137 FRAMEWORK-4.  
FT DISULFID 40 114 BY SIMILARITY.  
FT CONFLICT 15 15 G -> GG (IN REF. 1; CAA30727).  
FT CONFLICT 15 15 G -> H (IN REF. 2).  
FT CONFLICT 77 78 GY -> YG (IN REF. 4).  
FT CONFLICT 102 102 N -> D (IN REF. 4).  
FT CONFLICT 123 123 MISSING (IN REF. 4).  
FT NON\_TER 137 137  
SQ SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;  
  
Query Match 25.0%; Score 334.5; DB 1; Length 137;  
Best Local Similarity 57.4%; Pred. No. 5.5e-18;  
Matches 70; Conservative 14; Mismatches 27; Indels 11; Gaps 3;  
  
QY 2 VQLQQWAGLLKSWGTLSTCAVSGASF-SGYWSWIRQPPGKGLWIGINHRGTTYN 60  
Db 20 VQLQQSGPGLVPSQSLSTCVTGYSTSGYFWNIRQPPGNKLEWLGFIKYDGSNGYN 79  
  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAVYYCARTVAGTS-----DYWGQGLTVTV 114  
Db 80 PSLKRVSVITRDTSENQFPLKINSVTTEDTATYYC-----AGDNDHLVYFPDYWGQGLTVTV 135







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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; V00768; CAA24149.1; -.  
DR PIR; A02094; G2MS14.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-like; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOFC 141.  
FT DOMAIN 20 130 IG-like.  
FT NON TER 144 144  
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match 23.7%; Score 316.5; DB 1; Length 144;  
Best Local Similarity 52.0%; Pred. No. 1.2e-16;  
Matches 65; Conservative 16; Mismatches 35; Indels 9; Gaps 1;

QY 1 QVQLQOMGAGLKLKSWGTLSTCAVSGASFSGYWMIROPPGKLEWIGELNHRGTTYN 60  
DB 20 QVQLKESGPGVLVAPSQSLSTICTVSGFSLTGYGVNWRQPPGKLEWLGTIWNGSTIDYN 79  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTADTAVYVCARTVA-----GTSDYWGQGT 111  
DB 80 STLKSLRLTTKDNKSKSQVFLKMNLSLTQDDTARYYCASVSITYYGRSDKYFTLDYWGQGT 139  
QY 112 VTVSS 116  
DB 140 VTVSS 144

RESULT 11  
KV1A\_HUMAN STANDARD; PRT; 108 AA.  
ID P01593;  
AC 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=69234734; PubMed=4893682;  
RA Titani K., Shinoda T., Putnam F.W.;  
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The  
RT complete sequence and the location of the disulfide bridges.";  
RL J. Biol. Chem. 244:3550-3560(1969).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
DR PIR; A01861; KIHUAG.  
DR HSSP; P01607; 1REI.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-like; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 23.7%; Score 316; DB 1; Length 108;  
Best Local Similarity 54.8%; Pred. No. 9.5e-17;  
Matches 57; Conservative 22; Mismatches 25; Indels 0; Gaps 0;

QY 147 LTQSPAFMSATPGDKVSIACKASRDVDDVNMVYQGRGAPFIIEDATTLVPGISPRS 206  
DB 4 MTQSPFSLASVGDRTITCQASQDINHYLNWYQGPKKAPKILYDASNLSTGVPSRFS 63  
QY 207 GSGVGTDFTLTINNIDSEDAAYYFCLQHDNFPITFGGTKEIK 250  
DB 64 GSGVGTDFTLTISGLQPEDIAITYYCCQYDTLPRTFGGTKEIK 107

RESULT 12  
KV5A\_MOUSE STANDARD; PRT; 149 AA.  
ID P01633;  
AC 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-V region MPC11 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE OF 1-71 FROM N.A.  
RX MEDLINE=83001944; PubMed=6288267;  
RA Kelley D.E., Coleclough C., Perry R.P.;  
RT "Functional significance and evolutionary development of the  
RT 5'-terminal regions of immunoglobulin variable-region genes.";  
RL Cell 29:681-689(1982).  
RN [2]  
RP SEQUENCE OF 41-149 FROM N.A.  
RX MEDLINE=80176554; PubMed=6245773;  
RA Rabbits T.H., Hamlyn P.H., Matthysens G., Roe B.A.;  
RT "The variability, arrangement, and rearrangement of immunoglobulin  
RT genes.";  
RL Can. J. Biochem. 58:176-187(1980).  
RN [3]  
RP SEQUENCE OF 30-149.  
RX MEDLINE=7818617; PubMed=418775;  
RA Smith G.P.;  
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse  
RT myeloma MPC 11.";  
RL Biochem. J. 171:337-347(1978).  
CC -1- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS  
CC AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE  
CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL  
CC RESIDUE OF TYPICAL KAPPA CHAINS.  
CC -----  
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CC -----  
DR EMBL; J00561; AAA38776.1; -.  
DR PIR; A90823; KVM511.  
DR HSSP; P80362; 1WTL.  
DR InterPro; IPR007110; IG-like.



```
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; Repeat.
FT SIGNAL 1 29
FT CHAIN 30 149 IG KAPPA CHAIN V-V REGION MPC11.
FT DOMAIN 42 64 FRAMEWORK-1.
FT DOMAIN 65 75 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 76 90 FRAMEWORK-2.
FT DOMAIN 91 97 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 98 129 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 130 138 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 139 148 FRAMEWORK-4.
FT REPEAT 26 35
FT REPEAT 38 47
FT NON_TER 149 149
SQ SEQUENCE 149 AA; 16434 MW; B0480C87B682AC3E CRC64;

Query Match 23.7%; Score 316; DB 1; Length 149;
Best Local Similarity 53.2%; Pred. No. 1.3e-16;
Matches 59; Conservative 20; Mismatches 32; Indels 0; Gaps 0;

QY 140 GGSSETLTQSPAFMSATPGDKVISISCKASRDVDDVNMWYQQRPGAPIFIIEDATTLVP 199
DB 38 GVDGDIWMTQSHKFMSTSVGDRYSITCKASQDVSTVAMWYQQRPGQSPKLLIYSASYRT 97

QY 200 GISPRFSGSGYGTDTFTLTINNIDSEDAAYFYCLQHDNFPITFGGKVEIK 250
DB 98 GVPDRFTSGSGSDTFTFTISSVQAEIDLAVYYCQGHYSTPTPTGGGTKEIK 148

RESULT 13
KV1B_HUMAN STANDARD; PRT; 108 AA.
ID KV1B_HUMAN
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; Pubmed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin l-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; Pubmed=1234024;
RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the
RT Bence-Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC REGION OF THE KAPPA CHAIN REI.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91653; KIHUAV.
DR PDB; 1JV5; 30-JAN-02.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
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```
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6F6FB9 CRC64;

Query Match 23.6%; Score 315; DB 1; Length 108;
Best Local Similarity 54.8%; Pred. No. 1.1e-16;
Matches 57; Conservative 21; Mismatches 26; Indels 0; Gaps 0;

QY 147 LTQSPAFMSATPGDKVISISCKASRDVDDVNMWYQQRPGAPIFIIEDATTLVPGISPRS 206
DB 4 MTQSPSSLASVGVDRVITTCQASQDISDYLNMWYQQRPGAKPKLLIYDASNLSEGVSPRS 63

QY 207 GSGYGTDTFTLTINNIDSEDAAYFYCLQHDNFPITFGGKVEIK 250
DB 64 GGSAGAHFTFTISSIQPEDIALTYCQQYDLPWTFGGGTKEIK 107

RESULT 14
KV5_MOUSE STANDARD; PRT; 108 AA.
ID KV5_MOUSE
AC P01652;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region J606.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; Pubmed=6798111;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RT binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR PIR; A92811; KVM506.
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11810 MW; 8DE4DD31076F2APB CRC64;

Query Match 23.5%; Score 314; DB 1; Length 108;
Best Local Similarity 53.3%; Pred. No. 1.3e-16;
Matches 57; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 144 ETTLTQSPAFMSATPGDKVISISCKASRDVDDVNMWYQQRPGAPIFIIEDATTLVPGISP 203
DB 4 MTQSPSSLASVGVDRVITTCQASQDISDYLNMWYQQRPGAKPKLLIYDASNLSEGVSPRS 63
```

Db 1 DVQMIQSPSSLSASLGDIVTMTQASQGTSLNLNMFQOKPGKAPKLLIYGASNLDEGVPS 60

QY 204 RFGSGYGTDFTLTINNIDSEDAAYFCLQHDNFPPLTFGGGTVEIK 250

Db 61 RFGSGRYGTDFTLTISLDEDMATYFCLQHSYLPYTFGGGTKEIK 107

RESULT 15

KVSQ\_MOUSE

ID KVSQ\_MOUSE STANDARD; PRT; 108 AA.

AC P01650;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-V region UPC 61.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE.

RX MEDLINE=79195288; PubMed=109517;

RA Vrana M., Rudikoff S., Potter M.;

RT "The structural basis of a hapten-inhibitable kappa-chain idiotype.";

RL J. Immunol. 122:1905-1910(1979).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT

CC BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).

DR PIR; A92808; KVS61.

DR HSSP; P80362; 1WTL.

DR InterPro; IPR007110; Ig-1-like.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; Igv; 1.

DR PROSITE; PS50835; IG\_LIKE; 1.

KW Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 35 49 FRAMEWORK-2.

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 57 88 FRAMEWORK-3.

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 98 108 FRAMEWORK-4.

FT DISULFID 23 88 BY SIMILARITY.

FT NON\_TER 108 108

SQ SEQUENCE 108 AA; 11809 MW; FAEADA36076F2AFE CRC64;

Query Match 23.4%; Score 313; DB 1; Length 108;

Best local Similarity 53.3%; Pred. No. 1.6e-16;

Matches 57; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 144 ETTLTQSPAFMSATPGDKVISICASRDVDDVNMYQQRPGAPFIIEDATTLVPGISP 203

Db 1 DVQMIQSPSSLSASLGDIVTMTQASQGTSLNLNMFQOKPGKAPKLLIYGASILEDGVPS 60

QY 204 RFGSGYGTDFTLTINNIDSEDAAYFCLQHDNFPPLTFGGGTVEIK 250

Db 61 RFGSGRYGTDFTLTISLDEDMATYFCLQHSYLPYTFGGGTKEIK 107

Search completed: May 13, 2004, 15:02:06

Job time : 8.03884 secs



Db 40 QVKLQSGGLVPCGSLKLSCAASGSDPSRYWMSVWRQAPGKLEWIGEINPDSSTINY 99

QY 60 NPSLDGRVTISLDTSTNQISLKTSMATAADTAVYYCAR-TVAGTSDYWGQGLTVTVSSGS 118

Db 100 TPLKDKFISRDNAKNTLYLQMSKVRSEDITALYCARASYIGHSAYWGGTTVTVS--- 156

QY 119 ASAPTGGGGSGGGSGGGSGGGSETTLTQSPAFMSATPGDKVISICKASRDVDDVNM 178

Db 157 -----SGGGSGGGSGGGSGGGSDIELTQSPASLSASVGETVTITCRASGNINHYLAW 207

QY 179 YQORPGEAPIFIIEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAYYFCLQHDNFP 238

Db 208 YQOKGKSPQLLVYNAKTLADGVPRFRSGSGGTQYSLKINSLOPEDFGSYCQHFWTTP 267

QY 239 LTFGGGTKEIK 250

Db 268 YTFGGGTKEIK 279

RESULT 2

Q921A6 PRELIMINARY; PRT; 241 AA.

AC Q921A6; 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Anti-CEA 79 single chain Fv fragment (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

[1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98170165; PubMed=9509426;

RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D., Yi K.S., Suh P.G., Ryu S.H., Chung H.K., "Cloning and characterization of cDNAs encoding VH and VL of a monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and generation of a single-chain Fv molecule (scfv).";

RL Mol. Cells 7:816-819(1997).

DR EMBL; U88067; AAB48044.1; -. InterPro; IPR007110; Ig-like. InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00406; IGV; 2.

DR PROSITE; PS50835; IG\_LIKE; 2.

FT NON\_TER 1

FT NON\_TER 1

SQ SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

Query Match 45.4%; Score 606.5; DB 11; Length 241; Best Local Similarity 48.4%; Pred. No. 1.2e-39; Matches 124; Conservative 42; Mismatches 67; Indels 23; Gaps 6;

QY 1 QVQLQOWGAGLLKSMGTLISLTCAVSGASFSGYWMSWIRQPPGKLEWIGEIN-HRGSTTY 59

Db 1 QVKLQSGPELKKRGETVKISCKASGYTFPTYGMNWKQAPGKGLKMWGWINTYTGEPTY 60

QY 60 NPSLDGRVTISLDTSTNQISLKTSMATAADTAVYYCAR-TVAGTSDYWGQGLTVTVSSGS 118

Db 61 ADDEKGRFAFSLTSTASTAYLQINNKNEDTATYFCARKDLRYFDYWGQGTTVTVS--- 117

QY 119 ASAPTGGGGSGGGSGGGSGGGSETTLTQSPAFMSATPGDKVISICKASRDVDDVNM 178

Db 118 -----SGGGSGGGSGGGSGGGSDIELTQSPSSLSASLGKVTITCKASQDINKYIAM 168

QY 179 YQORPGEAPIFIIEDATL---VPGISPRFSGSGYGTDFLTINNIDSEDAAYYFCLQHDNFP 234

Db 169 YQHKPGKGP---RSATHTLHITYIQGIPSRFSGSGGRDYSFSSISNLEBEDIATYYCLHY 224

QY 235 DNFPPLTFGGGTKEIK 250

Db 225 DNLAH-TFGGGTKEIK 239

RESULT 3

Q7QM2 PRELIMINARY; PRT; 243 AA.

AC Q7QM2; 01-OCT-2003 (Tremblrel. 25, Created)

DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE scfv 6H8 protein (Fragment).

GN scfv 6H8.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=Balb/C;

RA Peter J.C., Eftekhari P., Billiald P., Wallukat G., "scfv single chain antibody variable fragment as inverse agonist for the beta-2 adrenergic receptor.";

RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

RL EMBL; AJ574851; CAE00495.1; -. NON\_TER 1

FT NON\_TER 1

SQ SEQUENCE 243 AA; 25976 MW; BEFF64D2DCFAF76 CRC64;

Query Match 44.0%; Score 588.5; DB 11; Length 243; Best Local Similarity 47.0%; Pred. No. 3e-38; Matches 118; Conservative 48; Mismatches 70; Indels 15; Gaps 4;

QY 1 QVQLQOWGAGLLKSMGTLISLTCAVSGASFSGYWMSWIRQPPGKLEWIGEIN-HRGSTTY 59

Db 1 QVQLQSGSELVPRGASVKLSCKASGYTFITYMHWKQRHGQGLEWIGNITYPGSGITNY 60

QY 60 NPSLDGRVTISLDTSTNQISLKTSMATAADTAVYYCARVAGTSDYWGQGLTVTVSSGSA 119

Db 61 DEKFNKGLITVDTSSSTAYMHLSSLASDSAVYYCARGGRL-DWGA GTTVTVS---- 115

QY 120 SAPTGGSGGGSGGGSGGGSGGGSETTLTQSPAFMSATPGDKVISICKASRDVDDVNM 179

Db 116 -----SGGGSGGGSGGGSGGGSDIQMTQSSSSFSVSLGDRVTITCKASEDIYNRLAWY 167

QY 180 QORPGEAPIFIIEDATTLVPGISPRFSGSGYGTDFLTINNIDSEDAAYYFCLQHDNFP 239

Db 168 QQKPGNAPRLISGATSLTGTGVPFRFSGSGSKDYTLSTSLQTEVDATYYCCQYWS-TR 226

QY 240 TFGGGTKEIK 250

Db 227 TFGGGTKEIK 237

RESULT 4

Q8WUX4 PRELIMINARY; PRT; 588 AA.

AC Q8WUX4; 01-MAR-2002 (Tremblrel. 20, Created)

DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

NCBI\_TaxID=9606;

[1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymph;

RA Strausberg R., Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL; BC019235; AAH19235.1; -. InterPro; IPR007110; Ig-like. InterPro; IPR003006; IG\_MHC. InterPro; IPR003596; IG\_v. Pfam; PF00047; Ig; 5.



DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;

Query Match 38.1%; Score 509; DB 4; Length 588;  
Best Local Similarity 41.0%; Pred. No. 1.4e-31;  
Matches 136; Conservative 23; Mismatches 81; Indels 92; Gaps 11;

QY 1 QVQLQQWAGAGLLKSWGTLSTLCVAVSGASFSGYWWSWIRQPPGKLEWIGELINHRGSTTYN 60  
DB 20 QVQLQQWAGAGLLKPSSETLSLTGCVYGSGFSGYWWSWIRQPPGKLEWIGELINHSGSTNYN 79  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTAADTAVVYCARTVAGTS-----DYWGQGTL 111  
DB 80 PSLKSRVTISVDTSKKQLSLKLSSVNAADTAVVYCARVITRASPGTDGRYGMVWGQGT 139  
QY 112 VTVSSGSASAPT-----GGGSGGGSGGSGG-----GSGGGSSETTLTQSPA 152  
DB 140 VTVSSGSASAPTLPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRG 199  
QY 153 FMSATPGDKVISISCKA---SRDV---DDVNMWYQORPG-----EAPIFIIED---ATT 196  
DB 200 FPSVLRGKGYAATSQVLLPSKDVMOGTDEHVCKVQHPNGNKEKNVPLPVIAELPPKVS 259  
QY 197 LVP-----GISPR-----FSGSGYGTD----- 213  
DB 260 FVPPRDGFPGNPRKSKLICQATGFSPRQIQVSWLREGKQVSGVTTDQVQAEAKESGPTT 319  
QY 214 ----FTLTINNIDSEDAAYYFCLQHDNFPPLTF 241  
DB 320 YKVTSTLTIKESDWLSQSMFTC-RVDHRLGLTF 350

RESULT 5

Q9BU10 PRELIMINARY; PRT; 597 AA.  
ID Q9BU10  
AC Q9BU10;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC002963; AAH02963.1; -  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match 38.1%; Score 509; DB 4; Length 597;  
Best Local Similarity 41.0%; Pred. No. 1.5e-31;  
Matches 136; Conservative 23; Mismatches 81; Indels 92; Gaps 11;

QY 1 QVQLQQWAGAGLLKSWGTLSTLCVAVSGASFSGYWWSWIRQPPGKLEWIGELINHRGSTTYN 60  
DB 20 QVQLQQWAGAGLLKPSSETLSLTGCVYGSGFSGYWWSWIRQPPGKLEWIGELINHSGSTNYN 79  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTAADTAVVYCARTVAGTS-----DYWGQGTL 111

DB 80 PSLKSRVTISVDTSKKQLSLKLSSVNAADTAVVYCARVITRASPGTDGRYGMVWGQGT 139  
QY 112 VTVSSGSASAPT-----GGGSGGGSGGSGG-----GSGGGSSETTLTQSPA 152  
DB 140 VTVSSGSASAPTLPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRG 199  
QY 153 FMSATPGDKVISISCKA---SRDV---DDVNMWYQORPG-----EAPIFIIED---ATT 196  
DB 200 FPSVLRGKGYAATSQVLLPSKDVMOGTDEHVCKVQHPNGNKEKNVPLPVIAELPPKVS 259  
QY 197 LVP-----GISPR-----FSGSGYGTD----- 213  
DB 260 FVPPRDGFPGNPRKSKLICQATGFSPRQIQVSWLREGKQVSGVTTDQVQAEAKESGPTT 319  
QY 214 ----FTLTINNIDSEDAAYYFCLQHDNFPPLTF 241  
DB 320 YKVTSTLTIKESDWLSQSMFTC-RVDHRLGLTF 350

RESULT 6

Q96AA6 PRELIMINARY; PRT; 618 AA.  
ID Q96AA6  
AC Q96AA6;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC017356; AAH17356.1; -  
DR PIR; S15590; S15590.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;

Query Match 38.1%; Score 509; DB 4; Length 618;  
Best Local Similarity 41.0%; Pred. No. 1.5e-31;  
Matches 136; Conservative 23; Mismatches 81; Indels 92; Gaps 11;

QY 1 QVQLQQWAGAGLLKSWGTLSTLCVAVSGASFSGYWWSWIRQPPGKLEWIGELINHRGSTTYN 60  
DB 20 QVQLQQWAGAGLLKPSSETLSLTGCVYGSGFSGYWWSWIRQPPGKLEWIGELINHSGSTNYN 79  
QY 61 PSLDGRVTISLDTSTNQISLKLTSMTAADTAVVYCARTVAGTS-----DYWGQGTL 111  
DB 80 PSLKSRVTISVDTSKKQLSLKLSSVNAADTAVVYCARVITRASPGTDGRYGMVWGQGT 139  
QY 112 VTVSSGSASAPT-----GGGSGGGSGGSGG-----GSGGGSSETTLTQSPA 152  
DB 140 VTVSSGSASAPTLPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRG 199  
QY 153 FMSATPGDKVISISCKA---SRDV---DDVNMWYQORPG-----EAPIFIIED---ATT 196  
DB 200 FPSVLRGKGYAATSQVLLPSKDVMOGTDEHVCKVQHPNGNKEKNVPLPVIAELPPKVS 259  
QY 197 LVP-----GISPR-----FSGSGYGTD----- 213  
DB 260 FVPPRDGFPGNPRKSKLICQATGFSPRQIQVSWLREGKQVSGVTTDQVQAEAKESGPTT 319

QY 214 ----FTLTINNIDSEDAAYFCLQHDNFPPLTF 241  
DB 320 YKVTSTLTIKESDWLSQSMFTC-RVDHRLGLTF 350

RESULT 7

Q9BQB8 PRELIMINARY; PRT; 597 AA.  
AC Q9BQB8; 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Muscle, and lymph;  
RA Strausberg R.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC006180; AAH06180.1; -.  
DR EMBL; BC001872; AAH01872.1; -.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig\_1like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 37 6%; Score 503; DB 4; Length 597;  
Best Local Similarity 40.7%; Pred. No. 4.3e-31;  
Matches 135; Conservative 23; Mismatches 82; Indels 92; Gaps 11;

QY 1 QVQLQWAGAGLKSMTLSLTCAVSGASFSGYWISWIRQPPGKLEWIGEINHRGTTYN 60  
DB 20 QVQLQWAGAGLKPSETLSLTGCVYGGSFSGYWSWIRQPPGKLEWIGEINHSGITVYN 79  
QY 61 PSLDGRVTISLDTSTNQISLKTSMTADTAVYYCARTVAGTS-----DYWGQGTL 111  
DB 80 PSLKSRVTISVDTSKQSLKLSVNAADTAVYYCARVITRASPGTDGRYGMVWGQGT 139  
QY 112 VTVSSGSASAPT-----GGGSGGGSGGG-----GSGGSETTLTQSPA 152  
DB 140 VTVSSGSASAPTLFPLVSCENSPSDTSSVAVGLAQDFLPDSITFSWKYKNSDISSTRG 199  
QY 153 FMSATPGDKVVISCKA---SRDV-----DDVNMWYQQRPG-----EAPIFILED---ATT 196  
DB 200 FPSVLRGKYAATSQVLLPSKDVMOGTDEHVCKVQHPPNGKKNVPLPVIAELPKVSV 259  
QY 197 LVP-----GISPR-----FSGSGYCTD----- 213  
DB 260 FVPFRDGFNGPRKSKLIGQATGSPRQIQVSWLREGKQYGSVTTDQVQAEAKESGPTT 319  
QY 214 ----FTLTINNIDSEDAAYFCLQHDNFPPLTF 241  
DB 320 YKVTSTLTIKESDWLSQSMFTC-RVDHRLGLTF 350

RESULT 8

Q925S1 PRELIMINARY; PRT; 218 AA.  
AC Q925S1; 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE MRP5 (Fragment).  
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX PubMed=11819679;  
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,  
RA Su C.;  
RT "Mechanism of exogenous nucleic acids and their precursors improving  
RT the repair of intestinal epithelium after irradiation in mice.";  
RL World J. Gastroenterol. 6:709-717(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Cui D., Zeng G., Yan X., Li X., Su C.;  
RT "Cloning of mouse genes related to repairing of intestinal epithelium  
RT of the irradiated mice by treatment with the intestinal RNA of mice of  
RT the same strain.";  
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
DR EMBL; AF240168; AAK43733.1; -.  
DR InterPro; IPR007110; Ig\_1like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 218  
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 34.1%; Score 456; DB 11; Length 218;  
Best Local Similarity 43.8%; Pred. No. 5.9e-28;  
Matches 98; Conservative 34; Mismatches 74; Indels 18; Gaps 4;

QY 1 QVQLQWAGAGLKSMTLSLTCAVSGASFSGYWISWIRQPPGKLEWIGEIN-HRGSTTY 59  
DB 3 QVQLQSGPELKKPGETVRISCKASGYFTTGMQWVQKMPGKLGWIGINTHSQVPKY 62  
QY 60 NPSLDGRVTISLDTSTNQISLKTSMTADTAVYYCAR-TVAGTSDYWGQGTLYTVS 118  
DB 63 AEEFKGRFAFSLETASTAYLIQISLNKEDTATYFCMRWDYDGFAYWGQGTTVVS--- 119  
QY 119 ASAPTGGGGSGGGSGGGSGGGSETTLTQSPAFMSATPGDKVISCKASRDVDD--- 174  
DB 120 -----SGGGSGGGSGGGSGGSDIVLTQSPASLAVSLGQRATISCRASESDNIGIS 170  
QY 175 DVNMWYQQRPGAPFIPIEDATTLVPGISPRFSGSGYGTDFTLTI 218  
DB 171 FMNWFQKPKQPPKLLIYAASKQSGVPAGLLASGSGTDFSLNI 214

RESULT 9

Q96EY0 PRELIMINARY; PRT; 613 AA.  
AC Q96EY0; 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011857; AAH11857.1; -.  
DR PIR; S15590; S15590.  
DR InterPro; IPR007110; Ig\_1like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 5.

DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match	33.2%;	Score 443.5;	DB 4;	Length 613;
Best Local Similarity	39.2%;	Pred. No. 2e-26;		
Matches 129;	Conservative 24;	Mismatches 85;	Indels 91;	Gaps 12;

QY	1	QVQLQQWGA	GLLKSMG	TLSLTCAV	SGASFTGY	WMIROPPG	KGLEWIG	EINHRG	STTYN	60					
		:	:	:	:	:	:	:	:						
Db	20	QVQLQESG	PGLVKPS	ETLSLTCT	IVSGGSI	SSYYWMI	RQPA	KGLEWIG	RIYTS	GSSTNYN	79				
QY	61	PSLDGRVT	ISLDST	NOISLKL	TSMTAD	TA	VYYCAR	-----	TVAGT	SDYWGQ	TLTV	114			
		:	:	:	:	:	:	:	:	:					
Db	80	PSLKS	RVTMSV	DTSKNQ	FLSKLS	SVTA	ADTA	VYYCAS	QPMEL	PTVG-	-LFYWGQ	TLTV	137		
QY	115	SSGSASAP	T-----	GGGSGGGG	GGG-----	GGGGS	GETTLQ	SPAFMS				155			
		:	:	:	:	:	:	:	:	:	:				
Db	138	SSGSASAP	TLFPLV	SCENSP	DTSSVA	VGCLAQ	DFLP	DSITF	SMKYK	NSDIS	TRGFPS	197			
QY	156	ATPGDKV	SISCKA	---SRD	V---DD	VNMVQ	QRRG	---EA	PIFI	ED---A	TLVLP	199			
		:	:	:	:	:	:	:	:	:	:				
Db	198	VLRG	GKYA	ATSQ	VLPLPS	KDVWG	GTDE	HVCKVQ	HPNG	NKEKNV	PLPVIA	ELPRK	VSFVP	257	
QY	200	-----	GISPR	-----	FSGSGY	GTD	-----					213			
		:	:	:	:	:	:	:	:	:	:				
Db	258	PRDGF	FGNPR	KSKLIC	QATG	FSFR	QIOV	SWLREG	KQVGS	GVTTD	QVQAE	AKES	GP	TTYKV	317
QY	214	-FTLT	INNID	SEDA	YFCL	OH	DNF	PLTF	241						
		:	:	:	:	:	:	:	:	:	:	:	:	:	
Db	318	TSTLT	IKESD	WLSQ	SMFTC	-RVD	H	RGLTF	345						

RESULT	ID	Q723Y6	PRELIMINARY;	PRT;	116 AA.
AC	Q723Y6;				
DT	01-OCT-2003	(TREMBLrel. 25, Created)			
DT	01-OCT-2003	(TREMBLrel. 25, last sequence update)			
DT	01-OCT-2003	(TREMBLrel. 25, last annotation update)			
DE	Rearranged VH4-34 V gene segment (Fragment).				
GN	VH4-34.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Hodgkin lymphoma;				
RA	Tinguely M., Rosengquist R., Sundstroem C., Amini R.M., Koppers R.,				
RA	Hansmann M.L., Brauning A.;				
RT	"Analysis of a clonally related mantle cell and Hodgkin lymphoma				
RT	indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg				
RT	cell precursor in a germinal center.";				
RL	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AJ564425; CAD92032.1; -.				
FT	NON_TER 1 1				
FT	NON_TER 116 116				
SO	SEQUENCE 116 AA; 12902 MW; CE3D8A846616C908 CRC64;				

Query Match	32.7%;	Score 437.5;	DB 4;	Length 116;
Best Local Similarity	72.0%;	Pred. No. 7.6e-27;		
Matches	85;	Conservative	8;	Mismatches 14;
				Indels 11;
				Gaps 1;

```
QY 1 QVQLQQQWGAAGLLKSNGLISLTCAVSGASFSGYYMSWTRPPGKGLEWIGELINHRGSTITYN 60
Db 1 QVQLQQWGAAGLLKPSSETLSLSCAVYGGSFSGYYMWNTRQPPGKGLEWIGELINHGSGTNYN 60
QY 61 PSLDGRVTTISLDTSTNOISLKLTSMTAADTAVVYCARTVAGTSDYWGQGLTVVTSGS 118
Db 61 PSLKSRVTTISVDTSKNQSLKLSSVTADTAVVYCAR-----GEIVVWPAS 107
```

RESULT 11	
095973	
ID 095973	PRELIMINARY;
	PRT; 150 AA.

DT	01-MAY-1999	(TREMBLrel. 10, Created)	
DT	01-MAY-1999	(TREMBLrel. 10, last sequence update)	
DT	01-OCT-2003	(TREMBLrel. 25, last annotation update)	
DE	VH4 heavy chain variable region precursor (Fragment).		
GN	IGM.		
OS	Homo sapiens (Human).		
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi		
CC	Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Sub C.-H., Song C.-H., Lee C.-H., Lee S.-K.;		
RT	"Clonal proliferation of Igm secreting B cell in the synovium of		
RT	Behcet's patient with arthritis."		
RL	Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF103795; AAC79084.1; --		
DR	HSSP; P01825; 7FAB.		
DR	InterPro; IPR007110; Ig-1like.		
DR	InterPro; IPR003596; Ig_v.		
DR	Pfam; PF00047; Ig; 1.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PSS0835; IG_LIKE; 1.		
KW	Signal.		
FT	SIGNAL	1	19
FT	CHAIN	20	>150
FT	NON_TER	150	150
FT	SEQUENCE	150 AA; 16315 MW; 85664E04938AA7C9 CRC64;	

[illegible]

```

RESULT 12
Q9UL73
ID Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment) .
OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998) .
DR EMBL; AF035041; AAD56277.1; -.

```



DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;

Query Match 31.2%; Score 416.5; DB 4; Length 119;  
Best Local Similarity 70.6%; Pred. No. 3.4e-25;  
Matches 84; Conservative 6; Mismatches 26; Indels 3; Gaps 1;

QY 1 QVQLQWAGALLKSWGTLSTLCAVSGASFSGYYSWIRQPPGKLEWIGELNHRGTTYN 60  
Db 1 QVQLQESGPGLVKPSSETLSLTCTVSGSICSYWSWIRQPPGKLEWIGIYISGSTYNT 60  
QY 61 PSLDGRVTISLDTSTNQISLKLSTMTADTAVVYCARTVAGTS--DYWGQTLVTYSS 116  
Db 61 PSLKSRVTISVDRSKNQFSLKLTSLTAADTAVVFCARLSNMGPIYFDYWGQTLVTYSS 119

RESULT 13  
ID Q96KX8 PRELIMINARY; PRT; 496 AA.

AC Q96KX8;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strauberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC016369; AAH16369.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 31.1%; Score 415.5; DB 4; Length 496;  
Best Local Similarity 42.8%; Pred. No. 2.4e-24;  
Matches 101; Conservative 20; Mismatches 54; Indels 61; Gaps 7;

QY 1 QVQLQWAGALLKSWGTLSTLCAVSGASF--SGYYSWIRQPPGKLEWIGELNHRGTT 58  
Db 20 QQLQESGPGLVKSSSETLSLTCTVSGSISSSSYWGWIRQPPGKLEWIANITYSGITY 79  
QY 59 YNPSLDGRVTISLDTSTNQISLKLSTMTADTAVVYCAR-----TVAGTSDYWGQTLV 112  
Db 80 YNPSLKSRVTISVDTSKNQLSLKYSVTADTAVVFCARHGYSRSGRTGAIDYWGQTLV 139  
QY 113 TVSSGSASAPTGSGSGSGSGSGSGSETTLTQSPAFMSATPGDKVISICKASRDV 172  
Db 140 TVSSASPTSPK-----VFPLSLCSTQPDGNVVIACLVQ--- 172  
QY 173 DDDVWVYQQRPGEAPIFIEDATLVPGISPRFSGSGYGTDFLTINNII-DSEDA 227  
Db 173 -----GFFPQEP-----LSVTWSESQG---VTARNFPPSQDAS 203

RESULT 14

Q7Z379  
ID Q7Z379 PRELIMINARY; PRT; 478 AA.  
AC Q7Z379;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein DKFZp686K04218 (Fragment).  
GN DKFZP686K04218.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amlid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX538066; CAD97996.1; -.  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match 30.2%; Score 403.5; DB 4; Length 478;  
Best Local Similarity 42.9%; Pred. No. 2e-23;  
Matches 100; Conservative 28; Mismatches 46; Indels 59; Gaps 10;

QY 1 QVQLQWAGALLKSWGTLSTLCAVSGASF-SG-YYSWIRQPPGKLEWIGELNHRGTT 58  
Db 19 QVQLQESGPGLVKPSQTLSTLTCTVSGSIGSGDYFWSWIRQAPRGLEWIGIYISGSTY 78  
QY 59 YNPSLDGRVTISLDTSTNQISLKLSTMTADTAVVYCARTVAGTS-DYWGQTLVTYSS 116  
Db 79 YNPSLKSRVTISIDTSKQFSLRLNSLTADTAVVFCARGLGTAFDIDWGQTLVTYSS 138  
QY 117 GSASAPTGSGSGSGSGSGSGSETTLTQSPAFMSATPGD-KVISICKASRDVDD 175  
Db 139 ASPTSP-----KVFLSLDSTPQDGNVVIACLVQ----- 167  
QY 176 VNWYQQRPGEAPIFIEDATLVPGISPRFSGSGYGTDFLTINNII-DSEDA 227  
Db 168 -GFFPQEP-----LSVTWSESQG---NVTARNFPPSQDAS 198

RESULT 15  
ID Q7Z374 PRELIMINARY; PRT; 492 AA.

AC Q7Z374;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein DKFZp686C02218 (Fragment).  
GN DKFZP686C02218.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amlid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX538077; CAD98001.1; -.  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 29.8%; Score 398; DB 4; Length 492;  
Best Local Similarity 41.9%; Pred. No. 5.5e-23;  
Matches 98; Conservative 23; Mismatches 53; Indels 60; Gaps 8;

QY 1 QVQLQWAGALLKSWGTLSTLCAVSGASF--GYYSWIRQPPGKLEWIGELNHRGTT 58



Db	32	QLQJESGPGLVKPSSETLSLCTVSGGSVSNRNYYWGWIRQPPGKGLEWIGSIYNNENTY	91
QY	59	YNPSLDGRVTISLDTSTNOISLKLTSMTAADTAVYYCARTYACT--SDYWGQGTIVTVS	115
Db	92	YSPSLKSRLTIFVDTSKNHFSRLRITSVTAADTAVYYCVRHVEGPGYGMFDPWGQGTIVTVS	151
QY	116	SGSASAPRTGGGGGGGGGGGGGGGGGGSETTLTQSPAFMSATPGD-KVISCKASRDVDD	174
Db	152	SASPTSP-----KVFPPLSLDSTPQDGNVVVACLIVQ-----	181
QY	175	DVNWYQQRPGEAIFILEDATLVPGISPRFSGSGYGTDFTLTNNI-DSEDA	227
Db	182	--GFFPQEP-----LSVTWSESGQ---NVTARNFPSPQDAS	212

Search completed: May 13, 2004, 15:07:00  
Job time : 34.6165 secs

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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:48:56 ; Search time 52.0738 Seconds  
(without alignments)  
1372.754 Million cell updates/sec

Title: US-10-072-301-31

Perfect score: 1348

Sequence: 1 QVTLKESGPTLVKPTQTTLT.....CQSDVLPPLTFGGTKVDIK 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: geneseqp19808:\*
- 2: geneseqp19908:\*
- 3: geneseqp20008:\*
- 4: geneseqp20018:\*
- 5: geneseqp20028:\*
- 6: geneseqp20038:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	844	62.6	256	3	AAY55072	Aay55072 Interleuk
2	844	62.6	260	3	AAY55075	Aay55075 Single ch
3	844	62.6	367	3	AAY55078	Aay55078 Single ch
4	844	62.6	381	3	AAY55079	Aay55079 Single ch
5	844	62.6	519	3	AAY55080	Aay55080 Single ch
6	844	62.6	546	3	AAY55074	Aay55074 Single ch
7	844	62.6	626	3	AAY55081	Aay55081 Single ch
8	844	62.6	640	3	AAY55082	Aay55082 Single ch
9	822.5	61.0	259	3	AAB09778	Aab09778 Antiviral
10	822.5	61.0	259	4	AAB70885	Aab70885 TMV 54K p
11	811.5	60.2	251	5	ABP45038	Abp45038 Human Bly
12	811.5	60.2	909	2	AAR50092	Aar50092 Humanised
13	803	59.6	248	5	ABP45349	Abp45349 Human Bly
14	801.5	59.5	255	5	ABP45592	Abp45592 Human Bly
15	800.5	59.4	249	5	ABP45310	Abp45310 Human Bly
16	789	58.5	248	5	ABP45865	Abp45865 Human Bly
17	787	58.4	240	4	AAB46044	Aab46044 Human TF
18	787	58.4	240	4	AAB46045	Aab46045 Human TF
19	786	58.4	248	5	ABP45410	Abp45410 Human Bly
20	786	58.3	240	4	AAB46010	Aab46010 Human MUC
21	781.5	58.0	243	5	ABP45924	Abp45924 Human Bly
22	781.5	58.0	249	5	ABP45177	Abp45177 Human Bly
23	779.5	57.8	272	2	AAR21260	Aar21260 ScFv sequ
24	779.5	57.8	285	2	AAR64810	Aar64810 ScFv anti
25	779	57.8	240	4	AAB46011	Aab46011 Human MUC

26	779	57.8	240	4	AAB46012	Aab46012 Human MUC
27	777	57.6	249	5	AAU75150	Aau75150 Amino aci
28	777	57.6	250	5	ABP45163	Abp45163 Human Bly
29	775	57.5	240	4	AAB46006	Aab46006 Human MUC
30	773	57.3	240	4	AAB45996	Aab45996 Human MUC
31	772	57.3	240	4	AAB46009	Aab46009 Human MUC
32	772	57.3	240	4	AAB46039	Aab46039 Human TF
33	771	57.2	240	4	AAB45991	Aab45991 Human MUC
34	769	57.0	240	4	AAB46018	Aab46018 Human MUC
35	769	57.0	240	4	AAB46021	Aab46021 Human MUC
36	769	57.0	266	5	ABG97826	Abg97826 Human sin
37	769	57.0	266	5	ABG35329	Abg35329 Thrombopo
38	767	56.9	240	4	AAB46013	Aab46013 Human MUC
39	767	56.9	240	4	AAB45992	Aab45992 Human MUC
40	767	56.9	240	4	AAB46017	Aab46017 Human MUC
41	767	56.9	240	4	AAB46014	Aab46014 Human MUC
42	766	56.8	240	4	AAB46040	Aab46040 Human TF
43	766	56.8	667	6	ABP97414	Abp97414 Anti-huma
44	765	56.8	240	4	AAB45997	Aab45997 Human MUC
45	765	56.8	240	4	AAB46038	Aab46038 Human TF

ALIGNMENTS

RESULT 1	
AAY55072	standard; protein; 256 AA.
ID	AAY55072 standard; protein; 256 AA.
AC	AAY55072;
XX	
DT	25-FEB-2000 (first entry)
XX	
DE	Interleukin-6 specific ScFv protein sequence.
XX	
KW	Gene isolation; membrane-bound protein; fusion protein; drug production;
KW	antigen-binding cell; secretable functional protein; antigenic protein;
KW	protein isolation; diagnosis; interleukin-6; ScFv.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	WO9960113-A1.
XX	
PD	25-NOV-1999.
XX	
PF	30-APR-1999; 99WO-JP002341.
XX	
PR	20-MAY-1998; 98JP-00138652.
PR	01-OCT-1998; 98JP-00279876.
XX	
PA	(CHUS ) CHUGAI SEIYAKU KK.
XX	
PI	Tsuchiya M, Saito M, Ohtomo T;
XX	
DR	WPI; 2000-039382/03.
DR	N-PSDB; AA240291.
XX	
PT	Efficient and selective isolation of a gene encoding membrane protein
PT	with low or no antigenic binding activity, for diagnosis, study of, and
PT	production of drugs treating abnormal functions of the protein.
XX	
PS	Example 1; Page 54-56; 120pp; Japanese.
XX	
CC	This sequence represents a ScFv specific for human interleukin-6. The
CC	invention relates to a method for isolating a gene encoding a membrane-
CC	bound protein, comprising introducing a vector into a cell, contacting an
CC	antigen with the cell expressing the fused protein encoded by the vector
CC	on its surface to select an antigen-binding cell, and isolating the cDNA.
CC	The vector contains DNA encoding a secretable functional protein with
CC	antigenicity and binding affinity, and a cDNA ligated to DNA downstream
CC	of the 3' end of the coding sequence. The method can be used to isolate a
CC	membrane-bound protein for diagnosis and study. It can also be used for

CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein

XX Sequence 256 AA;

Query Match 62.6%; Score 844; DB 3; Length 256;  
Best Local Similarity 65.6%; Pred. No. 3.1e-49;  
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTLTLCTFSGFSRLRTTGEVGVWVRQPPGKALEWIALIYWDDDKR 60  
Db 1 QVQLQESGPGLVRRPSQTLSTCTVSGYSI-TSDHAWSWVRQPPGRGLEWIGYISYGITT 59  
QY 61 YSPSLKSRLLITTKDTSKKQVLLTMNVDPADTATYYCTHEQYYDTSGPYYFDWGGQT 120  
Db 60 YNPSLKSRVTMLRDTSKNQFSRLSSVTAADTAVYYCAR-----SLARTTAMDYWGQS 113  
QY 121 LVTVSSGGGGSGGGSGGGSGGGSNIQVTQSPSSLSASVGDRTVMTCRASQDIRKNLN 180  
Db 114 LVTIVS-----SGGGSGGGSGGGSGGSDIQMTQSPSSLSASVGDRTVITTCRASQDISSYLN 168  
QY 181 WYQOKPGKAPKVLIVDASDLEFGIPSRFSGSGGTDFTLTSSLPEDIATYYCCQGSYDL 240  
Db 169 WYQOKPGKAPKLLIYTSRLHSGVPSRFSGSGGTDFTFTTSSLPEDIATYYCCQGNL 228  
QY 241 PLTFGGGTTKVDIK 253  
Db 229 PYTFGGGTTKVEIK 241

RESULT 2  
AAY55075  
ID AAY55075 standard; protein; 260 AA.

XX AAY55075;

DT 25-FEB-2000 (first entry)

DE Single chain Fv protein sequence shPM1(deltaBL).

KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretable functional protein; antigenic protein;  
KW protein isolation; diagnosis; ScFv.

OS Synthetic.

XX WO9960113-A1.

PD 25-NOV-1999.

PF 30-APR-1999; 99WO-JP002341.

PR 20-MAY-1998; 98JP-00138652.

PR 01-OCT-1998; 98JP-00279876.

PA (CHUS ) CHUGAI SEIYAKU KK.

PI Tsuchiya M, Saito M, Ohtomo T;

DR WPI; 2000-039382/03.

DR N-PSDB; AAZ40305.

PT Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
PT production of drugs treating abnormal functions of the protein.  
XX Example 7; Page 80-82; 120pp; Japanese.

XX This sequence represents a single chain Fv (ScFv) sequence. The invention  
CC relates to a method for isolating a gene encoding a membrane-bound  
CC protein, comprising introducing a vector into a cell, contacting an

CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the cDNA.  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for  
CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein

XX Sequence 260 AA;

Query Match 62.6%; Score 844; DB 3; Length 260;  
Best Local Similarity 65.6%; Pred. No. 3.1e-49;  
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTLTLCTFSGFSRLRTTGEVGVWVRQPPGKALEWIALIYWDDDKR 60  
Db 20 QVQLQESGPGLVRRPSQTLSTCTVSGYSI-TSDHAWSWVRQPPGRGLEWIGYISYGITT 78  
QY 61 YSPSLKSRLLITTKDTSKKQVLLTMNVDPADTATYYCTHEQYYDTSGPYYFDWGGQT 120  
Db 79 YNPSLKSRVTMLRDTSKNQFSRLSSVTAADTAVYYCAR-----SLARTTAMDYWGQS 132  
QY 121 LVTVSSGGGGSGGGSGGGSGGGSNIQVTQSPSSLSASVGDRTVMTCRASQDIRKNLN 180  
Db 133 LVTIVS-----SGGGSGGGSGGGSGGSDIQMTQSPSSLSASVGDRTVITTCRASQDISSYLN 187  
QY 181 WYQOKPGKAPKVLIVDASDLEFGIPSRFSGSGGTDFTLTSSLPEDIATYYCCQGSYDL 240  
Db 188 WYQOKPGKAPKLLIYTSRLHSGVPSRFSGSGGTDFTFTTSSLPEDIATYYCCQGNL 247  
QY 241 PLTFGGGTTKVDIK 253  
Db 248 PYTFGGGTTKVEIK 260

RESULT 3  
AAY55078  
ID AAY55078 standard; protein; 367 AA.

XX AAY55078;

DT 25-FEB-2000 (first entry)

DE Single chain Fv protein sequence shPM1-Kappa.

KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretable functional protein; antigenic protein;  
KW protein isolation; diagnosis; ScFv.

OS Synthetic.

XX WO9960113-A1.

PD 25-NOV-1999.

PF 30-APR-1999; 99WO-JP002341.

PR 20-MAY-1998; 98JP-00138652.

PR 01-OCT-1998; 98JP-00279876.

PA (CHUS ) CHUGAI SEIYAKU KK.

PI Tsuchiya M, Saito M, Ohtomo T;

DR WPI; 2000-039382/03.

DR N-PSDB; AAZ40308.

PT Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
PT production of drugs treating abnormal functions of the protein.



XX PS Example 7; Page 86-89; 120pp; Japanese.  
XX CC This sequence represents a single chain Fv (ScFv) sequence. The invention  
CC relates to a method for isolating a gene encoding a membrane-bound  
CC protein, comprising introducing a vector into a cell, contacting an  
CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the CDNA.  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a CDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for  
CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein  
XX SQ Sequence 367 AA;  
  
Query Match 62.6%; Score 844; DB 3; Length 367;  
Best Local Similarity 65.6%; Pred. No. 4.4e-49;  
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;  
  
QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSLRTTGEVGVWVRQPGKALEWLALIWDDDKR 60  
Db 20 QVQLQESGPGLVPRPSQTLSTCTVSGYSI-TSDHAWSWVRQPGRGLEWIGYISYSGITT 78  
QY 61 YSPSLKSRLLTITKDTSKKQVLTMTNVPADTATYYCTHEQYYVDTSQPYFDFWGGGT 120  
Db 79 YNPSLKSRLVTMLRDTSKNQFSLRLSSVTADTAVYYCAR-----SLARTTAMDYWGQGS 132  
QY 121 LVTVSSGGGGSGGGSGGGSGGGSNIQVTQSPSSLSASVGDRTVMTCRASQDIRKNLN 180  
Db 133 LVTVS-----SGGGSGGGSGGGSGGSDIQMTQSPSSLSASVGDRTVITCRASQDISSYLN 187  
QY 181 WYQOKPKGAPKVLIIYDASDLETGIPSRFSGSGSGTDFILTISLQPEDIATYYCQGSYLV 240  
Db 188 WYQOKPKGAPKVLIIYTSRLHSGVPSRFSGSGSGTDFITLSSLQPEDIATYYCQQGNTL 247  
QY 241 PLTFGGGTAKVDIK 253  
Db 248 PYTFGGGTKEIK 260  
  
RESULT 4  
AAY55079  
ID AAY55079 standard; protein; 381 AA.  
XX AC AAY55079;  
XX DT 25-FEB-2000 (first entry)  
XX DE Single chain Fv protein sequence shPM1-MCH4.  
XX KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretable functional protein; antigenic protein;  
KW protein isolation; diagnosis; ScFv.  
XX OS Synthetic.  
XX PN WO9960113-A1.  
XX PD 25-NOV-1999.  
XX PF 30-APR-1999; 99WO-JP002341.  
XX PR 20-MAY-1998; 98JP-00138652.  
XX PR 01-OCT-1998; 98JP-00279876.  
XX PA (CHUS ) CHUGAI SEIYAKU KK.  
XX PI Tsuchiya M, Saito M, Ohtomo T;  
XX

DR WPI; 2000-039382/03.  
DR N-PSDB; AAZ40309.  
XX PT Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
PT production of drugs treating abnormal functions of the protein.  
XX PS Example 7; Page 90-94; 120pp; Japanese.  
XX CC This sequence represents a single chain Fv (ScFv) sequence. The invention  
CC relates to a method for isolating a gene encoding a membrane-bound  
CC protein, comprising introducing a vector into a cell, contacting an  
CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the CDNA.  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a CDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for  
CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein  
XX SQ Sequence 381 AA;  
  
Query Match 62.6%; Score 844; DB 3; Length 381;  
Best Local Similarity 65.6%; Pred. No. 4.6e-49;  
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;  
  
QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSLRTTGEVGVWVRQPGKALEWLALIWDDDKR 60  
Db 20 QVQLQESGPGLVPRPSQTLSTCTVSGYSI-TSDHAWSWVRQPGRGLEWIGYISYSGITT 78  
QY 61 YSPSLKSRLLTITKDTSKKQVLTMTNVPADTATYYCTHEQYYVDTSQOPYFDFWGGGT 120  
Db 79 YNPSLKSRLVTMLRDTSKNQFSLRLSSVTADTAVYYCAR-----SLARTTAMDYWGQGS 132  
QY 121 LVTVSSGGGGSGGGSGGGSGGGSNIQVTQSPSSLSASVGDRTVMTCRASQDIRKNLN 180  
Db 133 LVTVS-----SGGGSGGGSGGGSGGSDIQMTQSPSSLSASVGDRTVITCRASQDISSYLN 187  
QY 181 WYQOKPKGAPKVLIIYDASDLETGIPSRFSGSGSGTDFILTISLQPEDIATYYCQGSYLV 240  
Db 188 WYQOKPKGAPKVLIIYTSRLHSGVPSRFSGSGSGTDFITLSSLQPEDIATYYCQQGNTL 247  
QY 241 PLTFGGGTAKVDIK 253  
Db 248 PYTFGGGTKEIK 260  
  
RESULT 5  
AAY55080  
ID AAY55080 standard; protein; 519 AA.  
XX AC AAY55080;  
XX DT 25-FEB-2000 (first entry)  
XX DE Single chain Fv protein sequence shPM1(deltaEL)-BvGS3.  
XX KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretable functional protein; antigenic protein;  
KW protein isolation; diagnosis; ScFv.  
XX OS Synthetic.  
XX PN WO9960113-A1.  
XX PD 25-NOV-1999.  
XX PF 30-APR-1999; 99WO-JP002341.  
XX PR 20-MAY-1998; 98JP-00138652.  
XX

PR 01-OCT-1998; 98JP-00279876.  
XX  
XX (CHUS ) CHUGAI SEIYAKU KK.  
PA  
XX  
XX Tsuchiya M, Saito M, Ohtomo T;  
PI  
XX WPI; 2000-039382/03.  
DR  
DR N-PSDB; AA240312.  
XX  
XX  
PT Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
PT production of drugs treating abnormal functions of the protein.  
PS  
PS Example 7; Page 95-100; 120pp; Japanese.  
XX  
XX This sequence represents a single chain Fv (ScFv) sequence. The invention  
CC relates to a method for isolating a gene encoding a membrane-bound  
CC protein, comprising introducing a vector into a cell, contacting an  
CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the CDNA.  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a CDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for  
CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein  
XX  
XX Sequence 519 AA;  
SQ

Query Match 62.6%; Score 844; DB 3; Length 519;  
Best Local Similarity 65.6%; Pred. No. 6.2e-49;  
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTTLTCTFSGFSRLRTGEGVGVNRQPPGKALEWLLAIYWD DDKR 60  
DB 20 QVQLQESGPGILVRPSQTLSTLCTVSGYSI-TSDHAMSVMRQPPGRLIEWIGYISYSGIT 78  
QY 61 YSPSLKSRLLITTKDTSKKQVLTMTNVPADTATYYCTHEQYYVDTSGQPYFDFWGGGT 120  
DB 79 YNPSLKSRYTMLRDTSKNQPSLRSLSSVTADTA VYYCAR-----SLARTTAMDYWGQS 132  
QY 121 LVTVSSGGGSGGGSGGGSGGGSNIQVTPSSLSASVGD RVTMTCRASQDIRKNLN 180  
DB 133 LVTVS-----SGGGSGGGSGGGSGGSDIQMTQSPSSLSASVGD RVTITCRASQDISSYLN 187  
QY 181 WYQKPKGAPKAPKLIYDASDLETGIPSRFSGSGGTDFILITISSLPEDIA TYYCQQS DYL 240  
DB 188 WYQKPKGAPKAPKLIYTSRLHSGVPSRFSGSGGTDFFTISSLPEDIA TYYCQQGNTL 247  
QY 241 PLTFGGGTKV D I K 253  
DB 248 PYTFGGGTKEIK 260

RESULT 6  
AAV55074  
ID AAV55074 standard; protein; 546 AA.  
XX  
AC AAV55074;  
XX  
XX 25-FEB-2000 (first entry)  
DT  
XX  
DE Single chain Fv protein sequence hPM1-BVGS3.  
XX  
KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW antigen-binding cell; secretable functional protein; antigenic protein;  
KW protein isolation; diagnosis; ScFv.  
XX  
XX Synthetic.  
OS  
XX  
PN WO960113-A1.

XX  
PD 25-NOV-1999.  
XX  
XX 30-APR-1999; 99WO-JP002341.  
PF  
XX  
XX 20-MAY-1998; 98JP-00138652.  
PR  
XX 01-OCT-1998; 98JP-00279876.  
PA  
XX (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Tsuchiya M, Saito M, Ohtomo T;  
XX  
XX WPI; 2000-039382/03.  
DR  
DR N-PSDB; AA240303.  
XX  
XX  
PT Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
PT production of drugs treating abnormal functions of the protein.  
PS  
PS Example 5; Page 73-78; 120pp; Japanese.  
XX  
XX This sequence represents a single chain Fv (ScFv) sequence. The invention  
CC relates to a method for isolating a gene encoding a membrane-bound  
CC protein, comprising introducing a vector into a cell, contacting an  
CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the CDNA.  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a CDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for  
CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein  
XX  
XX Sequence 546 AA;  
SQ

Query Match 62.6%; Score 844; DB 3; Length 546;  
Best Local Similarity 65.6%; Pred. No. 6.5e-49;  
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTTLTCTFSGFSRLRTGEGVGVNRQPPGKALEWLLAIYWD DDKR 60  
DB 20 QVQLQESGPGILVRPSQTLSTLCTVSGYSI-TSDHAMSVMRQPPGRLIEWIGYISYSGIT 78  
QY 61 YSPSLKSRLLITTKDTSKKQVLTMTNVPADTATYYCTHEQYYVDTSGQPYFDFWGGGT 120  
DB 79 YNPSLKSRYTMLRDTSKNQPSLRSLSSVTADTA VYYCAR-----SLARTTAMDYWGQS 132  
QY 121 LVTVSSGGGSGGGSGGGSGGGSNIQVTPSSLSASVGD RVTMTCRASQDIRKNLN 180  
DB 133 LVTVS-----SGGGSGGGSGGGSGGSDIQMTQSPSSLSASVGD RVTITCRASQDISSYLN 187  
QY 181 WYQKPKGAPKAPKLIYDASDLETGIPSRFSGSGGTDFILITISSLPEDIA TYYCQQS DYL 240  
DB 188 WYQKPKGAPKAPKLIYTSRLHSGVPSRFSGSGGTDFFTISSLPEDIA TYYCQQGNTL 247  
QY 241 PLTFGGGTKV D I K 253  
DB 248 PYTFGGGTKEIK 260

RESULT 7  
AAV55081  
ID AAV55081 standard; protein; 626 AA.  
XX  
AC AAV55081;  
XX  
XX 25-FEB-2000 (first entry)  
DT  
XX  
DE Single chain Fv protein sequence shPM1-kappa-BVGS3.  
XX  
KW Gene isolation; membrane-bound protein; fusion protein; drug production;  
KW

KW antigen-binding cell; secretable functional protein; antigenic protein;  
KM protein isolation; diagnosis; ScFv.  
XX Synthetic.  
OS  
XX WO960113-A1.  
PN  
XX 25-NOV-1999.  
PD  
XX  
PF 30-APR-1999; 99WO-JP002341.  
XX  
XX 20-MAY-1998; 98JP-00138652.  
PR 01-OCT-1998; 98JP-00279876.  
XX  
XX (CHUS ) CHUGAI SEIYAKU KK.  
XX  
XX Tsuchiya M, Saito M, Ohtomo T;  
PI  
XX WPI; 2000-039382/03.  
DR  
XX N-PSDB; AAZ40316.  
DR  
XX  
XX Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
PT production of drugs treating abnormal functions of the protein.  
XX  
XX Example 7; Page 103-109; 120pp; Japanese.  
PS  
XX  
XX This sequence represents a single chain Fv (ScFv) sequence. The invention  
CC relates to a method for isolating a gene encoding a membrane-bound  
CC protein, comprising introducing a vector into a cell, contacting an  
CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the vector  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for  
CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein  
XX  
SQ Sequence 626 AA;  
  
Query Match 62.6%; Score 844; DB 3; Length 626;  
Best Local Similarity 65.6%; Pred. No. 7.4e-49;  
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;

XX  
DT 25-FEB-2000 (first entry)  
XX  
XX Single chain Fv protein sequence shPM1-MCH4-BvGS3.  
DE  
XX  
KM Gene isolation; membrane-bound protein; fusion protein; drug production;  
KM antigen-binding cell; secretable functional protein; antigenic protein;  
KW protein isolation; diagnosis; ScFv.  
XX  
XX Synthetic.  
OS  
XX  
XX WO960113-A1.  
PN  
XX 25-NOV-1999.  
PD  
XX  
XX 30-APR-1999; 99WO-JP002341.  
PF  
XX  
XX 20-MAY-1998; 98JP-00138652.  
PR 01-OCT-1998; 98JP-00279876.  
XX  
XX (CHUS ) CHUGAI SEIYAKU KK.  
XX  
XX Tsuchiya M, Saito M, Ohtomo T;  
PI  
XX WPI; 2000-039382/03.  
DR  
XX N-PSDB; AAZ40321.  
DR  
XX  
XX Efficient and selective isolation of a gene encoding membrane protein  
PT with low or no antigenic binding activity, for diagnosis, study of, and  
PT production of drugs treating abnormal functions of the protein.  
XX  
XX Example 7; Page 111-117; 120pp; Japanese.  
PS  
XX  
XX This sequence represents a single chain Fv (ScFv) sequence. The invention  
CC relates to a method for isolating a gene encoding a membrane-bound  
CC protein, comprising introducing a vector into a cell, contacting an  
CC antigen with the cell expressing the fused protein encoded by the vector  
CC on its surface to select an antigen-binding cell, and isolating the cDNA.  
CC The vector contains DNA encoding a secretable functional protein with  
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream  
CC of the 3' end of the coding sequence. The method can be used to isolate a  
CC membrane-bound protein for diagnosis and study. It can also be used for  
CC producing drugs treating abnormal functions of the protein. Such a  
CC technique is efficient and selective, which is different from the prior-  
CC art transmembrane trap (TMT) method wherein an epitope recognised by an  
CC antibody is carried in a fused protein  
XX  
SQ Sequence 640 AA;  
  
Query Match 62.6%; Score 844; DB 3; Length 640;  
Best Local Similarity 65.6%; Pred. No. 7.6e-49;  
Matches 166; Conservative 29; Mismatches 46; Indels 12; Gaps 3;



	RESULT 9
ID	AAB09778
XX	AAB09778 standard; protein; 259 AA.
AC	XX AAB09778;
DE	DT 06-SEP-2000 (first entry)
XX	Anti-viral scFv-antibody against a component of the TMV replicase.
KW	Molecular pathogenecicide; plant disease; resistance; antibody; scFv;
KM	gene construct; pathogen; toxin; fusion protein; antimicrobial;
KX	deoxyribonuclease; RNase; ribosome inactivator; immunomodulator.
OS	Tobacco mosaic virus.
XX	Synthetic.
PN	WO200023593-A2.
PD	27-APR-2000.
PF	15-OCT-1999; 99WO-EP007844.
PR	16-OCT-1998; 98EP-00119630.
PR	16-OCT-1998; 98IN-MU000666.
PA	(FRAU ) FRAUNHOFER GES FORDERUNG ANGEWANDTEN.
PI	Fischer R, Schillberg S, Naehring J, Sack M, Monecke M, Liao Y;
PI	Spiegel H, Zimmermann S, Emans N, Holzem A,
DR	WI ; 2000-339692/29.
PT	New fusion proteins and gene constructs for expressing agents
PT	(antibodies, enzymes, vectors or molecular pathogenecicides), useful for
PS	protecting plants against pathogens and increasing resistance to disease.
XX	Example 6; Fig 23b; 193pp; English.
CC	The present invention describes a fusion protein (I) comprising at least
CC	one binding domain specifically recognising an epitope of a plant
CC	pathogen and at least one further domain comprising a protein or peptide
CC	sequence which is toxic to the pathogen or detrimental to its
CC	replication, transmission or life cycle. Also described is a
CC	pathogenicide (II) comprising (I) and a cellular targeting sequence
CC	and/or membrane localisation sequence and/or motif that leads to membrane
CC	anchoring; or at least one binding domain that specifically recognises a
CC	viral movement and/or replicase protein. The fusion protein,
CC	pathogenicide, polynucleotide, vectors, and compositions from the present
CC	invention are useful for the protection of a plant against the action of
CC	a pathogen. The kit from the present invention is useful for carrying out
CC	the diagnostic field or as research tools. The kit or its components,
CC	such as the fusion protein, pathogenicide, polynucleotides, vectors or
CC	compositions are useful in plant cell and plant tissue culture, in
CC	agriculture. They are extremely useful for breeding new varieties of
CC	plants that display improved properties such as resistance to pathogens.
CC	AAAS6587 to AAA56702 and AAB09774 to B097820 represent sequences used in
SO	Sequence 259 AA;
OY	Query Match            61.0%; Score 822.5; DB 3; Length 259; Best Local Similarity   61.2%; Pred. No. 8.7e-48; Matches     156; Conservative     39; Mismatches     53; Indels        7; Gaps          2  1 QVTIKESGPTLVKPTQTTLTLCFTSGFSRLRTGEGVGWRQPPGXALEMLALYYDDDKR 60      :::  :    :    :    :    :    :    :    : Db    3 QVTLKESGPGLKPSTLSTCSFGSFLSTSGMGWGIRPSPGGLEWLAIHWDDDKY 62  ::   ::   :    :    :    :    :    :    : OY    61 YSPSLKSRLTITKTDSKKQVLMTNVDPADATYYCYTHQQYYYDTSQGYPYFDFWGGGT 120  : :: :: :    :    :    :    :    :    :    :

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Db      63 YNPSLRSQLTISKDTSNQVFLRITNVDLTADTATYYCARGYYGNDSP-----FAYWGGGT 117
QY      121 LVTVSSGGGGSGGGSGGGSGG--GGSNIQVTQSPSLASVGDRTVMTCRASQDIRKN 178
Db      118 LITVSSGAGPTSGSGKRPGEKSTKAPDILVLSQSPKFMSTSVGDRVSITCKASQIVRTA 177
QY      179 LNMVQOKPGKAPKVLIVDASDLETGIPSRFSGSGSGTDFILTTISLQPEDIAATYYCOQSD 238
Db      178 VAMFQOKPGQSPKALIVLASNRHTGVPRFTGSGSGTDFLTISNVQSEDLADYFCLQHW 237
QY      239 YLPLTFGGGTIKVDIK 253
Db      238 NYPTFGSGTKLEIK 252

RESULT 10
AAB70885
ID      AAB70885 standard; protein; 259 AA.
XX
AC      AAB70885;
XX
DT      12-JUL-2001 (first entry)
XX
DE      TMV 54K protein derived monoclonal antibody scFv54-1.
XX
KM      Monoclonal antibody; detection; diagnosis; infection; scFv54-1.
XX
OS      Tobacco mosaic virus.
XX
PN      EP1092769-A2.
XX
PD      18-APR-2001.
XX
PF      18-AUG-2000; 2000EP-00117845.
XX
PR      15-OCT-1999; 99DE-01049855.
XX      19-APR-2000; 2000DE-01019473.
PA      (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
XX
PI      Fischer R, Helgers Y, Hoffmann K, Holzem A, Monecke M;
PI      Naehring J, Schillerberg S;
XX
DR      WPI; 2001-267745/28.
XX
PT      New polypeptide tag, useful for detection and isolation of fusion
PT      proteins, is derived from tobacco mosaic virus 54k protein and reacts
PT      specifically with antibodies.
XX
PS      Example 1; Page 7-8; 12pp; German.
XX
CC      This invention describes a novel polypeptide with tag sequence (I) or a
CC      sequence derived from (I) by replacement of one or more amino acids (aa),
CC      provided the three-dimensional/tertiary structure remains essentially
CC      unchanged. The invention also describes (1) expression vector encoding a
CC      fusion protein (FP) of a target polypeptide (II) and (I); (2) FP encoded
CC      by the vector of (1); (3) antibodies (Ab), or their fragments, directed
CC      against (I); and (4) kit containing the vector of (1) and optionally Ab.
CC      (I) are used for isolation and/or detection of fusion polypeptides that
CC      contain (I), by reaction with (I)-specific antibodies (Ab). Ab are used
CC      for isolation, purification and/or detection of polypeptides (also for
CC      determination of molecular weight, cell localization, post-translational
CC      modification and interaction with other factors), and for diagnosis of
CC      infection by tobacco mosaic virus (TMV). (I) is recognized by very
CC      specific, high-affinity antibodies that do not cross-react significantly
CC      with other cellular proteins (bacterial or eukaryotic). This sequence
CC      represents the monoclonal antibody scFv54-1 which is used to illustrate
CC      the method of the invention
XX
SQ      Sequence 259 AA;

Query Match      61.0%; Score 822.5; DB 4; Length 259;
Best Local Similarity 61.2%; Pred. No. 8,7e-48;

```



[illegible][illegible]

XX WPI; 1994-111012/14.  
DR N-PSDB; AAQ58896.  
XX  
PT New fusion protein contg. enzyme for prodnrg activation - coupled to  
PT antigen binding component, esp. scFv antibody fragment, partic. for  
PT treatment of tumours.  
XX  
PS Claim 13; Page 12-15; 35pp; German.  
XX  
CC The sequence AAR50092 comprises a humanised scFv-fragment against CEA  
CC fused to a human beta-glucuronidase. The fusion protein is useful for  
CC targeting beta-glucuronidase to cancer cells expressing CEA, where the  
CC enzyme is able to convert a prodnrg into its active form. Any fusion  
CC protein not bound to tumour can be removed by internalisation via the  
CC mannose-6-phosphate and galactose receptors. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX  
SQ Sequence 909 AA;

Query Match 60.2%; Score 811.5; DB 2; Length 909;  
Best Local Similarity 63.6%; Pred. No. 1.7e-46;  
Matches 161; Conservative 30; Mismatches 49; Indels 13; Gaps 5;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSLRTTGEVGVWVRQPPGKALEWLAITYWDDDKR 60  
Db 20 QVQLQESGPGLVRSQSLTSLCTVSGFTI-SSGYSMHWVRQPPGRGLEWIGYIQSGITN 78  
QY 61 YSPSLKSRLLITTKDTSKKQVLTMTNVPADTATYYCTHEQYYDTSGQPYFDFWGGGT 120  
Db 79 YNPSLKSRVLTMLVDTSKNQFSLRLSSVTAADTAVYYCAREDDYH-----WYFDVWGQGT 133  
QY 121 LVTVSSGGGGSGGGSGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKNLN 180  
Db 134 TVTVS-----SGGGSGGGSGGGSGGGSDIQLTQSPSSLSASVGDRTVITCSTSSSV-SYMH 187  
QY 181 WYQKPKGKAPKVLIDASDLETGIPSRFSGSGSGTDFILTSSLOPEDIATYYCQGSDDL 240  
Db 188 WYQKPKGKAPKLLIYSTSNLASGVSRFSGSGSGTDFITSSLOPEDIATYYCHQWGSY 247  
QY 241 PLTFGGGTKVDIK 253  
Db 248 P-TFGGQTKLEIK 259

RESULT 13  
ABP45349  
ID ABP45349 standard; protein; 248 AA.  
XX  
AC ABP45349;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Bly's binding scFv SEQ ID 1360.  
XX  
KW Bly's; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US019110.  
XX  
PR 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX  
DR WPI; 2002-114799/15.  
XX

PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.

PS Claim 1; Page 2025-2026; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to  
CC B Lymphocyte Stimulator (Bly's) polypeptides. Bly's is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Bly's. The antibodies bind to Bly's  
CC and so may be used to detect and quantitate the presence of Bly's in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Bly's. They may also be  
CC administered to treat diseases associated with aberrant Bly's expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention

SQ Sequence 248 AA;

Query Match 59.6%; Score 803; DB 5; Length 248;  
Best Local Similarity 63.2%; Pred. No. 1.7e-46;  
Matches 160; Conservative 32; Mismatches 55; Indels 6; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSLRTTGEVGVWVRQPPGKALEWLAITYWDDDKR 60  
Db 1 QVQLQESGPGLVKPSFTLSLCTVSGSIRS--YYSWIRQSPGRGLEWIGHIYHSGSTD 58  
QY 61 YSPSLKSRLLITTKDTSKKQVLTMTNVPADTATYYCTHEQYYDTSGQPYFDFWGGGT 120  
Db 59 YNPSLKSRVMTSIDTSKNQFSLNLTSTADTAVYYCARDHYDVLTGSGYLQAFDVGQGT 118  
QY 121 LVTVSSGGGGSGGGSGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKNLN 180  
Db 119 LVTVSSGGGGSGGGSGGGGS--ALDIQLTQSPSSLSASVGDRTVITCRASQIGRYLN 175  
QY 181 WYQKPKGKAPKVLIDASDLETGIPSRFSGSGSGTDFILTSSLOPEDIATYYCQGSDDL 240  
Db 176 WYQKPKGRAPRLIFVTSSLSHSDVPSRFSGSGSGTDFSLTISNLQPEDFATYYCQGS-YT 234  
QY 241 PLTFGGGTKVDIK 253  
Db 235 DPTFGGQTRLLEIK 247

RESULT 14  
ABP45592  
ID ABP45592 standard; protein; 255 AA.  
XX  
AC ABP45592;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Bly's binding scFv SEQ ID 1603.  
XX  
KW Bly's; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

KW	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX	common variable immunodeficiency; acquired immunodeficiency syndrome.
OS	Homo sapiens.
PN	WO200202641-A1.
PD	10-JAN-2002.
PF	15-JUN-2001; 2001WO-US019110.
PR	16-JUN-2000; 2000US-0212210P.
PR	17-OCT-2000; 2000US-0240816P.
PR	16-MAR-2001; 2001US-0276248P.
PR	21-MAR-2001; 2001US-0277379P.
PA	25-MAY-2001; 2001US-0293499P.
PI	(HUMA-) HUMAN GENOME SCI INC.
XX	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PT	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
PS	WPI; 2002-114799/15.
CC	Antibodies against B Lymphocyte Stimulating polypeptides, useful for the .
CC	diagnosis and treatment of cancers and immune disorders.
CC	Claim 1; Page 2316-2317; 3148pp; English.
CC	This invention describes novel antibodies that immunospecifically bind to
CC	B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC	tumour necrosis factor (TNF) super family and induces B cell
CC	proliferation and differentiation. The antibodies of the invention have
CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC	antirheumatic and antiAIDS activity and can be used in vaccines to
CC	inhibit the expression and activity of Blys. The antibodies bind to Blys
CC	and so may be used to detect and quantitate the presence of Blys in
CC	biological samples and may be used in this way to diagnose disease
CC	associated with aberrant expression of Blys. They may also be
CC	administered to treat diseases associated with aberrant Blys expression
CC	and activity such as cancer, immune, and autoimmune disorders and
CC	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC	immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC	the antibodies and fragments of the antibodies described in the method of
CC	the invention
XX	
SQ	Sequence 255 AA;
Query Match	59.5%; Score 801.5; DB 5; Length 255;
Best Local Similarity	62.0%; Pred. No. 2.2e-46;
Matches 163; Conservative 27; Mismatches 54; Indels 19; Gaps 6	
QY	1 QVTLKESGPTLVKPTQTLTLTCTFSGSFLRTTGEVGWVRQPEKALEWLALTY---WD 56   :::        ::   ::  :: ::   ::
DB	1 QVQLQQSGPGLVKPSQTLISCAISGDSVGSNGAAWMWIRQSPRGLEWLGRYYRSQWY 60   :::        ::   ::  :: ::   ::
QY	57 DDKRYSPLSKSRLLTTTKDTTSKKOVVLMTNVDPADATYYCTHEQYYD-TSGOPYY--- 112    :::        ::   ::  :: ::   ::
DB	61 SD--YGASVRSRITINADTSKNQFSLQNLNSVTPEDTAVVYYCARSGRYDILTG--YSSGG 116    :::        ::   ::  :: ::   ::
QY	113 --FDFWGGTLVTVSSGGGSGGGGGSGGGSNIQVTPSPSSLASVGDRTVMTCR 170   :::        ::   ::  :: ::   ::
DB	117 GGMDEVWGRLTVTS-----SGGGSGGGGGSGGGSIDIQMTQSPSTLSASIGDRVITTCR 171   :::        ::   ::  :: ::   ::
QY	171 ASODIRKLNLMWYQOKPKAPKVLIYDASDLETGIPSRFSGSGGTDFILTISSLPEDIA 230   :::        ::   ::  :: ::   ::
DB	172 ASEGITYHWLAWYQOKPKAPKLLIYKAASSLASGAPSRFGSGSGTDFTLTISSLPDDFA 231   :::        ::   ::  :: ::   ::
QY	231 TYQCQSGLDYLPITFGGGTKVDIK 253              ::   ::  :: ::   ::
DB	232 TYCCQQSYSNYPITFGGGTKLEIK 254              ::   ::  :: ::   ::

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RESULT.15
ABP45310
ID ABP45310 standard; protein; 249 AA.
XX
AC ABP45310;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1321.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
XX 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DX WPI; 2002-114799/15.
XX
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 1979-1980; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytosolic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 249 AA;
XX
Query Match 59.4%; Score 800.5; DB 5; Length 249;
Best Local Similarity 64.3%; Pred. No. 2.5e-46;
Matches 164; Conservative 27; Mismatches 55; Indels 9; Gaps 4;
QY 1 QVTLKESGPTLVKPTQTLTLTCTFSGFSRLTTGEGVGVWVRQPPGKALEWLAIIYWD DDKR 60
1 QVQLQGWGAGLLKRPSETLSITCAVYGSGF--SGYVWSWIRQPPGKGLEWIGEINHSGSTN 58
DB

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QY	61	YSPSLKSRLLTITKDTSKKQVLTMTNVPADTATYCTHEQY YD-TSGQPY-YFDFWGO	118
Db	59	YNPSLKS RVTISVDTSKNQFSLKLSVTADTAVYYCARGPRYYDILTG YRYNWFDPWGR	118
QY	119	GTIVTVSSGGGGSGGGSGGGSGGGSNIQVTQSPSSLASVGDRTMTCRASQDIRKN	178
Db	119	GTIVTVS-----SGGGSGGGSGGGSGGSDIVMTQSPSTLSASVGDRTVITCRASQGISW	173
QY	179	LNMYOQKPGKAPKVL IYDASDLETGIPSRFSGSGGTDFILTISSLQPED IATYYCQOSD	238
Db	174	LNMYOQKPGRAPKVL IYKASTLESVPSRFSGSGGTDFILTISSLQPED FATYYCQOSY	233
QY	239	YLPLTFGGGTKVDIK	253
Db	234	STPWTFGGGTKLEIK	248

Search completed: May 13, 2004, 15:01:01  
Job time : 53.0738 secs



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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:53:42 ; Search time 13.8782 Seconds  
(without alignments)  
941.146 Million cell updates/sec

Title: US-10-072-301-31  
Perfect score: 1348  
Sequence: 1 QVTLKESGPTLVKPTQTTLT.....CQGS DYLP LTFGGGTRKVDIK 253

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/iaa/PCrUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	764	56.7	248	2	US-08-887-352B-22 Sequence 22, Appl
2	764	56.7	248	3	US-09-109-207C-22 Sequence 22, Appl
3	764	56.7	248	3	US-09-296-005-22 Sequence 22, Appl
4	764	56.7	248	4	US-09-920-171-22 Sequence 22, Appl
5	762	56.5	244	4	US-08-918-148-77 Sequence 77, Appl
6	762	56.5	248	2	US-08-887-352B-23 Sequence 23, Appl
7	762	56.5	248	3	US-09-109-207C-23 Sequence 23, Appl
8	762	56.5	248	3	US-09-296-005-23 Sequence 23, Appl
9	762	56.5	248	4	US-09-920-171-23 Sequence 23, Appl
10	746.5	55.4	245	4	US-08-918-148-76 Sequence 76, Appl
11	742	55.0	359	4	US-09-646-028-16 Sequence 16, Appl
12	742	55.0	361	4	US-09-646-028-13 Sequence 13, Appl
13	736	54.6	264	3	US-08-564-164A-4 Sequence 4, Appl
14	734.5	54.5	240	1	US-08-488-113B-148 Sequence 148, App
15	734.5	54.5	240	1	US-08-477-484B-148 Sequence 148, App
16	734.5	54.5	240	2	US-08-646-360-148 Sequence 148, App
17	734.5	54.5	240	3	US-08-839-765-148 Sequence 148, App
18	734.5	54.5	240	3	US-09-136-389-148 Sequence 148, App
19	734.5	54.5	240	4	US-09-610-838-148 Sequence 148, App
20	734.5	54.5	240	4	US-09-918-148-78 Sequence 148, App
21	730.5	53.4	245	4	US-08-918-148-78 Sequence 78, Appl
22	720.5	53.4	235	2	US-08-190-199A-61 Sequence 61, Appl
23	714.5	53.0	245	4	US-08-918-148-75 Sequence 75, Appl
24	711	52.7	269	3	US-08-646-265A-109 Sequence 109, App
25	708.5	52.6	263	2	US-08-752-844-66 Sequence 66, Appl
26	708.5	52.6	263	4	US-09-293-533-66 Sequence 66, Appl
27	707	52.4	301	2	US-08-661-052-14 Sequence 14, Appl

28	707	52.4	301	3	US-09-188-082-14 Sequence 14, Appl
29	707	52.4	301	4	US-09-364-088-14 Sequence 14, Appl
30	707	52.4	301	4	US-09-102-716-14 Sequence 14, Appl
31	707	52.4	553	2	US-08-661-052-16 Sequence 16, Appl
32	707	52.4	553	3	US-09-188-082-16 Sequence 16, Appl
33	707	52.4	553	4	US-09-364-088-16 Sequence 16, Appl
34	707	52.4	553	4	US-09-102-716-16 Sequence 16, Appl
35	701.5	52.0	249	2	US-08-797-689-18 Sequence 18, Appl
36	701.5	52.0	249	4	US-09-984-186-18 Sequence 18, Appl
37	697.5	51.7	482	4	US-09-509-031-16 Sequence 16, Appl
38	685.5	50.9	277	2	US-08-256-790-2 Sequence 2, Appl
39	681.5	50.6	282	2	US-08-860-174A-10 Sequence 10, Appl
40	680.5	50.5	284	3	US-08-564-164A-2 Sequence 2, Appl
41	675	50.1	273	2	US-08-403-853-18 Sequence 18, Appl
42	672	49.9	243	1	US-07-958-140-2 Sequence 2, Appl
43	672	49.9	243	5	PCT-US93-09166-2 Sequence 2, Appl
44	664	49.3	240	4	US-10-092-246-36 Sequence 36, Appl
45	661	49.0	637	1	US-08-235-838-16 Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-08-887-352B-22  
Sequence 22, Application US/08887352B  
Patent No. 5994511  
GENERAL INFORMATION:  
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,352B  
FILING DATE: 03-Jul-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P1123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 248 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-887-352B-22

Query Match 56.7%; Score 764; DB 2; length 248;  
Best Local Similarity 60.7%; Pred. No. 1.4e-53;  
Matches 156; Conservative 30; Mismatches 57; Indels 14; Gaps 4;

QY	1	QVTLKESGPTLVKPTQTTLTCTFSGFSRLRTGEGVGVNRQPPGKALEWLAITYWDDKR	60
DB	1	EVQLVESGGGLVQPGGSLRLSCAVSGYSI-TSGYSWNIHQAPGKLEWVASITYDGSIN	59
QY	61	YPSLSKRLTITKDTSKQVLLMTNVPADTATYYCTHEQYVYDTSGQPYFDPMGQGT	120
DB	60	YNPSYKGRITISRDSKMTFYIQMNSLRADETAIVYVCARGSHYFG---HWHFAVWGQGT	115

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QY      121 LVTVSSGGGSGGGSGGGGSNTQTSPSSLASVGDRVMTTCRASODI----R   176
        ||||| | ||||| : ||||| : ||||| : ||||| : ||||| :
Db      116 LVTVS-----SEGGSGEGGSGEGGSDTLTQSPPSSLASVGDRVTTTCRASKPVDEGD 170
        ||||| | ||||| : ||||| : ||||| : ||||| : ||||| :
QY      177 KNLNMYYQQKP GKAPKVLIIYDASDLETGTISRFGSGSGCTDFILTISSLQPEPIATYYCQQ 236
        ||||| | ||||| : ||||| : ||||| : ||||| : ||||| :
Db      171 SYLNMYQQQPKGAKPKLLIYAASYLESQVPSRFSGSGSCTDFLTLISSLQPEDFATYYCQQ 230
        ||||| | ||||| : ||||| : ||||| : ||||| : ||||| :
QY      237 SDYLPLTFGGGKTVDIK 253
        | |||| | ||||| : ||||| : ||||| : ||||| :
Db      231 SHEDPYTFGGGTKEIK 247
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RESULT 2
US-09-109-207C-22
; Sequence 22, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 22
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-248
; OTHER INFORMATION: sfv sequence derived from MAE11
US-09-109-207C-22

```

Query Match	56.7%	Score 764	DB 3	Length 248
Best Local Similarity	60.7%	Pred. No. 1.4e-53		
Matches 156	Conservative 30	Mismatches 57	Indels 14	Gaps 4
QY	1	QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTTGEVGVWVRQPPGKALEWLLALIWDDDKR	60	
Db	1	EVQLVESGGGLVQPGSGSLRLSCAVSGYSI-TSGYSMNWIRQAPGKLEWVASITYDGSTN	59	
QY	61	YSPSLKSLTLITKDTSKQVVLMTNVDPADTATYYCTHEQYYYDTSQOPYYFDPMGGGT	120	
Db	60	YNPSVKGRITISRDDSKNTFYLOMNSLRADETAIVYYCARGSHYFG---HWHFAVMGGGT	115	
QY	121	LVTVSSGGGGSGGGSGGGSGGGSNIOVTQSPSSLASAVGDRVTMTCRASQDI---R	176	
Db	116	LVTVS-----SEGGGSEGGGSEGGGSDIQLTQSPSSLASAVGDRVTITCRASKPVPDGGSD	170	
QY	177	KNLNWYQOKPGKAPKVLIVDASDLETGIPSRFSGSGSGTDFILTTISSLOPEDIAATYYCQ	236	
Db	171	SYLNWYQOKPGKAPKLLIYAASYLESGVPSRFSGSGSGTDFLLTISLQPEDFATYYCQ	230	
QY	237	SDYLP.LTFGGGGTKVDIK	253	
Db	231	SHEDPYTFGGGTKEIK	247	

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RESULT 3
US-09-296-005-22
; Sequence 22, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296, 005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352

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; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 22
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-248
; OTHER INFORMATION: sfv sequence derived from MAE11
US-09-296-005-22

```

Query Match	56.7%;	Score 764;	DB 3;	Length 248;
Best Local Similarity	60.7%;	Pred. No. 1.4e-53;		
Matches 156;	Conservative 30;	Mismatches 57;	Indels 14;	Gaps 4;
QY	1	QVTLKESGPTLVKPTQTLLTCTFSGSLRTTGEGVGNRQPPGKALEMLALIYWDDKR	60	
Dp	1	EVQLVESGGGLVQPGGSLRLSCAVSGYSI-TSGYMNWIRQAPGKGLEWVASITYDGSITN	59	
QY	61	YSPSLKSRLLITTKDTSKKQVLTMTNVDPADTAYVCTHEQYYDYDTSGQPYFDPMGGGT	120	
Dp	60	YNPSVKGRITISRDDSKNTFYLMNSLRADETAYVYCARGSHYFG---HMHFAVMGGGT	115	
QY	121	LVTVSSGGGSGGGGSGGGGSGGGSNIQVTCGSPSSLASVGDRTVMTCRASQDI----R	176	
Dp	116	LVTVS-----SEGGGSEGGGSEGGGSDIQLTQSPSSLASVGDRTVITCRASKPYDGEED	170	
QY	177	KNLNMYQQKPKGAPKVLIIYDASDLETGIPSRFSGSGSGTDFILTISSLOPEDIATYYCQQ	236	
Dp	171	SYLNMYQQKPKGAPKVLIIYASYLESGVPSRFSGSGSGTDFLTISSLOPEDFATYYCQQ	230	
QY	237	SDYLPITFGGGTKVDIK	253	
Dp	231	SHEDPYTFGGGTKEIK	247	

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RESULT 4
US-09-920-171-22
; Sequence 22, Application US/09920171
; Patent No. 6682735
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 22
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sfv sequence derived from MAE11
US-09-920-171-22

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Query Match          56.7%; Score 764; DB 4; Length 248;  
Best Local Similarity 60.7%; Pred. NO. 1.4e-53;  
Matches 156; Conservative 30; Mismatches 57; Indels 14; Gaps  
  
QY      1 QVTLKESGPIIVKPQTQLTILCTFSGSFSLRTGTGEVGWVRQPFGKALEWLALIIYWDDKR 60  
       :|::|||:::||::|||::|||::|||::|||::|||::|||::|||::|||:  
Db      1 EVQLVESGGGLVQPGSGSLRLSCAVSGLYSITSGYSMNWIRQAAPKGLEWVASITYDGSTN 59  
  
QY      61 YSPSLKSRLTIITTKDTSKQOVLLTMNTVPADATAYCYCTHEQQYYDTSGGPYYFDFFWGCGT 120  
       |:|::|||::|||::|||::|||::|||::|||::|||::|||::|||:
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Db 60 YNPSVKGRITISRDSKNTFYLMNSLRAEDTAVYYCARGSHYFG---HMFAVMGQGT 115  
QY 121 LVTVSSGGGGGGGGGGGGGSGGSGSNIQVTQSPSSLASVGDRTVMTCRASQDI----R 176  
Db 116 LVTWVS-----SEGGSSEGGSEGGSDIQLTQSPSSLASVGDRTVITCRASKPVDGEGD 170  
QY 177 KNLNMYQOKPGKAPKVLIDYDASDLETGIPSRFSSGSGGTDFTLTSSLOPEDDIATYYCCQ 236  
Db 171 SYLNWYQOKPGKAPKLLIYASYLESGVPSRFSSGSGGTDFTLTSSLOPEDFATYYCCQ 230  
QY 237 SDYLPITFGGGTKVDIK 253  
Db 231 SHEDPYTFGGGTKEIK 247

RESULT 5  
US-08-918-148-77  
; Sequence 77, Application US/08918148A  
; Patent No. 6342220  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camellia  
; APPLICANT: W.  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Fendly, Brian M.  
; APPLICANT: Gurney, Austin L.  
; TITLE OF INVENTION: Agonist Antibodies  
; FILE REFERENCE: P0979  
; CURRENT APPLICATION NUMBER: US/08/918,148A  
; CURRENT FILING DATE: 1997-08-25  
; NUMBER OF SEQ ID NOS: 79  
; SEQ ID NO 77  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: artificial  
US-08-918-148-77

Query Match 56.5%; Score 762; DB 4; Length 244;  
Best Local Similarity 60.6%; Pred. No. 1.9e-53;  
Matches 154; Conservative 33; Mismatches 51; Indels 16; Gaps 4;  
QY 1 QVTLKESGPTLVKPTQTTLTCTFSGFSRLTTEGVGVNRQPPGKALEWLALYWD-DK 59  
Db 3 QVQLVQSGGGLVPRGSLSLSCAVSGITLRT--YGMHWVRQAPGKGLEWVASISFDGRSE 60  
QY 60 RYSPSLKSLRLITTKDTSKKQVLTMTNVPADTATYYCTHEQYYDTSQOPYFDFWQGG 119  
Db 61 YYADSVQGRFTISRDSKNTLYQMNSLRAEDTAVYYCAR-----GAHYGFDIWQGG 112  
QY 120 TLVTSSGGGGGGGGGGGGGSGGSGSNIQVTQSPSSLASVGDRTVMTCRASQDIRKNL 179  
Db 113 TMTVTVS-----SGGGTGGGGGGGGSDIQMTQSPSTLSASIGDRTVITCRASEGIYHWL 167  
QY 180 NMYQOKPGKAPKVLIDYDASDLETGIPSRFSSGSGGTDFTLTSSLOPEDDIATYYCCQSDY 239  
Db 168 AMYQOKPGKAPKLLIYKASSLSASGAPSRFSSGSGGTDFTLTSSLOPEDFATYYCCQYSN 227  
QY 240 LPLTFGGGTKVDIK 253  
Db 228 YPLTFGGGTLEIK 241

RESULT 6  
US-08-887-352B-23  
; Sequence 23, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
; TITLE OF INVENTION: Improving Polypeptides  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way

CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,352B  
FILING DATE: 03-Jul-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P1123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 248 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
US-08-887-352B-23

Query Match 56.5%; Score 762; DB 2; Length 248;  
Best Local Similarity 60.3%; Pred. No. 2e-53;  
Matches 155; Conservative 32; Mismatches 56; Indels 14; Gaps 4;  
QY 1 QVTLKESGPTLVKPTQTTLTCTFSGFSRLTTEGVGVNRQPPGKALEWLALYWD-DDKR 60  
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSI-TSGYSNHWIRQAPGKLEWVASIKYSGETK 59  
QY 61 YSPSLKSLRLITTKDTSKKQVLTMTNVPADTATYYCTHEQYYDTSQOPYFDFWQGGT 120  
Db 60 YNPSVKGRITISRDSKNTFYLMNSLRAEDTAVYYCARGSHYFG---HMFAVMGQGT 115  
QY 121 LVTVSSGGGGGGGGGGGGGSGGSGSNIQVTQSPSSLASVGDRTVMTCRASQDI----R 176  
Db 116 LVTWVS-----SEGGSSEGGSEGGSDIQLTQSPSSLASVGDRTVITCRASKPVDGEGD 170  
QY 177 KNLNMYQOKPGKAPKVLIDYDASDLETGIPSRFSSGSGGTDFTLTSSLOPEDDIATYYCCQ 236  
Db 171 SYLNWYQOKPGKAPKLLIYASYLESGVPSRFSSGSGGTDFTLTSSLOPEDFATYYCCQ 230  
QY 237 SDYLPITFGGGTKVDIK 253  
Db 231 SHEDPYTFGGGTKEIK 247

RESULT 7  
US-09-109-207C-23  
; Sequence 23, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; CURRENT FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 23  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Artificial  
; LOCATION: 1-248  
; OTHER INFORMATION: sfv sequence derived from MAB11







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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,164A
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR94/00714
; FILING DATE: 15-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93/07241
; FILING DATE: 16-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin F.
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: ST93030-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3816
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264 amino acids
; TYPE: amino acid
; TOPOLOGY: 1linear
; MOLECULE TYPE: protein
; US-08-564-164A-4
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Query Match          54.6%; Score 736; DB 3; Length 264;
Best Local Similarity 57.7%; Pred. No. 2.5e-51;
Matches 146; Conservative 32; Mismatches 61; Indels 14; Gaps 3;
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QY      1 QVTLKESGPTLVKPTQTLLTCTFSGFSLRTTGEVGVWVRQPPGKALEWLALYWDDEKR 60
      11 QVQLQESGPGELGQPAQISITCTVSGFSL--SSYGVHWVRQSPGKLEWLGIWRGGGT 68
QY      61 YSPSLKSRLLITKDTSKQVVLMTNVDPADTATYYCTHEQYYVDTSGQPYFDFWGGGT 120
      69 YNAAFMRSLITKDNSKQVFFKLNLSLOPDDTAMYCAKR-----GGPGYFDWVGQGT 121
QY      121 LVTVSSGGGGSGGGSGGGSGGGSGGSGNTQVTPSSLSASVGDRTVMTCRASQDIRKNLN 180
      122 TVTVS-----SGGGSGGGSGGGSGGGSDIELTQSPASLSASVGEIVTWTCRASENTYSNLA 176
QY      181 WYQOKPGKAPKVLIIYDASDLETGIPSRFSGSGSGTDFILTISSLOPEDIAITYCCQSDYL 240
      177 WYQOKGKSPQLLVYAATKPGNGVPSRFSGSGGTQFSLKINSLOPEDLGNYCLHFGYT 236
QY      241 PLTFGGGTGVDIK 253
      237 PYRFGGGTKLETK 249
DB
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```

RESULT 14
US-08-488-113B-148
; Sequence 148, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: 1linear
; MOLECULE TYPE: protein
; US-08-488-113B-148
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Query Match          54.5%; Score 734.5; DB 1; Length 240;
Best Local Similarity 57.9%; Pred. No. 2.9e-51;
Matches 147; Conservative 31; Mismatches 61; Indels 15; Gaps 4;
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QY      1 QVTLKESGPTLVKPTQTLLTCTFSGFSLRTTGEVGVWVRQPPGKALEWLALYWDDEK 59
      1 EIQLVQSGGGLVKGSGSVRISCAASGYTF--TNYGMWVRQAPGKLEWGMWINTHTGEP 58
QY      60 RYSPSLKSRLLITKDTSKQVVLMTNVDPADTATYYCTHEQYYVDTSGQPYFDFWGGG 119
      59 TYADSFKGRFTFSLDSDKNTAYLIQINSRAEDTAVYFCTRA-----GYDWYFDWVGQ 111
QY      120 TLVTVSSGGGGSGGGSGGGSGGGSGGSGNTQVTPSSLSASVGDRTVMTCRASQDIRKNL 179
      112 TVTVS-----SGGGSGGGSGGGSGGGSDIOMTQSPSSLSASVGDRTVITCRASQDINSYL 166
QY      180 NMWQOKPGKAPKVLIIYDASDLETGIPSRFSGSGSGTDFILTISSLOPEDIAITYCCQSDY 239
      167 SWFOQKPGKAPKTLIYRANRLBSGVPSRFSGSGSGTDTYTLTISSLOPEDFGIYYCCQYDE 226
QY      240 LPLTFGGGTGVDIK 253
      227 SPWTFGGGTGLEMK 240
DB
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RESULT 15
US-08-477-484B-148
; Sequence 148, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
```

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; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
;
; PRIOR APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
;
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
;
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-477-484B-148
    
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Query Match 54.5%; Score 734.5; DB 1; Length 240;  
 Best Local Similarity 57.9%; Pred. No. 2.9e-51;  
 Matches 147; Conservative 31; Mismatches 61; Indels 15; Gaps 4;

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   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1 EIQLVSGGGLVKPGGSVRISCAASGYTF--TNYGMNVRQAPGKLEWGWINTHTGEP 58
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 60 RYSPSLKSLRLTITKDTSKQVLTMTNVDPADTATYCTHEQYYDTSQOPYPDFWGGG 119
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 59 TYADSFGRFTFSLDDSKNTAYLQINSLRADTAIFYFCTRR-----GYDWYFDVWGGG 111
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 120 TLVTYSSGGGGSGGGSGGGSSNIQVTSPPSSLSASVGDVMTTCRASQDIRKNL 179
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 112 TTVTVS-----SGGGSGGGSGGGSDIQMTQSPSSLSASVGDVMTTCRASQDINSYL 166
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 180 NWYQKPGKAPKVLIVDASDLETGIRPSRSGSGSGTDFILITISSIQPEDIATYYCCQSDY 239
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 167 SWFOQKPGKAPKTLIVRANRLSEGVSRFSGSGSGTDYTLTISLQYEDFGIYYCCQYDE 226
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 240 LPLTFGGGTTKVDIK 253
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 227 SPWTFGGGTTLEMK 240
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
    
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Search completed: May 13, 2004, 15:10:50  
 Job time : 13.8782 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 15:07:07 ; Search time 37.4587 Seconds  
(without alignments)  
1879.405 Million cell updates/sec

Title: US-10-072-301-31  
Perfect score: 1348  
Sequence: 1 QVTLKESGPTLVKPTQTLLT.....CQGS DYLP LFRGGG TKVDIK 253

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
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15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
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17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1348	100.0	253	14	US-10-072-301-23	Sequence 23, Appl
2	1348	100.0	253	14	US-10-072-301-31	Sequence 31, Appl
3	1348	100.0	253	14	US-10-071-866-23	Sequence 23, Appl
4	1348	100.0	253	14	US-10-071-866-31	Sequence 31, Appl
5	1348	100.0	253	15	US-10-360-828-23	Sequence 23, Appl
6	1348	100.0	253	15	US-10-360-828-31	Sequence 31, Appl
7	821.5	60.9	286	12	US-10-406-830-8	Sequence 8, Appl
8	811.5	60.2	251	10	US-09-880-748-1049	Sequence 1049, Ap
9	811.5	60.2	251	12	US-10-293-418-1049	Sequence 1049, Ap
10	803	59.6	248	10	US-09-880-748-1360	Sequence 1360, Ap
11	803	59.6	248	12	US-10-293-418-1360	Sequence 1360, Ap
12	801.5	59.5	255	10	US-09-880-748-1603	Sequence 1603, Ap
13	801.5	59.5	255	12	US-10-293-418-1603	Sequence 1603, Ap
14	800.5	59.4	249	10	US-09-880-748-1321	Sequence 1321, Ap
15	800.5	59.4	249	12	US-10-293-418-1321	Sequence 1321, Ap

16	794	58.9	253	14	US-10-072-301-17	Sequence 17, Appl
17	794	58.9	253	14	US-10-072-301-25	Sequence 25, Appl
18	794	58.9	253	14	US-10-071-866-17	Sequence 17, Appl
19	794	58.9	253	14	US-10-071-866-25	Sequence 25, Appl
20	794	58.9	253	15	US-10-360-828-17	Sequence 17, Appl
21	794	58.9	253	15	US-10-360-828-25	Sequence 25, Appl
22	789	58.5	248	10	US-09-880-748-1876	Sequence 1876, Ap
23	789	58.5	248	12	US-10-293-418-1876	Sequence 1876, Ap
24	787	58.4	248	10	US-09-880-748-1421	Sequence 1421, Ap
25	787	58.4	248	12	US-10-293-418-1421	Sequence 1421, Ap
26	781.5	58.0	243	10	US-09-880-748-1935	Sequence 1935, Ap
27	781.5	58.0	243	12	US-10-293-418-1935	Sequence 1935, Ap
28	781.5	58.0	249	10	US-09-880-748-1188	Sequence 1188, Ap
29	781.5	58.0	249	12	US-10-293-418-1188	Sequence 1188, Ap
30	777	57.6	250	10	US-09-880-748-1174	Sequence 1174, Ap
31	777	57.6	250	12	US-10-293-418-1174	Sequence 1174, Ap
32	777	57.6	287	12	US-10-406-830-5	Sequence 5, Appl
33	769	57.0	266	12	US-10-257-864A-108	Sequence 108, Appl
34	769	57.0	291	12	US-10-406-830-10	Sequence 10, Appl
35	765	56.8	250	15	US-10-423-847-12	Sequence 12, Appl
36	764.5	56.7	333	14	US-10-059-261-61	Sequence 61, Appl
37	764	56.7	248	9	US-09-920-171-22	Sequence 22, Appl
38	764	56.7	248	14	US-10-113-996-22	Sequence 22, Appl
39	762	56.5	248	9	US-09-920-171-23	Sequence 23, Appl
40	762	56.5	248	10	US-09-880-748-1004	Sequence 1004, Ap
41	762	56.5	248	12	US-10-293-418-1004	Sequence 1004, Ap
42	762	56.5	248	14	US-10-113-996-23	Sequence 23, Appl
43	761	56.5	240	9	US-09-192-854-2	Sequence 2, Appl
44	761	56.5	240	9	US-09-968-561A-2	Sequence 2, Appl
45	761	56.5	240	10	US-09-968-744A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-10-072-301-23  
; Sequence 23, Application US/10072301  
; Publication No. US20030152913A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF  
; FILE REFERENCE: 25636-718  
; CURRENT APPLICATION NUMBER: US/10/072,301  
; CURRENT FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 23  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Clone 15.150.24  
US-10-072-301-23

Qy	Query Match	100.0%;	Score 1348;	DB 14;	Length 253;
	Best Local Similarity	100.0%;	Pred. No. 2e-87;		
	Matches 253;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1 QVTIKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVGWVROPPGKALEWLLAIYWDDDKR	60			
Db	1 QVTIKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVGWVROPPGKALEWLLAIYWDDDKR	60			
Qy	61 YSPSLKSLRLTITTKDTSKKQVYVLTMTNVPADATATYCTHGOYYVDTSGOPYFDFWGGGT	120			
Db	61 YSPSLKSLRLTITTKDTSKKQVYVLTMTNVPADATATYCTHGOYYVDTSGOPYFDFWGGGT	120			
Qy	121 LVTYSSGGGSGGGSGGGSGGGSGGGSNIQVTPSSLSASVGDRTVTMTCRASQDIRKNTN	180			
Db	121 LVTYSSGGGSGGGSGGGSGGGSGGGSNIQVTPSSLSASVGDRTVTMTCRASQDIRKNTN	180			

Qy	181	WYQOKPGKAPKVL IYDASDLETGIPSRFSGSGSGTDFILTTISLQED IATYYCCQSPYL	240
Db	181	WYQOKPGKAPKVL IYDASDLETGIPSRFSGSGSGTDFILTTISLQED IATYYCCQSPYL	240
Qy	241	PLTFGGGATKVDIK	253
Db	241	PLTFGGGATKVDIK	253

```

RESULT 2
US-10-072-301-31
; Sequence 31, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Ji
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24 Variant
US-10-072-301-31

```

[illegible]

```

RESULT 3
US-10-071-866-23
; Sequence 23, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST F
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1

```

```

; SEQ ID NO 23
;
; LENGTH: 253
;
; TYPE: PRT
;
; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: Clone 15.150.24
US-10-071-866-23

```

	Query Match	100.0%;	Score 1348;	DB 14;	Length 253;	
	Best Local Similarity	100.0%;	Pred. No. 2e-87;			
	Matches 253;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 QVTLKESGPTLVKPTQLTLLTCTFSGSFLRTTGEGWVRQPFGKALEWLALTYWDDEKR	60				
Dp	1 QVTLKESGPTLVKPTQLTLLTCTFSGSFLRTTGEGWVRQPFGKALEWLALTYWDDEKR	60				
QY	61 YSPSLKSRLTTTKDTSKKQVLTMTNVDPADATATYYCTHEQQYYYDTSGQPYFFDFWGQGT	120				
Dp	61 YSPSLKSRLTTTKDTSKKQVLTMTNVDPADATATYYCTHEQQYYYDTSGQPYFFDFWGQGT	120				
QY	121 LVTSSGGGGGGGGGGGGGGGGGGNIQVTPSPSSLASAVGDRTMTCRASQDIRKNLN	180				
Dp	121 LVTSSGGGGGGGGGGGGGGGGGGNIQVTPSPSSLASAVGDRTMTCRASQDIRKNLN	180				
QY	181 WYQOKPGKAPRVLYLDASDLETGIPSRFSGSGSGTDFILTISSLPEDIAITYYCOQSDYL	240				
Dp	181 WYQOKPGKAPRVLYLDASDLETGIPSRFSGSGSGTDFILTISSLPEDIAITYYCOQSDYL	240				
QY	241 PLTFGGGGRVNDIK	253				
Dp	241 PLTFGGGGRVNDIK	253				

```

RESULT 4
US-10-071-866-31
; Sequence 31, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST P
; TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Clone 15.150.24 Variant
US-10-071-866-31

```

Query Match	100.0%;	Score 1348;	DB 14;	Length 253;
Best Local Similarity	100.0%;	Pred. No. 2e-87;		
Matches 253;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	QVTLKESGPTLVKPTQTLTLTCTFSGFSRLRTGEGVGNVRQPPGKALEMLALIYWDDBKR	60	
Db	1	QVTLKESGPTLVKPTQTLTLTCTFSGFSRLRTGEGVGNVRQPPGKALEMLALIYWDDBKR	60	
QY	61	YSPSLKSRLLTIITKDTSKKQVLTMTNVDPADATATYCTHEQYYYDDTSGQPYFDFMGQT	120	
Db	61	YSPSLKSRLLTIITKDTSKKQVLTMTNVDPADATATYCTHEQYYYDDTSGQPYFDFMGQT	120	
QY	121	LVTVSSGGGGSGGGSGGGSGGGGSNIQVTSPPSLASVGDRTVMTCRASQDIRKNULN	180	
Db	121	LVTVSSGGGGSGGGSGGGSGGGGSNIQVTSPPSLASVGDRTVMTCRASQDIRKNULN	180	
QY	181	WYQOKPGKAPKVLIIYDASDLETGIPSRFSGSGSGTDFILTTISSLOPEDATATYCCQOSDYL	240	

Db 181 WYQKPKGKAPKVLIDASDLETGIPSRFSGSGSDTDFILTISSLPEDIATYYCCQSDYL 240  
QY 241 PLTFGGGTTKVDIK 253  
Db 241 PLTFGGGTTKVDIK 253

## RESULT 5

US-10-360-828-23  
; Sequence 23, Application US/10360828  
; Publication No. US20030206909A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shaobing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS  
; FILE REFERENCE: 25636-727  
; CURRENT APPLICATION NUMBER: US/10/360,828  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: US 10/071,866  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/072,301  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/133,978  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.24  
US-10-360-828-23

Query Match 100.0%; Score 1348; DB 15; Length 253;  
Best Local Similarity 100.0%; Pred. No. 2e-87;  
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTTGEVGVWVROPKGALWALIIYWDGDKR 60  
Db 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTTGEVGVWVROPKGALWALIIYWDGDKR 60  
QY 61 YSPSLKSLRLTITKDTSKQVLLTMNVPADATATYCTHEQYYDTSQOPYFDFWGGGT 120  
Db 61 YSPSLKSLRLTITKDTSKQVLLTMNVPADATATYCTHEQYYDTSQOPYFDFWGGGT 120  
QY 121 LVTVSSGGGSGGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKUNL 180  
Db 121 LVTVSSGGGSGGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKUNL 180  
QY 181 WYQKPKGKAPKVLIDASDLETGIPSRFSGSGSDTDFILTISSLPEDIATYYCCQSDYL 240  
Db 181 WYQKPKGKAPKVLIDASDLETGIPSRFSGSGSDTDFILTISSLPEDIATYYCCQSDYL 240  
QY 241 PLTFGGGTTKVDIK 253  
Db 241 PLTFGGGTTKVDIK 253

## RESULT 6

US-10-360-828-31  
; Sequence 31, Application US/10360828  
; Publication No. US20030206909A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shaobing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS  
; FILE REFERENCE: 25636-727  
; CURRENT APPLICATION NUMBER: US/10/360,828  
; CURRENT FILING DATE: 2003-02-07

; PRIOR APPLICATION NUMBER: US 10/071,866  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/072,301  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 10/133,978  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 31  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.24 Variant  
US-10-360-828-31

Query Match 100.0%; Score 1348; DB 15; Length 253;  
Best Local Similarity 100.0%; Pred. No. 2e-87;  
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTTGEVGVWVROPKGALWALIIYWDGDKR 60  
Db 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTTGEVGVWVROPKGALWALIIYWDGDKR 60  
QY 61 YSPSLKSLRLTITKDTSKQVLLTMNVPADATATYCTHEQYYDTSQOPYFDFWGGGT 120  
Db 61 YSPSLKSLRLTITKDTSKQVLLTMNVPADATATYCTHEQYYDTSQOPYFDFWGGGT 120  
QY 121 LVTVSSGGGSGGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKUNL 180  
Db 121 LVTVSSGGGSGGGGSGGGSNIQVTPSSLSASVGDRTVMTCRASQDIRKUNL 180  
QY 181 WYQKPKGKAPKVLIDASDLETGIPSRFSGSGSDTDFILTISSLPEDIATYYCCQSDYL 240  
Db 181 WYQKPKGKAPKVLIDASDLETGIPSRFSGSGSDTDFILTISSLPEDIATYYCCQSDYL 240

QY 241 PLTFGGGTTKVDIK 253  
Db 241 PLTFGGGTTKVDIK 253

## RESULT 7

US-10-406-830-8  
; Sequence 8, Application US/10406830  
; Publication No. US20040071696A1  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, GREGORY P.  
; APPLICANT: HORAK, EVA M.  
; APPLICANT: WEINER, LOUIS M.  
; APPLICANT: JAMES, MARKS D.  
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE  
; FILE REFERENCE: 407T-000410US  
; CURRENT APPLICATION NUMBER: US/10/406,830  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US 60/370,276  
; PRIOR FILING DATE: 2002-04-05  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 286  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic antibody.  
US-10-406-830-8

Query Match 60.9%; Score 821.5; DB 12; Length 286;  
Best Local Similarity 66.1%; Pred. No. 2.7e-50;  
Matches 168; Conservative 28; Mismatches 43; Indels 15; Gaps 6;

QY 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTTGEVGVWVROPKGALWALIIYWDGDKR 60  
Db 1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTTGEVGVWVROPKGALWALIIYWDGDKR 60



Db	23	QVQLQESGGPGELVHPSETLSLTCTVSGGSEFRS--YYWSMIR-PPGKLEWIGYIFYSGSTN	79
QY	61	YSPSLKSRLLITTKDTSKKQVLTMTNVDADTATYYCTHEQYYYDTSQPYFDPMGGGT	120
Db	80	YNPSLKSRVLTISVDTSKNQFSLKLSLTAAADTAVYYCARGHL-----GELGMFDPMGGT	134
QY	121	LVTVSSGGGGSGGGSGGGSGGGSGGGSGNIQVTQSPSSLASVGDRTVMTCRASQDIRKUNL	180
Db	135	LVTVS-----SSGGSGSGGGSGGGSGGGSDIQMTQSPSSLASVGDRTVITCQASQDISNYLN	189
QY	181	WYQQKPKGAPKRLIYDASDLETGIPSRFSGSGSGTDFILFTSSLPEDIATYYC-QQSDY	239
Db	190	WYQQKPKGAPKRLIFAA SRLASGVPSRFSGSGSGTDFSLTISLQPDGFATYYCLQDSDY	249
QY	240	LPLTFGGGTQVDIK	253
Db	250	-PLTFGGGTQVEIK	262

## RESULT 8

```

US-09-880-748-1049
; Sequence 1049, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1049
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1049

```

Query Match	60.2%;	Score 811.5;	DB 10;	Length 251;
Best Local Similarity	63.0%;	Pred. No. 1.2e-49;		
Matches 160;	Conservative 31;	Mismatches 58;	Indels 5;	Gaps 3;

QY	1 QVTLKESGPTLVKPTQTLLTCTFSGFSLRTTGEGWVRÖPBGKALEMLALIYWDDKR 60
Dd	1 ÖLÖQÖESGPGLVBPSETLSLTCTVSGGFISSRTSYMGWIRÖPPGKGPEMIGNITYTKTY 60
QY	61 YSPSLKSRLTTTKDTSKKÖVLJTMNVDPADTATYYCTHEÖYYDDTSGÖPYFPDFWGÖGT 120
Dd	61 YSPSLKSRAVTISVDTSKNÖLSLKLNSTYAADTAIVYYCARAGYDLLT-GYPFYFDSSWKGT 119
QY	121 LVTVSSGGGSGGGGSGGGGSNIÖVTÖSPSSLASVGDRVTMTCRASÖDIRKNLN 180
Dd	120 LVTVSSGGGSGGGGSGGGGS--ALÖIYLÖSPATLSLSPÖERATLSCRASÖSVSYLA 176
QY	181 WYÖQKPÖKAPKVLIYDASDLÖTGISRFSGSGSGTDÖILTISSLÖPEDIAIYYCQÖSDYL 240
Dd	177 WYÖQKPGQAPRLLIYDASNRAIGIPARFSGSGSGTDFLTITISSLEPEDFAVYYCQÖRSNM 236
QY	241 P-LTFGGGGTKVDIK 253
Dd	237 PFLTFGGGGTKVEIK 250

## RESULT 9

```

US-10-293-418-1049
? Sequence 1049, Application US/10293418
? Publication No. US20030223996A1
? GENERAL INFORMATION:
? APPLICANT: Ruben et al.
? TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
? FILE REFERENCE: PF523P2
? CURRENT APPLICATION NUMBER: US/10/293,418
? CURRENT FILING DATE: 2002-11-27
? PRIOR APPLICATION NUMBER: 60/331,469
? PRIOR FILING DATE: 2001-11-16
? PRIOR APPLICATION NUMBER: 60/340,817
? PRIOR FILING DATE: 2001-12-19
? PRIOR APPLICATION NUMBER: 09/880,748
? PRIOR FILING DATE: 2001-06-15
? PRIOR APPLICATION NUMBER: 60/293,499
? PRIOR FILING DATE: 2001-05-25
? PRIOR APPLICATION NUMBER: 60/277,379
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/276,248
? PRIOR FILING DATE: 2001-03-16
? PRIOR APPLICATION NUMBER: 60/240,816
? PRIOR FILING DATE: 2000-10-17
? PRIOR APPLICATION NUMBER: 60/212,210
? PRIOR FILING DATE: 2000-06-16
? NUMBER OF SEQ ID NOS: 3247
? SEQ ID NO 1049
? LENGTH: 251
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-293-418-1049

```

Query Match	60.2%;	Score 811.5;	DB 12;	length 251;
Best Local Similarity	63.0%;	Pred. No. 1.2e-49;		
Matches 160;	Conservative 31;	Mismatches 58;	Indels 5;	Gaps 3;

QY		1 QVTLKESGPTLVKPTQTLLTCTPSGSFLRTTGEGVGWOPPGKALEMLALIYWDDDKR	60
Dd		1 QLOQESGBGLVKPSETLSLTCIVSGGFISRTSYMGWRQPFGKEPMIGNIYYTKTY	60
QY		61 YSPSLSKRLITTKDTSKKQVVLTMTNVDPADATAYYCTHEQYYYDTSGOPYFDFWGQGT	120
Dd		61 YSPSLSKRVLTISVDTSKNQSLSLKNSTVTAADTAVVYCARAGYDLLT-GYPFYFDSSNGKT	119
QY		121 LVTWSSGGGGSGGGSGGGSGSNIQVTSPPSLASVGDVRTMTCRASQDIRKNLN	180
Dd		120 LVTVSSGGGGSGGGSGGGSGS---ALIEVLTSPATLSLPERATLSCRASQSVSYYLA	176
QY		181 WYQQEKPKAPKVLIYDASDLLETGIPSRFSGSGSGTDPILTISSLOPEDIAITYYCQSQSDYL	240
Dd		177 WYQQEKGQAPELLIYDASNRAITGIPARFSGSGSGTDFTLTIISSLEPEDFAVYYCQQRSMW	236
QY		241 P-LTFGGGKTVDIK	253
Dd		237 PFLTGGGKTVEIK	250

## RESULT 10

US-09-880-748-1360  
: Sequence 1360, Application US/09880748  
: Publication No. US20030059937A1  
: GENERAL INFORMATION:  
: APPLICANT: Ruben et al.  
: TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blyss  
: FILE REFERENCE: PF523  
: CURRENT APPLICATION NUMBER: US/09/880,748  
: CURRENT FILING DATE: 2001-06-15  
: PRIOR APPLICATION NUMBER: 60/212,210  
: PRIOR FILING DATE: 2000-06-15  
: PRIOR APPLICATION NUMBER: 60/240,816  
: PRIOR FILING DATE: 2000-10-17  
: PRIOR APPLICATION NUMBER: 60/276,248  
: PRIOR FILING DATE: 2001-03-16

## RESULT 9



; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1360
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1360

Query Match 59.6%; Score 803; DB 10; Length 248;

Best Local Similarity 63.2%; Pred. No. 4.6e-49;
Matches 160; Conservative 32; Mismatches 55; Indels 6; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTTLTLCTFSGFSLRTTGEVGVWVRQPPGKALEWLALIWDDDKR 60
Db 1 QVQLQESGPGLVKPSSETLSLCTVSGSIRS--YVWSWIRQSPGRGLEWIGHIYHSGSTD 58
QY 61 YSPSLKSRLLTTTKDTSKKQVVLMTNVDPADTATYYCTHEQYYDDTSGQPYFDFWGQGT 120
Db 59 YNPSLSRSRVMTSIDTSKNQFSLNLTSVTAADTAVYYCARDHYDVLGTSYLAQAFDVGQGT 118
QY 121 LVTYSSGGGGSGGGSGGGSGGSGSNIQVTQSPSSLSASVGDRTVMTCRASQDIRKNLN 180
Db 119 LVTYSSGGGGSGGGSGGGSGGGS--ALDIQLTQSPSSLSASVGDRTVITCRASQSIGRYLN 175
QY 181 WYQOKPGKAPKVLIVDASDLETGIPSRFSGSGSGTDFILTISSLQPEDVATYYCCQSDYL 240
Db 176 WYQOKPGRAPRLIFVTSSLHSDVPSRFSGSGSGTDFSLTISNLPEDFATYYCQQS-YT 234
QY 241 PLTFGGGTAKVDIK 253
Db 235 DPTFGQGTRLLEIK 247

RESULT 11

US-10-293-418-1360
; Sequence 1360, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1360
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1360

Query Match 59.6%; Score 803; DB 12; Length 248;
Best Local Similarity 63.2%; Pred. No. 4.6e-49;
Matches 160; Conservative 32; Mismatches 55; Indels 6; Gaps 3;

QY 1 QVTLKESGPTLVKPTQTTLTLCTFSGFSLRTTGEVGVWVRQPPGKALEWLALIWDDDKR 60
Db 1 QVQLQESGPGLVKPSSETLSLCTVSGSIRS--YVWSWIRQSPGRGLEWIGHIYHSGSTD 58
QY 61 YSPSLKSRLLTTTKDTSKKQVVLMTNVDPADTATYYCTHEQYYDDTSGQPYFDFWGQGT 120
Db 59 YNPSLSRSRVMTSIDTSKNQFSLNLTSVTAADTAVYYCARDHYDVLGTSYLAQAFDVGQGT 118
QY 121 LVTYSSGGGGSGGGSGGGSGGSGSNIQVTQSPSSLSASVGDRTVMTCRASQDIRKNLN 180
Db 119 LVTYSSGGGGSGGGSGGGSGGGS--ALDIQLTQSPSSLSASVGDRTVITCRASQSIGRYLN 175
QY 181 WYQOKPGKAPKVLIVDASDLETGIPSRFSGSGSGTDFILTISSLQPEDVATYYCCQSDYL 240
Db 176 WYQOKPGRAPRLIFVTSSLHSDVPSRFSGSGSGTDFSLTISNLPEDFATYYCQQS-YT 234
QY 241 PLTFGGGTAKVDIK 253
Db 235 DPTFGQGTRLLEIK 247

RESULT 12

US-09-880-748-1603
; Sequence 1603, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1603
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1603

Query Match 59.5%; Score 801.5; DB 10; Length 255;
Best Local Similarity 62.0%; Pred. No. 6.1e-49;
Matches 163; Conservative 27; Mismatches 54; Indels 19; Gaps 6;

QY 1 QVTLKESGPTLVKPTQTTLTLCTFSGFSLRTTGEVGVWVRQPPGKALEWLALIWDDDKR 56
Db 1 QVQLQESGPGLVKPSQTLISCAISGDSVGSNGAAMWIRQSPGRGLEWLGRTYRSQRY 60
QY 57 DDKRYSPSLKSRLLTTTKDTSKKQVVLMTNVDPADTATYYCTHEQYYD-TSGQPY--- 112
Db 61 SD--YGASVRSRITINADTSKNQFSLQLNSVTPEDTAVYYCARESGRYDILTG--YISGG 116
QY 113 --FDFWGQGTLVTVSSGGGGSGGGSGGGSGGSGSNIQVTQSPSSLSASVGDRTVMTCR 170
Db 117 GGMVDWGRGTLTVTS-----SGGGSGGGSGGGSGGGSDIQMTQSPSTLSASIGDRVITTCR 171
QY 171 ASQDIRKNLNWYQOKPGKAPKVLIVDASDLETGIPSRFSGSGSGTDFILTISSLQPEDIA 230
Db 172 ASGGLYHMLAWYQOKPGKAPKVLIVKASSLASGAPSRFSGSGSGTDFLTISSLQPDdfa 231
QY 231 TTYCQQSDYLLPLTFGGGTAKVDIK 253
Db 232 TTYCQQYSNYPPLTFGGGTAKLEIK 254





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:50:27 ; Search time 11.4218 Seconds  
(without alignments)  
2130.694 Million cell updates/sec

Title: US-10-072-301-31

Perfect score: 1348

Sequence: 1 QVTLKESGPTLVKPTQTTLT.....CQSDYLPRTFGGKVDIK 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:\*

1: pirl:\*

2: pirl2:\*

3: pirl3:\*

4: pirl4:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	611	45.3	268	2	A56446	Ig heavy chain V r
2	578.5	42.9	249	2	S41374	single chain Fv an
3	551	40.9	124	2	A49002	Ig heavy chain V r
4	538.5	39.9	138	2	S31513	Ig heavy chain - h
5	534.5	39.7	374	2	S69339	Ig heavy chain V r
6	533.5	39.6	233	2	JC5322	p53 specific singl
7	487	36.1	119	2	S18555	Ig heavy chain V r
8	485.5	36.0	125	1	MHDMC	Ig heavy chain V-I
9	474.5	35.2	121	1	G1HME	Ig heavy chain V-I
10	470.5	34.9	118	2	S18556	Ig heavy chain V r
11	469.5	34.8	121	1	A36005	Ig heavy chain V-I
12	468	34.7	108	1	K1HUR	Ig heavy chain V-I
13	468	34.7	129	2	S52789	Ig kappa chain V r
14	462	34.3	110	2	S44118	Ig kappa chain V-J
15	456	33.8	108	1	K1HUA	Ig kappa chain V-I
16	456	33.8	108	2	B49047	Ig kappa chain V r
17	456	33.8	125	2	S40349	Ig kappa chain V-J
18	449	33.3	107	2	S36264	Ig lambda chain V
19	448	33.2	108	1	K1HUS	Ig kappa chain V-I
20	447	33.2	107	2	S36269	Ig lambda chain V-I
21	445	33.0	122	2	S11740	Ig heavy chain V
22	445	33.0	123	2	S40331	Ig kappa chain - h
23	443	32.9	108	2	S19674	Ig kappa chain V r
24	443	32.9	129	2	S52793	Ig kappa chain V r
25	442	32.8	108	1	K1HUA	Ig kappa chain V-I
26	442	32.8	124	2	S40348	Ig kappa chain V-J
27	441	32.7	125	2	S40316	Ig kappa chain - h
28	441	32.7	127	2	S40367	Ig kappa chain V-J
29	440	32.6	107	2	S36262	Ig lambda chain V

30	439	32.6	129	2	S40317	Ig kappa chain - h
31	437	32.4	139	2	S40365	Ig kappa chain - h
32	435	32.3	108	1	K1HUR	Ig kappa chain V-I
33	435	32.3	108	1	K1HUR	Ig kappa chain V-I
34	435	32.3	120	1	G1HUC	Ig heavy chain V-I
35	434	32.2	108	2	I39154	Ig kappa chain (BR
36	432	32.0	109	2	S31981	Ig kappa chain - h
37	431	32.0	105	2	S36266	Ig lambda chain V
38	431	32.0	129	2	S52792	Ig kappa chain V r
39	430	31.9	117	2	S46376	Ig kappa chain V-J
40	429	31.8	125	2	S40350	Ig kappa chain - h
41	429	31.8	143	2	PT0174	Ig kappa chain pre
42	428	31.8	109	2	S31998	Ig heavy chain - h
43	427	31.7	108	2	S36279	Ig kappa chain V
44	427	31.7	117	2	S43528	Ig kappa chain V r
45	427	31.7	117	2	S42263	Ig kappa chain V r

ALIGNMENTS

RESULT 1

A56446

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C,Species: Mus musculus (house mouse)

C,Date: 19-Jan-1996 #sequence\_rev19-Jan-1996 #text\_change 16-Aug-1996

C,Accession: A56446

R,Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A,Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident

A,Reference number: A56446; MUID:95229583; PMID:7713873

A,Accession: A56446

A,Status: preliminary

A,Molecule type: mRNA

A,Residues: 1-268 <TAN>

A,Cross-references: GB:U20617

C,Keywords: heterotetramer; immunoglobulin

Query Match 45.3%; Score 611; DB 2; Length 268;

Best Local Similarity 49.6%; Pred.No.1.3e-34;

Matches 126; Conservative 42; Mismatches 70; Indels 16; Gaps 6;

Qy	1	QVTLKESGPTLVKPTQTTLTCTPSGFSRLRTGEGVGVNRQPPKALEWLALIV-WDDK	59
Db	3	QVTLQESGAEVLVKGASVLSCTTSGFNKDT--YHNVKORPEQGLEWIGRIAPANGIT	60
Qy	60	RYSPLSKRLTITKDTSKQVLTMTNVDPADATATYCTHEQYVYDTSQOPYFDFWGGG	119
Db	61	KYDPKFGKATIAADTSSNTAVYLQLSLTSEDTAVVYCAS---YVLR---YENYWGQG	113
Qy	120	TLVTWSSGGGSGGGSGGGSGGSGNSIQVTPSPSSASVGDRTVMTCRASQDIRKL	179
Db	114	TLVTWS-----SGGGSGGGSGGGSDIELTQSPAIMSASLGEKVTMSCRASSV-NFI	167
Qy	180	NWYQKPKGKAPKVLTYDASDLETGIPSRFSGSGGTDPIITLTISSLSQPEDATYYCQGS	239
Db	168	YNYQKSDASPKLWVYTSHPGVPARFSGSGSGNSYSLTISMEGEDATYYCQGF	227
Qy	240	LPLTFGGGKVDIK 253	
Db	228	SPFTFGSGTKLEIK 241	

RESULT 2

S41374

single chain Fv antibody - mouse

C,Species: Mus musculus (house mouse)

C,Date: 06-Jan-1995 #sequence\_rev19-Jan-1995 #text\_change 06-Jan-1995

C,Accession: S41374

R,Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A,Description: Construction and functional characterization of a single chain Fv antibod

A,Reference number: S41374

A/Accession: S41374  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-249 <ART>  
A/Cross-references: EMBL:Z29480

Query Match	42.9%	Score 578.5;	DB 2;	Length 249;
Best Local Similarity	44.8%	Pred. No. 1.9e-32;		
Matches 116;	Conservative 50;	Mismatches 74;	Indels 19;	Gaps 5;

[illegible]

```

RESULT 3
A49002
Ig heavy chain V region, rheumatoid factor RF antibody - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A49002
R:Stuber, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, H.W.J.; Gaskin, F.
A:Title: A rheumatoid factor from a normal individual encoded by VH2 and V kappa II gene
A:Reference number: A49002; MUID:92352481; PMID:1322670
A:Accession: A49002
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-124 <STU>
A:Cross-references: GB:M90808; NID:g185515; PIDN:AAA52989.1; PID:g567176
A:Experimental source: EBV-transformed lymphoblastoid cell line SSH23
A>Note: sequence extracted from NCBI backbone (NCBIN:110261, NCBIP:110262)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-99/Domain: immunoglobulin homology <IMM>

```

	Query Match	40.9%;	Score 551;	DB 2;	Length 124;	
	Best Local Similarity	81.7%;	Pred. No. 6.9e-31;			
	Matches 103;	Conservative 10;	Mismatches 11;	Indels 2;	Gaps 1;	
OY	1 QVTLKESGPTLVKPQTLLTLLCTFSGSFLRTTGEGVGWROBP GKALLEWLLAIYMDDDR	60				
Db	1 QITLKESGPTLVVRPQTGLTLLCTFSGFSLSTSGVGVGWIRQPPGKALLEWLLAIYMNDDR	60				
OY	61 YSPSLKSRLTITKTDSKKQVLLTMNVPADPATYYCTHEQYYYDTSQGYPYFDWGQGT	120				
Db	61 YSPSLKSRLTITKTDSKNQVLLTMNDPVDATYYCAH--WTVDSSGYLLGFDMGQGT	118				
OY	121 LVTVSS 126					
Db	119 LVTVSS 124					

RESULT 4  
S31513  
Ig heavy chain - human  
C;Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C/Accession: S31513  
R/Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A/Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
A/Reference number: S31509  
A/Accession: S31513  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-138 <CHA>  
A/Cross-references: EMBL:X69861; NID:g33084; PIDN:CAA49495.1; PID:g33085  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;30-114/Domain: immunoglobulin homology <IMM>

```

Query Match          39.9%; Score 538.5; DB 2; Length 138;
Best Local Similarity 80.8%; Pred. No. 5.4e-30;
Matches 101; Conservative 7; Mismatches 14; Indels 3; Gaps 1;

QY      1 QVTLKESGPTLVKPTQTLTLTCTFSGFSLRTTGEVGVWRQPPGKALEMLAIYWDDDKR 60
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      16 QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGIRQPPGKLTLEMLAIYWDDDKR 75

QY      61 YSPSLKSRLLITTKDTSKKQVLLTMTNVPADATATYYCTHEQYYYDTSQGPYYFDWGGGT 120
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      76 YSPSLKSRLLITTKDTSQNQVLLTMTNMDPVDIATYYCAHRPGIAVTGGN---FDYWGCGT 132

QY      121 LVTVS 125
      |||||
Db      133 LVTVS 137

```

RESULT 5  
S69339  
Ig heavy chain V region precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C:Accession: S69339, S72664  
R:Khamlich, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; MUID:95262687; PMID:7744049  
A:Accession: S69339  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <KHA>  
A:Cross-references: EMBL:X81695  
R:Khamlich, A.A.  
submitted to the EMBL Data Library, September 1994  
A:Reference number: S72664  
A:Accession: S72664  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140, 'C', 142-374 <KH2>  
A:Cross-references: EMBL:X81695  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

	Query Match	39.7%;	Score 534.5;	DB 2;	Length 374;	
	Best Local Similarity	81.0%;	Pred. No. 2.8e-29;			
	Matches 102;	Conservative	8;	Mismatches 13;	Indels 3;	Gaps 1;
OY	1 QVTLKESGPTLVKPTQTLLTCTFSGFSRLRTGEGVGWVRQPPGKALEWLALITYWDDDKR	60				
	:     :     :     :     :     :     :		:	:   :     :     :     :		
Dd	20 QITLKESGPLVKPQTQLLTCTCFSGFSLSKSGVGWGIRQPPGQALEWLALIFWDDDKR	79				
OY	61 YSPSLKSRLTIKTDSKKQAVLTMNTNVPADATATYYCTHEQQYYYDTSQPYYFDFFWGGGT	120				
	:     :     :     :     :     :		:	:   :     :     :     :		
Dd	80 YSPSLRHLTIKTDSKNQAVLTMNTNVPADATATYYC--GYSVVEGGYGGRFHFWGGGT	136				
OY	121 LVTVSS	126				
Dd	137 LVTVSS	142				











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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 14:49:01 ; Search time 7.1233 Seconds  
(without alignments)  
1849.388 Million cell updates/sec

Title: US-10-072-301-31  
Perfect score: 1348  
Sequence: 1 QVTLKESGPTLVKPTQTTLT.....CQSDYLPPLTFGGGTXVDIK 253

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	485.5	36.0	125	1 HV2D_HUMAN	P01817 homo sapien
2	474.5	35.2	121	1 HV2E_HUMAN	P01818 homo sapien
3	468	34.7	108	1 KV1P_HUMAN	P01608 homo sapien
4	468	34.7	108	1 KV1Y_HUMAN	P80362 homo sapien
5	456	33.8	108	1 KV1B_HUMAN	P01594 homo sapien
6	448	33.2	108	1 KV1Q_HUMAN	P01609 homo sapien
7	442	32.8	108	1 KV1A_HUMAN	P01593 homo sapien
8	435	32.3	108	1 KV1O_HUMAN	P01607 homo sapien
9	435	32.3	108	1 KV1S_HUMAN	P01611 homo sapien
10	435	32.3	120	1 HV2B_HUMAN	P01815 homo sapien
11	425	31.5	108	1 KV1C_HUMAN	P01595 homo sapien
12	425	31.5	108	1 KV1H_HUMAN	P01600 homo sapien
13	423	31.4	108	1 KV1E_HUMAN	P01597 homo sapien
14	423	31.4	108	1 KV1V_HUMAN	P04430 homo sapien
15	423	31.4	129	1 KV1G_HUMAN	P04431 homo sapien
16	418	31.0	108	1 KV1G_HUMAN	P01599 homo sapien
17	418	31.0	108	1 KV1M_HUMAN	P01605 homo sapien
18	415	30.8	108	1 KV1R_HUMAN	P01610 homo sapien
19	413	30.6	108	1 KV1K_HUMAN	P01603 homo sapien
20	411	30.5	147	1 HV2H_HUMAN	P04438 homo sapien
21	408.5	30.3	107	1 KV1D_HUMAN	P01596 homo sapien
22	408.5	30.3	109	1 KV1T_HUMAN	P01612 homo sapien
23	406	30.1	129	1 KV1S_HUMAN	P04432 homo sapien
24	405	30.0	108	1 KV1S_MOUSE	P01652 mus musculu
25	404	30.0	108	1 KV1L_HUMAN	P01604 homo sapien
26	403	29.9	108	1 KV1N_HUMAN	P01606 homo sapien
27	402.5	29.9	119	1 HV2C_HUMAN	P01816 homo sapien
28	401	29.7	108	1 KV5Q_MOUSE	P01650 mus musculu
29	401	29.7	108	1 KV5T_MOUSE	P01653 mus musculu
30	397	29.5	108	1 KV1F_HUMAN	P01598 homo sapien
31	391	29.0	108	1 KV5R_MOUSE	P01651 mus musculu
32	389	28.9	126	1 HV2A_HUMAN	P01814 homo sapien
33	388	28.8	108	1 KV5O_MOUSE	P01648 mus musculu

34	387	28.7	108	1 KV5L_MOUSE	P01645 mus musculu
35	387	28.7	117	1 KV1J_HUMAN	P01602 homo sapien
36	386	28.6	108	1 KV5K_MOUSE	P01644 mus musculu
37	386	28.6	108	1 KV5M_MOUSE	P01646 mus musculu
38	385	28.6	108	1 KV5N_MOUSE	P01647 mus musculu
39	382	28.3	112	1 KV1U_HUMAN	P01613 homo sapien
40	381	28.3	108	1 KV5P_MOUSE	P01649 mus musculu
41	378	28.0	108	1 KV5J_MOUSE	P01643 mus musculu
42	373.5	27.7	144	1 HV43_MOUSE	P01819 mus musculu
43	372	27.6	117	1 KV1I_HUMAN	P01601 homo sapien
44	367	27.2	128	1 KV5E_MOUSE	P01637 mus musculu
45	363.5	27.0	133	1 KV4B_HUMAN	P06313 homo sapien

ALIGNMENTS

RESULT 1									
HV2D_HUMAN	STANDARD;	PRT;	125 AA.						
ID	HV2D_HUMAN								
AC	P01817;								
DT	21-JUL-1986 (Rel. 01, Created)								
DT	21-JUL-1986 (Rel. 01, Last sequence update)								
DT	10-OCT-2003 (Rel. 42, Last annotation update)								
DE	Ig heavy chain V-II region MCE.								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE.								
RX	MEDLINE=81118242; PubMed=6780622;								
RA	Gerber-Jenson B., Kazin A., Kehoe J.M., Scheffel C., Erickson B.W.,								
RA	litman G.W.;								
RT	"Molecular basis for the temperature-dependent insolubility of								
RT	cryoglobulins. X. The amino acid sequence of the heavy chain variable								
RT	region of MCE."								
RL	J. Immunol. 126:1212-1216(1981).								
CC	-I- MISCELLANEOUS: THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM								
CC	CRYOIMMUNOGLOBULIN.								
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.								
DR	PIR; A02092; MHUMC.								
DR	HSSP; P01825; 7FAB.								
DR	GO; GO:0005576; C:extracellular; NAS.								
DR	GO; GO:0003823; F:antigen binding; NAS.								
DR	GO; GO:0006955; P:immune response; NAS.								
DR	InterPro; IPR007110; Ig-like.								
DR	InterPro; IPR003596; Ig_v.								
DR	PIfam; PF00047; Ig; 1.								
DR	SMART; SM00406; IGv; 1.								
DR	PROSITE; PS50835; IG LIKE; 1.								
KW	Immunoglobulin V region; Pyrrolidone carboxylic acid.								
FT	DOMAIN 1 113								
FT	MOD_RES 1 1								
FT	NON_TER 125 125								
SQ	SEQUENCE 125 AA; 13783 MW; 7A1ADP4C40F47BBS CRC64;								
Query Match									
Best Local Similarity 73.8%; Score 485.5; DB 1; Length 125;									
Matches 93; Conservative 11; Mismatches 21; Indels 1; Gaps 1;									
QY	1	QVTLKESGPTLVKPTQTLLTCTFSGFSRLTGTGEGVWVRQPGKALEMLALTYWDDDKR	60						
DB	1	QVTLKESGPTLVKPTETLLTCTFSGFSLSLSTSGVGVMIRQRPKALEMLAFINWDDDKR	60						
QY	61	YSPSLKSRLLTITKDTSKQVVLMTNVDPADTATYCTHEQYVYDTSQGPYFDWGGGT	120						
DB	61	YSPSLKSRLLTITKDTSRNQVVLITTMDPVDSGTFFCAHRPPWRPT-GNLGGFDXWGGGT	119						
QY	121	LVTVSS 126							
DB	120	LVTVSS 125							

```

RESULT 2
HV2E_HUMAN
ID HV2E_HUMAN STANDARD; PRT; 121 AA.
AC P01818;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region HE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70114712; PubMed=5264153;
RA Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.;
RT "Subgroups of amino acid sequences in the variable regions of
RL immunoglobulin heavy chains";
RL Proc. Natl. Acad. Sci. U.S.A. 64:997-1003 (1969).
CC -1- MISCELLANEOUS: THIS GAMMA-1 CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02093; GIHUE.
DR HSSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyroli done carboxylic acid.
FT DOMAIN 1 120 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13483 MW; 88A5082C273753B4 CRC64;

Query Match 35.2%; Score 474.5; DB 1; Length 121;
Best Local Similarity 71.7%; Pred. No. 1e-30;
Matches 91; Conservative 10; Mismatches 19; Indels 7; Gaps 2;

QY 1 QVTLKESGPTLVKPTQTTLTCTFSGSRLRTGEGVGVWRQPGKALEWLA-LIYWDGDK 59
DB 1 QVTLKENGPTLVKPTETTLTCTLSGSLTTDGVAVGWIRQGPGRALWLAWLTYWDGDK 60

QY 60 RYSPSLKSLRTITKDTSKQVLTMTNVDPAATATYCTHEQYVYDTSQPYFDFWGCG 119
DB 61 RYSPSLKSLRTITKDTSKQVLTMTNVDPAATATYCTHEQYVYDTSQPYFDFWGCG 114

QY 120 TLVTVSS 126
DB 115 TKVAVSS 121

RESULT 3
KVLP_HUMAN
ID KVLP_HUMAN STANDARD; PRT; 108 AA.
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
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RT Cum.);";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080 (1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnikol H.U., Hees M., Langer B., Ponstingl H.,
RA Steinmetz-Kayne M., Suter L., Watanabe S.;
RL (in) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RL New York (1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91638; KIHURY.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match 34.7%; Score 468; DB 1; Length 108;
Best Local Similarity 84.1%; Pred. No. 2.8e-30;
Matches 90; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 147 NIQVTSPPSSISASVGDRTVMTCRASODIRKLNLMYQOKPGKAPKVLIDASDLETGIPS 206
DB 1 DIQMTQSPSSISASVGDRTVITCQASQDISIFLNMVQOKPGKAPKLLIYDASKLEAGVPS 60

QY 207 RYSGSGSGTFTLTITSLQPEDIAITYCQOSDYLPITFGGTRVDIK 253
DB 61 RYSGTSGSGTFTFTITSLQPEDIAITYCQQFDNLPITFGGTRVDIK 107

RESULT 4
KVLY_HUMAN
ID KVLY_HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7993911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
RT structural origin of altered domain interactions in immunoglobulin
RT light-chain dimers.";
RL Biochemistry 33:14848-14857 (1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popl R.A., Solomon A.;
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RT "Characterization and preliminary crystallographic data on the VL-  
RT related fragment of the human ki Bence Jones protein Wat.";  
RL J. Mol. Biol. 147:185-193(1981).  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
DR PDB; 1WTL; 01-NOV-94.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT CONFLICT 30 31 TN -> SD (IN REF. 2).  
FT STRAND 4 7  
FT STRAND 10 13  
FT TURN 15 16  
FT STRAND 19 25  
FT TURN 30 31  
FT STRAND 33 38  
FT TURN 40 41  
FT STRAND 45 49  
FT TURN 50 52  
FT STRAND 53 54  
FT TURN 56 57  
FT TURN 60 61  
FT STRAND 62 67  
FT TURN 68 69  
FT STRAND 70 75  
FT HELIX 80 82  
FT STRAND 84 90  
FT STRAND 98 98  
FT STRAND 102 106  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;  
Query Match 34.7%; Score 468; DB 1; length 108;  
Best Local Similarity 84.1%; Pred. No. 2.8e-30;  
Matches 90; Conservative 8; Mismatches 9; Indels 0; Gaps 0;  
QY 147 NIQVTPSSLSASVGDRTVMTCRASQDIRKLNLMYQOKPGKAPKVLITYDASDLFTGIPS 206  
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQDITNVNMFQQRPGQAPKVLITYGASILETGVP 60  
QY 207 RFSGSGSGTDFILTISSLPEDIAITYCQOSDYLPITFGGKTKVDIK 253  
Db 61 RFSGSGSGTDFITTISSLPEDIAITYCQQYDYLPLTFGGGKTKVDIK 107  
RESULT 5  
KV1B\_HUMAN STANDARD; PRT; 108 AA.  
ID KV1B\_HUMAN  
AC P01594;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig kappa chain V-I region AU.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=72189444; PubMed=5028201;

RA Schiechl H., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
RT protein Au).";  
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY.  
RX MEDLINE=77022433; PubMed=1234024;  
RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,  
RA Schwager P., Steigemann W., Schramm H.J.;  
RT "The structure determination of the variable portion of the  
RT Bence-Jones protein Au.";  
RL Biophys. Struct. Mech. 1:139-146(1975).  
CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY  
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V  
CC REGION OF THE KAPPA CHAIN REI.  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
DR PIR; A91653; KIHUAU.  
DR PDB; 1JY5; 30-JAN-02.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11939 MW; E801187EE6F6FB9 CRC64;  
Query Match 33.8%; Score 456; DB 1; length 108;  
Best Local Similarity 81.3%; Pred. No. 2.5e-29;  
Matches 87; Conservative 9; Mismatches 11; Indels 0; Gaps 0;  
QY 147 NIQVTPSSLSASVGDRTVMTCRASQDIRKLNLMYQOKPGKAPKVLITYDASDLFTGIPS 206  
Db 1 DIQMTQSPSSLSASVGDRTVITTCASQDISDYNLMYQOKPGKAPKVLITYDASNLSSGVPS 60  
QY 207 RFSGSGSGTDFILTISSLPEDIAITYCQOSDYLPITFGGKTKVDIK 253  
Db 61 RFSGSGSGAHTFTTISSLPEDIAITYCQQYDYLPLTFGGGKTKVEIK 107  
RESULT 6  
KV1Q\_HUMAN STANDARD; PRT; 108 AA.  
ID KV1Q\_HUMAN  
AC P01609;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Scw.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75059271; PubMed=4435756;  
RA Eulitz M., Hilschmann N.;  
RT "The primary structure of a human immunoglobulin L-chain of  
RT kappa-type (Bence-Jones protein Scw.), II: The chymotryptic peptides  
RT and the complete amino acid sequence.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).

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CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01875; KIHUSW.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 FRAMEWORK-2.
FT DOMAIN 35 49 FRAMEWORK-3.
FT DOMAIN 50 56 FRAMEWORK-4.
FT DOMAIN 57 88 FRAMEWORK-5.
FT DOMAIN 89 97 FRAMEWORK-6.
FT DISULFID 98 107 FRAMEWORK-7.
FT NON TER 108 108 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11764 MW; 32CECDDDF9644414 CRC64;

Query Match
Best Local Similarity 78.5%; Score 448; DB 1; Length 108;
Matches 84; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 147 NIQVTSPLSASVGDRTMTGRASQDIRKLNWYQOKPKAPKVLIDASDLTGIPS 206
Db 1 DIQMTQSPSSLSASVGDRTVITTCQASQDIRKLNWYDQKPKAPRLIYGASTLETGVP 60
QY 207 RFGSGSGTDFILTISSLOPEDIAITYCCQSDYLPLTRGGTKVDIK 253
Db 61 RFGSGSGTDFILTISSLOPEDIAITYCCQSDYDNLPTFGQGTREVK 107

RESULT 7
KVIA_HUMAN
ID KVIA_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region AG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;
RA Tiltant K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01861; KIHUAG.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 FRAMEWORK-2.
FT DOMAIN 35 49 FRAMEWORK-3.
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FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 108 108
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match
Best Local Similarity 79.4%; Score 442; DB 1; Length 108;
Matches 85; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 147 NIQVTSPLSASVGDRTMTGRASQDIRKLNWYQOKPKAPKVLIDASDLTGIPS 206
Db 1 DIQMTQSPSSLSASVGDRTVITTCQASQDIRKLNWYDQKPKAPRLIYGASTLETGVP 60
QY 207 RFGSGSGTDFILTISSLOPEDIAITYCCQSDYLPLTRGGTKVDIK 253
Db 61 RFGSGSGTDFILTISSLOPEDIAITYCCQSDYDNLPTFGQGTREVK 107

RESULT 8
KVIO_HUMAN
ID KVIO_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region Rel.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Bpp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91663; KIHURE.
DR PDB; IREI; 17-FEB-84.
DR PDB; 1AR2; 12-NOV-97.
DR PDB; 1BMW; 29-DEC-99.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
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QY	121	LVTVSS	126
Db	115	PVTVSS	120

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RESULT 11
KVLC_HUMAN
ID          KVLC_HUMAN          STANDARD;      PRT;      108 AA.
AC          P01595;
DT          21-JUL-1986 (Rel. 01, Created)
DT          21-JUL-1986 (Rel. 01, Last sequence update)
DT          10-OCT-2003 (Rel. 42, Last annotation update)
DE          Ig kappa chain V-I region B1.
OS          Homo sapiens (Human).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX          NCBI_TaxID=9606;
RN          [1]

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RX	MEDLINE=73029807; PubMed=4563064;
RA	Braun M., Leibold W., Barnikol H.U., Hilschmann N.;
RT	"Principle of antibody structure. The primary structure of a
RT	monoclonal kappa I-type immunoglobulin V-chain (Bence Jones protein
RT	Bl). 3. The complete amino acid sequence and the genetic
RT	significance of the variability principles for the mechanism of
RT	antibody formation.";
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:1284-1306(1972).
CC	-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER
CC	-I- MISCELLANEOUS: This is a Bence-Jones protein.
DR	PIR; A01863; KIHUBI.
DR	HSSP; P01607; 1REI.
DR	GO; GO:0005576; C:extracellular; NAS.
DR	GO; GO:0003823; F:antigen binding; NAS.
DR	GO; GO:0006955; P:immune response; NAS.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_V.
DR	Pfam; PF00047; Ig_1.
DR	SMART; SMO0406; IGV; 1.
KM	PROSITE; PS50835; IG_LIKE; 1.
DR	Immunoglobulin V region; Bence-Jones protein.
FT	DOMAIN 1 23 FRAMEWORK-1.
FT	DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN 35 49 FRAMEWORK-2.
FT	DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN 57 88 FRAMEWORK-3.
FT	DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN 98 107 FRAMEWORK-4.
FT	DISULFID 23 88 BY SIMILARITY.
FT	NON TER 108 108
SQ	SEQUENCE 108 AA; 12026 MW; 7A83983986A431E7 CRC64;

Query Match	31.5%	Score 425;	DB 1;	Length 108;
Best Local Similarity	76.6%	Pred. No. 6.7e-27;		
Matches 82; Conservative	10;	Mismatches 15;	Indels 0;	Gaps 0;

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QY      147 NIQVTSPPSISASVGDRVTMTCRASODIRKLNLMWYOQPKGAPKVLITYDASDLETGPS 206
       :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||::~|||
Db      1 DIQMTOSSPSPISASVGDSVTITTCOASQDIRNSLIWYOQPKGAPKFLITYDAENLELGYPS 60
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QY      207 RFGSGSGTDFILTTSSIQPEDATYYCQGSDDLPLTFGGGKVDIK 253
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Db      61 RFRGSGSGTDFALSSIQPEDATYYCQGYNLPLYTFGGGKYLEIK 107

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RESULT 12		
KV1H HUMAN		
ID	KV1H HUMAN	STANDARD; PRT; 108 AA.
AC	P01600;	
DT	21-JUL-1986 (Rel. 01, Created)	
DT	21-JUL-1986 (Rel. 01, Last sequence update)	
DT	15-JUL-1999 (Rel. 38, Last annotation update)	
DE	Ig kappa chain V-I region Hau.	

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;

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RP  SEQUENCE.
RX  MEDLINE=71032830; PubMed=4097974;
RA  Watanabe S., Hilschmann N.;
RT  "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT  chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT  subgroups.";
RL  Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC  -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC  -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR  PIR; A01868; KIHUHU.
DR  HSSP; P80362; 1WTL.
DR  GO; GO:0005576; C:extracellular; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110, Ig-like.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig_1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG LIKE; 1.
KW  Immunoglobulin V region; Bence-Jones protein.
FT  DOMAIN 1 23 FRAMEWORK-1.
FT  DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN 35 49 FRAMEWORK-2.
FT  DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN 57 88 FRAMEWORK-3.
FT  DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT  DOMAIN 98 107 FRAMEWORK-4.
FT  DISULFID 23 88 BY SIMILARITY.
FT  NON TER 108 108
SQ  SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

```

Query Match	31.5%	Score 425;	DB 1;	length 108;
Best Local Similarity	76.6%;	Pred. No. 6.7e-27;		
Matches 82;	Conservative 11;	Mismatches 14;	Indels 0;	Gaps 0;

```
QY      147 NIQTQSSSLASVGDRTVTMTCRASQDIRKNLWNYYQQPKAPKVLITYASDLETGIPS 206
       :|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||
Db      1 DIQMGTSSSLASVGDRTVITTCRASQGISLSYLWYQQPKAPQVLITYAASSLPSCVPS 60
```

```
QY      207  RFSGSGSGTDFILTISSLPEDIAITYCCQSDYLPITFGGKVDIK 253
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      61  RFSGSGSGTDFILTISSLPEDFATYYCCQNYITPTSFQGRVEIK 107
```

```

RESULT 13
KVLE_HUMAN
ID_KVLE_HUMAN      STANDARD;      PRT;      108 AA.
AC      P01597;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-I region DBE.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=72053133; PubMed=5124396;
RA      Milstein C.P., Deverson E.V.;
RT      "The amino acid sequence of a human kappa light chain.";
RL      Biochem. J. 123:945-958(1971).
CC      -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR      PIR; A01865; K1HUDE.
DR      HSSP; P01607; 1REI.
DR      GO; GO:0005576; C:extracellular; NAS.
DR      GO; GO:0003823; F:antigen binding; NAS.
DR      GO; GO:0006955; P:immune response; NAS.

```



```
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match
Best Local Similarity 31.4%; Score 423; DB 1; Length 108;
Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 147 NIQVTSPLSASVGDRTVMTGRASQDIRKNLWYQOKPGKAPKVLIDASDLETGIPS 206
DB 1 BIZMTQSPSSLSASVGDRTVITCRAGQSVNXYLWYQOKPGKAPKVLIFAASSLKGVP 60

QY 207 RESGSGGTDFILTISSLOPEDIAITYCCQSDYLPITFGGTRVDI 252
DB 61 RFGSGSGTDFLTITISGLPEDPATYYCQQSYTPTFTGPGTKVEM 106

RESULT 14
KV1W_HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwalet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; KIHUBN.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match
Best Local Similarity 31.4%; Score 423; DB 1; Length 108;
Matches 81; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
```

```
QY 147 NIQVTSPLSASVGDRTVMTGRASQDIRKNLWYQOKPGKAPKVLIDASDLETGIPS 206
DB 1 DIQLTQSPSSLSASVGDRTVITCRASQSVNYVWAFQOKPGKAPKSLIYDASTLQSGVPS 60

QY 207 RESGSGGTDFILTISSLOPEDIAITYCCQSDYLPITFGGTRVDI 253
DB 61 NFGSGSGTDFILTISSLOPEDPATYYCQQXNSYPTFTGQTKVQIK 107

RESULT 15
KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G., Combriato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL Nucleic Acids Res. 12:6995-7006(1984).

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CC -----
DR EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; KIHUWK.
DR HSSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 FRAMEWORK-4.
FT DOMAIN 120 129 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match
Best Local Similarity 31.4%; Score 423; DB 1; Length 129;
Matches 83; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 143 GGSNIIQVTSPLSASVGDRTVMTGRASQDIRKNLWYQOKPGKAPKVLIDASDLET 202
DB 19 GARCDIQTQSPSSLSASVGDRTVITCRASQISINYLWYQOKPGKAPKLIYAASSLOS 78

QY 203 GIPSRFSGSGGTDFILTISSLOPEDIAITYCCQSDYLPITFGGTRVDI 253
DB 19 GIPSRFSGSGGTDFILTISSLOPEDPATYYCQQSYTPTFTGPGTKVEM 253
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Mon May 17 11:03:45 2004

us-10-072-301-31.rsp

Page 8

Db 79 GVTSRFSGSGGTDFTLTITSSIQPEDSATYCCQGSYSLITEGQTRLEIK 129

Search completed: May 13, 2004, 15:02:06  
Job time : 7.1233 secs

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Db 40 QVKLQSGGGLVKEPGSLKLSCAASGSDF--SRYWMSWVRQAPGKLEWIGEINPDSSTI 97

QY 60 RYSPSLKSRLLTTKDTSKQVLTMTNVPADTATYCTHEQYVYDTSQPYFDFWGG 119

Db 98 NYTPSLKDKFLISRDNAKNTLYLQMSKVSSEDALYYCARASYGSHA-----YWGQG 150

QY 120 TLVTVSSGGGGGGGGGGGGGGGSGGSGNIOVTQSPSSLASVGDRTVMTCRASQDIRKNL 179

Db 151 TTVTVS-----SGGGSGGGGGGGGGGSDIELTQSPSSLASVGETVITTCRASGNIHNYL 205

QY 180 NWYQOKPGKAPKVLIVDASDLETGIPSRFSGSGGTDIFILTISSLOPEDIAATYCCQSDY 239

Db 206 AMYQOKQKSPQLLVYNAKTLADGVPSPRFSGSGGTQYSLKINSLQPEDFGSYCCQHFMT 265

QY 240 LPLTFGGGTKVDIK 253

Db 266 TPYTFGGGTKLEIK 279

RESULT 2

Q921A6 PRELIMINARY; PRT; 241 AA.

AC Q921A6; 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Anti-CEA 79 single chain Fv fragment (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98170165; PubMed=9509426;

RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D., Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;

RT "Cloning and characterization of cDNAs encoding VH and VL of a monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and generation of a single-chain Fv molecule (scFv).";

RL Mol. Cells 7:816-819(1997).

DR EMBL; U88067; AAB48044.1; -

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00406; IGV; 2.

DR PROSITE; PS50835; IG\_LIKE; 2.

FT NON\_TER 1

FT NON\_TER 241

SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 48.4%; Score 652; DB 11; Length 241;

Best Local Similarity 51.2%; Pred. No. 3.6e-48;

Matches 132; Conservative 41; Mismatches 61; Indels 24; Gaps 7;

QY 1 QVTLKESGPTLVKPTQTTLTCTFSGFSRLTTEGVGVWRQPPGKALEWLLI-YWDDK 59

Db 1 QVKLQSGSELVPRPGASVYKLSCKASGYFTT-YMHWKQRHGGGLEWIGNIYPGSGIT 58

QY 60 RYSPSLKSRLLTTKDTSKQVLTMTNVPADTATYCTHEQYVYDTSQPYFDFWGG 119

Db 59 TYADDFKGRFAFSLETSASTAYLQINLNKEDTATYFCARDLL-----RYFDWGG 111

QY 120 TLVTVSSGGGGGGGGGGGGGSGGSGNIOVTQSPSSLASVGDRTVMTCRASQDIRKNL 179

Db 112 TTVTVS-----SGGGSGGGGGGGGGGSDIELTQSPSSLASVGETVITTCRASQDINXYI 166

QY 180 NWYQOKPGKAPK---VLIVDASDLETGIPSRFSGSGGTDIFILTISSLOPEDIAATYCC 235

Db 167 AMYQHKPKGPRSAHTLHIY----IQGIPSRFSGSGGGRDYFSFISINLEPEDIAATYCTL 222

QY 236 QSDYLPPLTFGGGTKVDIK 253

Db 223 HYDNLH-TFGGGTKLEIK 239

RESULT 3

Q7QM2 PRELIMINARY; PRT; 243 AA.

AC Q7QM2; 01-OCT-2003 (Tremblrel. 25, Created)

DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE scFv 6H8 protein (Fragment).

GN scFv 6H8.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Balb/C;

RA Peter J.C., Eftekhari P., Billiald P., Wallukat G.;

RT "scFv single chain antibody variable fragment as inverse agonist for the beta-2 adrenergic receptor.";

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ574851; CAE00495.1; -

FT NON\_TER 1

SQ SEQUENCE 243 AA; 25976 MW; BEFF64D2DCF4F76 CRC64;

Query Match 46.1%; Score 621; DB 11; Length 243;

Best Local Similarity 50.8%; Pred. No. 1.7e-45;

Matches 129; Conservative 40; Mismatches 67; Indels 18; Gaps 6;

QY 1 QVTLKESGPTLVKPTQTTLTCTFSGFSRLTTEGVGVWRQPPGKALEWLLIY-WDDK 59

Db 1 QVKLQSGSELVPRPGASVYKLSCKASGYFTT-YMHWKQRHGGGLEWIGNIYPGSGIT 58

QY 60 RYSPSLKSRLLTTKDTSKQVLTMTNVPADTATYCTHEQYVYDTSQPYFDFWGG 119

Db 59 NYDEKFNKGIIVDTSSSTAYMHLSSLASEDSAYYCAR-----GGRG-LDVWGAG 109

QY 120 TLVTVSSGGGGGGGGGGGGGSGGSGNIOVTQSPSSLASVGDRTVMTCRASQDIRKNL 179

Db 110 TTVTVS-----SGGGSGGGGGGGGGGSDIQMTQSSSFVSLSGDRVITTCRASQDINYL 164

QY 180 NWYQOKPGKAPKVLIVDASDLETGIPSRFSGSGGTDIFILTISSLOPEDIAATYCCQSDY 239

Db 165 AMYQOKPGNAPRLISGATSLETGVPSPRFSGSGGKDYLTLSITSLQTEVATYCCQY-W 223

QY 240 LPLTFGGGTKVDIK 253

Db 224 STRTFGGGTKLEIK 237

RESULT 4

Q9UL96 PRELIMINARY; PRT; 121 AA.

AC Q9UL96; 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035018; AAD56254.1; -.



DR	HSSP; P01825; 7FAB.		
DR	InterPro; IPR007110; IG_1like.		
DR	InterPro; IPR003596; IG_v.		
DR	Pfam; PF00047; IG; 1.		
DR	SMART; SM00406; IGv; 1.		
DR	PROSITE; PS50835; IG_Like; 1.		
FT	NON_TER	1	
FT	NON_TER	121	
SQ	SEQUENCE	121 AA; 13695 MW;	D582D450596BDD35 CRC64;

Query Match	40.8%	Score 549.5;	DB 4;	Length 121;
Best Local Similarity	82.5%;	Pred. No. 1e-39;		
Matches 104; Conservative	6;	Mismatches 11;	Indels 5;	Gaps 1;

```

Oy      1 QVTLKESGPIIVKPTQTLTLTCTFSGFSRLTTEGGVGVWRQPPGKALEWLAIIYWD DDKR 60
      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 QITLKESGPIIVKPTQTLTLTCTFSGFSRLTSGMDVGWIRQPPGKALEWLAIIYWD DDKR 60

```

```
OY      61 YSPSLKRLTITKDTSKKQVLTMVNDPADTAIYYCTHEQYYYDTSQQPYYPFWGOGT   120
        |||||         |    :|||       |||          |||::|||
DB      61 YSPSLKRLTITKDTSKNQVDLTMTFMDEPDATAIYYCAHRK-----SGDGYYFDYWGGGT   115
```

QY	121	LVTVSS	126
Db	116	LVTVSS	121

## RESULT 5

ID	Q925S1	PRELIMINARY;	PRT;	218 AA.
AC	Q925S1;			
DT	01-DEC-2001	(TREMBLrel. 19,	Created)	
DT	01-DEC-2001	(TREMBLrel. 19,	Last sequence update)	
DT	01-OCT-2003	(TREMBLrel. 25,	Last annotation update)	
DE	MRP5 (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c;			
RX	PubMed=11819679;			
RA	Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,			
RA	Su C.;			
RT	"Mechanism of exogenous nucleic acids and their precursors improving			
RT	the repair of intestinal epithelium after irradiation in mice.";			
RL	World J. Gastroenterol. 6:709-717(2000).			
RN	[2]			

RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Cui D., Zeng G., Yan X., Li X., Su C.;  
RT "Cloning of mouse genes related to repairing of intestinal epithelium  
RT of the irradiated mice by treatment with the intestinal RNA of mice of  
RT the same strain.";  
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80 (2001).  
DR EMBL; AF240168; AAK3733.1; -.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig\_2.  
DR SMART; SM00406; IGV\_1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
FT NON TER 218 218  
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match	36.8%;	Score 496.5;	DB 11;	Length 218;
Best Local Similarity	44.8%;	Pred. No. 7.8e-35;		
Matches 103; Conservative	42;	Mismatches 66;	Indels 19;	Gaps 6;

Oy 1 QVTLKESGPTLVKPTQTLLTCTFSGSFLRTTGEGVGWVRQPPGKALEWLALTYDDDK-59  
||::||| ||:::||: | :||: ||| :::  
Db 3 QVTLQGSGPELKKPGETVARISCKASGYTFTTA--GMQVQVKMPFGKLKWIGVINTHSGVP 60

```

QY      60 RYSPSLKSRLLTTTKDTSKQVLLTMNVNDEADATATYYCTHEQYYVDTSGQPYFDFWGG 119
      ::::: ::::: ::::: ::::: :::::
Db      61 KYAEFFKGRPAFSLETSASTAYLIQISLNKNEDEATATYFCM--RWDYDGG-----FAYWGG 113
      ::::: ::::: ::::: ::::: :::::
QY      120 TLVTVSSGGSGSGSGSGSGSGSGSNIQVTSPSLSASVGDVYTMTCRASQDIR--- 176
      ||||| ||||| ||||| ||||| ::::: ::::: ::::: ::::: :::::
Db      114 TTVTVS-----SGGGSGSGSGSGSGSDIVLTQSPASLAVSLGQRATISCSASESDVNIG 168
      ||||| ||||| ||||| ||||| ::::: ::::: ::::: ::::: :::::
QY      177 -KNLWYQQKPKGAKPKVLIVDASDLETGIPSRFSGSGSGTDFILTISSLQ 225
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db      169 ISFMNWFQQKPGQPPKLLIYASKGSGVPAGLLASGSGTDFSLNIYPM 218

```

## RESULT 6

ID	Q811U5	PRELIMINARY;	PRT;	118 AA.
AC	Q811U5;			
DT	01-JUN-2003 (TREMBLrel. 24, Created)			
DT	01-JUN-2003 (TREMBLrel. 24, last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, last annotation update)			
DE	Anti-human Fc gamma receptor III 3G8 gamma heavy chain variable region (Fragment).			
DE	Mus musculus (Mouse).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			

RP SEQ

RA	Bruenke J., Valerius T., Repp R., Fey G.H.;	
RL	Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AY173025; AAC18227.1; -	
DR	GO; GO:0004872; F:receptor activity; IEA.	
DR	InterPro; IPR003599; Ig.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003596; Ig_v.	
DR	pfam; PF00047; Ig; 1.	
DR	SMART; SM00409; IG; 1.	
DR	SMART; SM00406; IGV; 1.	
DR	PROSITE; PS50835; IG_LIKE; 1.	
KW	Receptor.	
FT	NON_TER	1
FT	NON_TER	118
SO	SEQUENCE	118 AA; 12979 MW; F57JB07033742E99 CRC64;

Query Match	33.4%;	Score 450;	DB 11;	Length 118;
Best Local Similarity	66.7%;	Pred. No. 3.6e-31;		
Matches	84;	Conservative	17;	Mismatches 17;
		Indels	8;	Gaps 1;

QY	1 QVTLKESGPTLVKPTQTLTJLCTFSGSFLRTTGEVGWVRÖPPGKALEMNLALTYWDDDKR	60
	: ::       :       :       :       :	
Db	1 QVTLKESGPILÖPSÖTLSTLCFSFGSFLRTSGMGVGRÖPPSGKLEMLHIWDDDKR	60
QY	61 YSPSLKSRLTIITKDITSKKÖVVLMTNVPADATATYYCTHEÖYYYDTSÖOPYFDFWGÖGT	120
	: : : :   :   :   :   :   :   :   :   :   :   :   :	
Db	61 YNPALKSRLLTISKDTSSNQVFELKIASVDATATATYYCAÖI-----NPAMFAWMGÖGT	112
QY	121 LVTVSS	126
	:	
Db	113 LVTVSA	118

## RESULT 7

ID	Q96SA9	PRELIMINARY;	PRT;	107 AA.
AC	Q96SA9;			
DT	01-DEC-2001 (TREMBlrel. 19, Created)			
DT	01-DEC-2001 (TREMBlrel. 19, last sequence update)			
DT	01-OCT-2003 (TREMBlrel. 25, last annotation update)			
DE	Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain variable region (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98375893; PubMed=9712075;  
RA Adderson E.B., Shikman A.R., Ward K.E., Cunningham M.W.;  
RT "Molecular analysis of polyclonal antibodies from  
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin  
RT antibody V region genes";  
RL J. Immunol. 161:2020-2031(1998).  
DR EMBL; U96396; AAB68785.1; -.  
DR PIR; B49047; B49047.  
DR PIR; S34083; S34083.  
DR PIR; S34086; S34086.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 107  
SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;

Query Match 33.3%; Score 448.5; DB 4; Length 107;  
Best Local Similarity 82.2%; Pred. No. 4.3e-31;  
Matches 88; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY 147 NIQVQSPSSLSASVGDRTVMTCRASQDIRKLNLMWYQOKPGKAPKVLIDASDLFTGIPS 206  
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQOKPGKAPKLLIYAASSLSQGVPS 60  
QY 207 RFSGSGSGTDFILTISSLOPEDIAITYCCQSDYLPITFGGKVDIK 253  
DB 61 RFSGSGSGTDFILTISSLOPEDFATYYCQOS-YSTLTFGGKVEIK 106

RESULT 8  
Q9UL77 PRELIMINARY; PRT; 108 AA.  
AC Q9UL77;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035037; AAD56273.1; -.  
DR PIR; B49047; B49047.  
DR PIR; S34083; S34083.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 108  
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 31.8%; Score 429; DB 4; Length 108;  
Best Local Similarity 78.5%; Pred. No. 2.1e-29;  
Matches 84; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 147 NIQVQSPSSLSASVGDRTVMTCRASQDIRKLNLMWYQOKPGKAPKVLIDASDLFTGIPS 206  
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQOKPGKAPKLLIYAASSLSQGVPS 60  
QY 207 RFSGSGSGTDFILTISSLOPEDIAITYCCQSDYLPITFGGKVDIK 253  
DB 61 RFSGSGSGTDFILTISSLOPEDFATYYCQOSYSTSWTFEGKVEIK 107

RESULT 9  
Q9UL81 PRELIMINARY; PRT; 107 AA.  
AC Q9UL81;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035033; AAD56269.1; -.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 107  
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 31.5%; Score 424.5; DB 4; Length 107;  
Best Local Similarity 78.5%; Pred. No. 5e-29;  
Matches 84; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 147 NIQVQSPSSLSASVGDRTVMTCRASQDIRKLNLMWYQOKPGKAPKVLIDASDLFTGIPS 206  
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQOKPGKAPKLLIYAASSLSQGVPS 60  
QY 207 RFSGSGSGTDFILTISSLOPEDIAITYCCQSDYLPITFGGKVDIK 253  
DB 61 RFSGSGSGTDFILTISSLOPEDFATYYCQOS-YSAITFGPGTKVDIR 106

RESULT 10  
Q96PF6 PRELIMINARY; PRT; 116 AA.  
AC Q96PF6;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Kappa 1 light chain variable region (Fragment).  
DE SDNK1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21361171; PubMed=11468171;  
RA Comenzo R.L., Zhang Y., Martinez C., Oseman K., Herrera G.A.;  
RT "The tropism of organ involvement in primary systemic amyloidosis:





